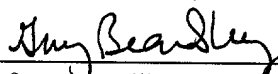


PATENT
ATTORNEY DOCKET NO. 06132/047002

Certificate of Mailing	
Date of Deposit: <u>June 15, 2001</u>	Label Number: <u>EL509219211US</u>
I hereby certify under 37 C.F.R. § 1.8(a) that this correspondence is being deposited with the United States Postal Service as Express Mail Post Office to Addressee with sufficient postage on the date indicated above and is addressed to: BOX PATENT APPLICATION, Assistant Commissioner for Patents, Washington, D.C. 20231.	
<u>Guy Beardsley</u> Printed name of person mailing correspondence	 Signature of person mailing correspondence

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Harold Kleanthous et al.	Art Unit:	Not Yet Assigned
Serial No.:	Not Yet Assigned	Examiner:	Not Yet Assigned
Filed:	June 15, 2001	Customer No.:	21559
Title:	Identification of Polynucleotides Encoding Novel Helicobacter Polypeptides in the Helicobacter Genome		

Assistant Commissioner For Patents
Washington, D.C. 20231

STATEMENT UNDER 37 C.F.R. § 1.821

As part of the patent application filed herewith, enclosed is a sequence listing in accordance with the requirements of 37 C.F.R. §§ 1.821 through 1.825 and consisting of 883 pages.

As required by 37 C.F.R. § 1.821(c), the sequence listing appears as a separate part of the application and is found after the Combined Declaration and Power of Attorney. Each sequence in the application appears separately in the sequence listing. And each sequence in the sequence listing is assigned a separate sequence identifier.

As required by 37 C.F.R. § 1.821(d), the sequence identifiers are used throughout the application description and claims to refer to their respective sequences.

As required by 37 C.F.R. § 1.821(e), enclosed is a diskette containing a copy of the sequence listing in computer readable form.

As required by 37 C.F.R. § 1.821(f), I hereby state that the contents of the computer readable form are the same as the contents of the paper copy.

As required by 37 C.F.R. § 1.821(g), I hereby state that this submission contains no new matter.

If there are any charges, or any credits, please apply them to Deposit Account No. 03-2095.

Respectfully submitted,

Date: June 15, 2001

Susan M. Michaud
Susan M. Michaud, Ph.D.
Reg. No. 42,885

Clark & Elbing LLP
176 Federal Street
Boston, MA 02110
Telephone: 617-428-0200
Facsimile: 617-428-7045
F:\06132\06132.047002 Sequence Statement.wpd



21559

PATENT TRADEMARK OFFICE

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Kleanthous, Harold
Al-Garawi, Amal
Miller, Charles
Tomb, Jean Francois
Oomen, Raymond P.
- (ii) TITLE OF THE INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES ENCODING
NOVEL HELICOBACTER POLYPEPTIDES IN THE HELICOBACTER GENOME
- (iii) NUMBER OF SEQUENCES: 638
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Clark & Elbing LLP
(B) STREET: 176 Federal Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Clark, Paul T.
(B) REGISTRATION NUMBER: 30,162
(C) REFERENCE/DOCKET NUMBER: 06132/047001
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617-428-0200
(B) TELEFAX: 617-428-7045
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1613 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 64...1551

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TAAGAAAAAC	CGCTAGAGTG	CAATACAATT	CTTGAAAGAT	ATGAAATTAA	AAAAGGAGAC	60
TTT	ATG	TTA	AAA	ATC	AAA	108
Met	Leu	Lys	Ile	Lys	Leu	
1			5		10	15
GCT	GAA	TGC	AGT	TTA	GTT	156
Ala	Glu	Cys	Ser	Leu	Val	
			20		25	30
TGG	GTC	AAA	AAT	AAA	GAG	204
Trp	Val	Lys	Asn	Lys	Glu	
		35			40	45
GGC	GTA	TTT	TTA	GAC	CAA	252
Gly	Val	Phe	Leu	Asp	Gln	
		50			55	60
GAA	GAT	GAT	GTG	CAT	TTA	300
Glu	Asp	Asp	Val	His	Leu	
		65			70	75
ACC	CTT	AAA	AAA	CTC	GCT	348
Thr	Leu	Lys	Lys	Leu	Ala	
				85		90
TGT	GGT	GCA	CAT	TCT	AAA	396
Cys	Gly	Ala	His	Ser	Lys	
			100			105
CTG	TTT	TTG	GGC	TTG	AAA	444
Leu	Phe	Leu	Gly	Leu	Lys	
		115			120	125
TCC	AAC	AAA	AAA	GAA	AGC	492
Ser	Asn	Lys	Lys	Glu	Ser	
		130			135	140
TTG	CAC	AAA	CCT	TGC	GAA	540
Leu	His	Lys	Pro	Cys	Glu	
		145			150	155
GCT	AAA	GAA	GCG	TTA	AAA	588
Ala	Lys	Glu	Ala	Leu	Lys	
		160			165	170
ATC	GTT	AAA	GAT	CTA	GTC	636
Ile	Val	Lys	Asp	Leu	Val	
				180		185

TAT Tyr	ATG Met	GCT Ala	GAA Glu 195	GTG Val	GCG Ala	CAA Gln	AAA Lys	GTG Val 200	GCT Ala	AAA Lys	GAA Glu	AAC Asn	CAT His 205	TTA Leu	GAA Glu	684
ATC Ile	CAT His	GTT Val 210	CAT His	GAT Asp	GAA Glu	AAA Lys	TTT Phe 215	TTA Leu	GAA Glu	GAA Glu	AAG Lys	AAA Lys 220	ATG Met	AAC Asn	GCC Ala	732
TTT Phe 225	TTA Leu	GCG Ala	GTC Val	AAT Asn	AAA Lys	GCC Ala 230	TCT Ser	CTT Leu	AGC Ser	GTC Val	AAT Asn 235	CCT Pro	CCT Pro	CGC Arg	TTG Leu	780
ATC Ile 240	CAT His	TTA Leu	GTC Val	TAT Tyr 245	AAG Lys	CCT Pro	AAA Lys	AAA Lys	GCG Ala	AAG Lys 250	AAA Lys	AAA Lys	ATC Ile	GCT Ala	TTA Leu 255	828
GTG Val	GGT Gly	AAG Lys	GGC Gly	TTG Leu 260	ACT Thr	TAT Tyr	GAT Asp	TGT Cys	GGG Gly 265	GGT Gly	TTG Leu	AGC Ser	TTG Leu 270	AAA Lys	CCG Pro	876
GCC Ala	GAT Asp	TAC Tyr 275	ATG Met	GTT Val	ACT Thr	ATG Met	AAA Lys	GCG Ala 280	GAT Asp	AAA Lys	GGC Gly	GGT Gly	GGC Gly 285	TCT Ser	GCG Ala	924
GTG Val	ATT Ile	GGG Gly 290	CTT Leu	TTA Leu	AAC Asn	GCA Ala	TTA Leu 295	GCC Ala	AAA Lys	CTA Leu	GGC Gly	GTG Val 300	GAG Glu	GCT Ala	GAA Glu	972
GTG Val	CAT His 305	GGC Gly	ATT Ile	ATT Ile	GGG Gly	GCT Ala 310	ACA Thr	GAA Glu	AAC Asn	ATG Met	ATA Ile 315	GGC Gly	CCA Pro	GCC Ala	GCT Ala	1020
TAT Tyr 320	AAA Lys	CCA Pro	GAT Asp	GAT Asp	ATT Ile 325	TTG Leu	ATC Ile	TCC Ser	AAA Lys	GAA Glu 330	GGC Gly	AAG Lys	AGC Ser	ATA Ile	GAG Glu 335	1068
GTC Val	CGT Arg	AAT Asn	ACC Thr 340	GAC Asp	GCT Ala	GAG Glu	GGG Gly	CGT Arg	TTG Leu 345	GTT Val	TTA Leu	GCG Ala	GAT Asp	TGT Cys 350	TTG Leu	1116
AGC Ser	TAC Tyr	GCT Ala 355	CAA Gln	GAT Asp	TTA Leu	AAC Asn	CCT Pro	GAT Asp 360	GTG Val	ATC Ile	GTG Val	GAT Asp	TTT Phe 365	GCG Ala	ACC Thr	1164
CTT Leu	ACT Thr	GGG Gly 370	GCA Ala	TGC Cys	GTT Val	GTA Val	GGC Gly 375	TTA Leu	GGC Gly	GAA Glu	TTC Phe	ACT Thr 380	TCA Ser	GCG Ala	ATC Ile	1212
ATG Met	GGG Gly 385	CAT His	AAT Asn	GAA Glu	GAG Glu	TTA Leu 390	AAA Lys	AAC Asn	CTC Leu	TTT Phe	GAA Glu 395	ACT Thr	TCA Ser	GGG Gly	TTA Leu	1260
GAA Glu 400	TCC Ser	GGC Gly	GAA Glu	TTA Leu	TTA Leu 405	GCC Ala	AAA Lys	CTC Leu	CCC Pro	TTT Phe 410	AAC Asn	CGC Arg	CAT His	TTA Leu	AAG Lys 415	1308
AAA Lys	TTG Leu	ATT Ile	GAA Glu	TCT Ser	AAA Lys	ATC Ile	GCT Ala	GAT Asp	GTG Val	TGC Cys	AAT Asn	ATT Ile	TCT Ser	TCT Ser	TCA Ser	1356

	420	425	430	
CGC TAT GGC GGT GCG ATC ACA GCG GGC TTG TTT TTA AAT GAA TTT ATT				1404
Arg Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe Leu Asn Glu Phe Ile				
	435	440	445	
AGA GAT GAG TTT AAG GAT AAG TGG CTA CAC ATT GAC ATT GCA GGC CCT				1452
Arg Asp Glu Phe Lys Asp Lys Trp Leu His Ile Asp Ile Ala Gly Pro				
	450	455	460	
GCT TAT GTG GAA AAA GAA TGG GAT GTG AAT AGC TTT GGA GCG AGT GGG				1500
Ala Tyr Val Glu Lys Glu Trp Asp Val Asn Ser Phe Gly Ala Ser Gly				
	465	470	475	
GCT GGC GTG AGA GCT TGC ACA GCT TTT GTG GAA GAG CTT TTG AAA AAG				1548
Ala Gly Val Arg Ala Cys Thr Ala Phe Val Glu Glu Leu Leu Lys Lys				
	480	485	490	495
GCT TGAAATGGGC TTGTCTGTAG GCATTGTGGG TTTGCCTAAT GTGGGCAAAT CCAGCA				1607
Ala				
CCTTTA				1613

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Leu	Lys	Ile	Lys	Leu	Glu	Lys	Thr	Thr	Phe	Glu	Asn	Ala	Lys	Ala
1				5					10					15	
Glu	Cys	Ser	Leu	Val	Phe	Ile	Ile	Asn	Lys	Asp	Phe	Ser	His	Ala	Trp
			20					25					30		
Val	Lys	Asn	Lys	Glu	Leu	Leu	Glu	Thr	Phe	Lys	Tyr	Glu	Gly	Glu	Gly
			35				40					45			
Val	Phe	Leu	Asp	Gln	Glu	Asn	Lys	Ile	Leu	Tyr	Ala	Gly	Val	Lys	Glu
	50					55					60				
Asp	Asp	Val	His	Leu	Leu	Arg	Glu	Ser	Ala	Cys	Leu	Ala	Val	Arg	Thr
65					70					75				80	
Leu	Lys	Lys	Leu	Ala	Phe	Lys	Ser	Val	Lys	Val	Gly	Val	Tyr	Thr	Cys
			85						90					95	
Gly	Ala	His	Ser	Lys	Asp	Asn	Ala	Leu	Leu	Glu	Asn	Leu	Lys	Ala	Leu
			100					105					110		
Phe	Leu	Gly	Leu	Lys	Leu	Gly	Leu	Tyr	Glu	Tyr	Asp	Thr	Phe	Lys	Ser
		115				120					125				
Asn	Lys	Lys	Glu	Ser	Val	Leu	Lys	Glu	Ala	Ile	Val	Ala	Leu	Glu	Leu
	130					135					140				
His	Lys	Pro	Cys	Glu	Lys	Thr	Cys	Ala	Asn	Ser	Leu	Glu	Lys	Ser	Ala
145					150					155				160	
Lys	Glu	Ala	Leu	Lys	Tyr	Ala	Glu	Ile	Met	Thr	Glu	Ser	Leu	Asn	Ile
			165					170						175	

GGCGAAATCG GGTTAATTTT AGCAGGGATT GCCAGCTATA CCGGTCAT ATG CAT TTA	57
Met His Leu	
1	
GGG TTA GCC ATT TTA GTC GCA GGG ATT GGG GGC TTT GTG GGG GAT CAG	105
Gly Leu Ala Ile Leu Val Ala Gly Ile Gly Gly Phe Val Gly Asp Gln	
5 10 15	
ATC TAT TTT TAC ATC GGC CGC ACC AAT AAA GCT TAC ATC CAA AAA AAG	153
Ile Tyr Phe Tyr Ile Gly Arg Thr Asn Lys Ala Tyr Ile Gln Lys Lys	
20 25 30 35	
CTA GAA AAA CAA CGC CGA AAA CTA GCC CTA GCC CAT TTA TTG TTG CAA	201
Leu Glu Lys Gln Arg Arg Lys Leu Ala Leu Ala His Leu Leu Leu Gln	
40 45 50	
AAA CAC GGC TGG TTT ATC ATT TTT ATC CAA CGC TAT ATG TAT GGC ATG	249
Lys His Gly Trp Phe Ile Ile Phe Ile Gln Arg Tyr Met Tyr Gly Met	
55 60 65	
CGC ACC ATC ATT CCC ATT AGC ATA GGT CTC ACG CGT TAT AGC GCT TTA	297
Arg Thr Ile Ile Pro Ile Ser Ile Gly Leu Thr Arg Tyr Ser Ala Leu	
70 75 80	
AAA TTC GCT ATC ATC AAT CTC ATT AGC GCG ATG GTG TGG GCG AGC ATT	345
Lys Phe Ala Ile Ile Asn Leu Ile Ser Ala Met Val Trp Ala Ser Ile	
85 90 95	
ACC ATT ATT CTA GCG TGG TAT TTA GGA GAA GAG TTA TTG CAT GCG TTA	393
Thr Ile Ile Leu Ala Trp Tyr Leu Gly Glu Glu Leu Leu His Ala Leu	
100 105 110 115	
GGG TGG CTT AAA AAA CAC CCT TAT GCG CTA ATA TTA CTA TTA GTA TCT	441
Gly Trp Leu Lys Lys His Pro Tyr Ala Leu Ile Leu Leu Leu Val Ser	
120 125 130	
TTC TTG GCG TTA GTG CTG TGG TAT TTC CAA TAC TAT AGT AAG AAA AAC	489
Phe Leu Ala Leu Val Leu Trp Tyr Phe Gln Tyr Tyr Ser Lys Lys Asn	
135 140 145	
CGC TAGAGTGCAA TACAATTCTT GAAAGATATG AAATTAAAAA AGGAGACTTT ATGTTA	548
Arg	
AAAATCAAAT TA	560

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met His Leu Gly Leu Ala Ile Leu Val Ala Gly Ile Gly Gly Phe Val
 1 5 10 15
 Gly Asp Gln Ile Tyr Phe Tyr Ile Gly Arg Thr Asn Lys Ala Tyr Ile
 20 25 30
 Gln Lys Lys Leu Glu Lys Gln Arg Arg Lys Leu Ala Leu Ala His Leu
 35 40 45
 Leu Leu Gln Lys His Gly Trp Phe Ile Ile Phe Ile Gln Arg Tyr Met
 50 55 60
 Tyr Gly Met Arg Thr Ile Ile Pro Ile Ser Ile Gly Leu Thr Arg Tyr
 65 70 75 80
 Ser Ala Leu Lys Phe Ala Ile Ile Asn Leu Ile Ser Ala Met Val Trp
 85 90 95
 Ala Ser Ile Thr Ile Ile Leu Ala Trp Tyr Leu Gly Glu Glu Leu Leu
 100 105 110
 His Ala Leu Gly Trp Leu Lys Lys His Pro Tyr Ala Leu Ile Leu Leu
 115 120 125
 Leu Val Ser Phe Leu Ala Leu Val Leu Trp Tyr Phe Gln Tyr Tyr Ser
 130 135 140
 Lys Lys Asn Arg
 145

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 61...600
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TAAAAACGCT ATAATAAATC AAAATTCTAC AACCAATCCG TTATATTAAA GGAAATCAAA 60
 ATG AAT GAA ACG CTC AAA GAA GAA CTT TTA CAA AGC ATC AGA GAA GTG 108
 Met Asn Glu Thr Leu Lys Glu Glu Leu Leu Gln Ser Ile Arg Glu Val
 1 5 10 15
 AAA GAC TAC CCT AAA AAA GGG ATT TTA TTC AAA GAC ATT ACC ACG CTA 156
 Lys Asp Tyr Pro Lys Lys Gly Ile Leu Phe Lys Asp Ile Thr Thr Leu
 20 25 30
 CTC AAC TAC CCT AAA CTC TTT AAC AAA CTC ATT GAC ACG CTC AAA AAA 204
 Leu Asn Tyr Pro Lys Leu Phe Asn Lys Leu Ile Asp Thr Leu Lys Lys
 35 40 45
 CGC TAT CTC GCT CTC AAT ATA GAC TTT ATC GTG GGC ATT GAA GCG AGA 252
 Arg Tyr Leu Ala Leu Asn Ile Asp Phe Ile Val Gly Ile Glu Ala Arg
 50 55 60
 GGG TTT ATT TTA GGC TCT GCT CTC GCT TAT GCG CTT GGG GTG GGT TTT 300
 Gly Phe Ile Leu Gly Ser Ala Leu Ala Tyr Ala Leu Gly Val Gly Phe

Ala Phe Arg Gly Ile Lys Gly Val Arg Val Val Leu Ile Asp Asp Leu
115 120 125
Leu Ala Thr Gly Gly Thr Ala Leu Ala Ser Leu Glu Leu Ile Lys Ala
130 135 140
Leu Gln Ala Glu Cys Ile Glu Ala Cys Phe Leu Ile Gly Leu Lys Glu
145 150 155 160
Leu Pro Gly Ile Gln Leu Leu Glu Glu Arg Val Lys Thr Phe Cys Leu
165 170 175
Leu Glu Leu Glu
180

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...357
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTCGCTAAA AAGGATATTT TAACAGA ATG TTT ACC CAA TGG TTT ATT CTC ACT	54
Met Phe Thr Gln Trp Phe Ile Leu Thr	
1 5	
ATC GCT ATT GTT TTT ATC CTT TAT ATG GGT GTG CGC ACT TTC TTT TTT	102
Ile Ala Ile Val Phe Ile Leu Tyr Met Gly Val Arg Thr Phe Phe Phe	
10 15 20 25	
AAA ACC GTG GCT AAA CGG CAA GAA CGC ACC AAC GCA TCC ATG AAG CTC	150
Lys Thr Val Ala Lys Arg Gln Glu Arg Thr Asn Ala Ser Met Lys Leu	
30 35 40	
ACC TTA CAA GAA GCT GAA ATT TTG ATC CAA AAA CAC CAG TTG CAA CTC	198
Thr Leu Gln Glu Ala Glu Ile Leu Ile Gln Lys His Gln Leu Gln Leu	
45 50 55	
CAA AGG GCT TTG GGC AAT ATT GAT ATT CTC ACC CAA GAA ATG AGC TCG	246
Gln Arg Ala Leu Gly Asn Ile Asp Ile Leu Thr Gln Glu Met Ser Ser	
60 65 70	
TTA AAA ACA GAA CTA AAA GCC CTT AAA CAG CGC AAC TCT GAA TAC AAA	294
Leu Lys Thr Glu Leu Lys Ala Leu Lys Gln Arg Asn Ser Glu Tyr Lys	
75 80 85	
GGC GAA TCG GAT AAA TAT AAA AAT CGT ATT AAA GAA TTG GAG CAA AAA	342
Gly Glu Ser Asp Lys Tyr Lys Asn Arg Ile Lys Glu Leu Glu Gln Lys	
90 95 100 105	
ATA GAA GCT CTC CTT TAAAAACGCT ATAATAA	374

Ile Glu Ala Leu Leu
110

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Phe	Thr	Gln	Trp	Phe	Ile	Leu	Thr	Ile	Ala	Ile	Val	Phe	Ile	Leu	
1				5				10					15			
Tyr	Met	Gly	Val	Arg	Thr	Phe	Phe	Phe	Lys	Thr	Val	Ala	Lys	Arg	Gln	
			20					25					30			
Glu	Arg	Thr	Asn	Ala	Ser	Met	Lys	Leu	Thr	Leu	Gln	Glu	Ala	Glu	Ile	
		35					40					45				
Leu	Ile	Gln	Lys	His	Gln	Leu	Gln	Leu	Gln	Arg	Ala	Leu	Gly	Asn	Ile	
	50				55					60						
Asp	Ile	Leu	Thr	Gln	Glu	Met	Ser	Ser	Leu	Lys	Thr	Glu	Leu	Lys	Ala	
65				70				75						80		
Leu	Lys	Gln	Arg	Asn	Ser	Glu	Tyr	Lys	Gly	Glu	Ser	Asp	Lys	Tyr	Lys	
			85					90					95			
Asn	Arg	Ile	Lys	Glu	Leu	Glu	Gln	Lys	Ile	Glu	Ala	Leu	Leu			
			100				105						110			

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 78...728
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAAAAAGAAA	ACGCAACGCA	TTAAGGTTTT	TTGTGCAATT	TTTTGATTTC	TCTTTAGAAA	60						
GTTTTATTAC	CACCTTA	ATG AAA	ATC CTA	GCC CTT	TTA ATC	GCT ATC	ATA	110				
		Met	Lys	Ile	Leu	Ala	Leu	Ile	Ala	Ile	Ile	
		1			5				10			
GGG CAT	GAG ATC	ATG CAT	GGC TTG	AGC GCG	TTT TTA	TTT GGG	GAT AGG	158				
Gly His	Glu Ile	Met His	Gly Leu	Ser Ala	Phe Leu	Phe Gly	Asp Arg					
	15		20			25						

AGC Ser	ACT Thr	AAA Lys	GAC Asp	GCT Ala	AGG Arg	CGT Arg	TTG Leu	AGT Ser	TTA Leu	AAC Asn	Pro	CCT Ile	ATC Arg	AGG His	CAT His	TTA Leu	206
303540																	
GAC Asp	ATG Met	ATG Met	GGT Gly	TCG Ser	GTG Val	CTT Leu	TTA Leu	CCG Pro	GCT Ala	TTA Leu	TTA Leu	CTC Leu	ATT Ile	TTT Phe	CAA Gln	254	
455055																	
GCC Ala	CCT Pro	TTT Phe	TTG Leu	TTT Phe	GGG Gly	TGG Trp	GCC Ala	AAA Lys	CCC Pro	GTG Val	CCT Pro	GTT Val	GAT Asp	ATG Met	CGC Arg	302	
60657075																	
TAC Tyr	ATT Ile	GTC Val	TCT Ser	CAA Gln	AAA Lys	GGC Gly	TCT Ser	CTA Leu	GCA Ala	TGC Cys	GTA Val	GTG Val	GTG Val	AGT Ser	TTA Leu	350	
808590																	
GCC Ala	GGG Gly	GTG Val	GCT Ala	TAT Tyr	AAT Asn	TTC Phe	ACT Thr	CTG Leu	GCC Ala	GTT Val	CTG Leu	CTC Leu	GCT Ala	TTC Phe	ATC Ile	398	
95100105																	
ACG Thr	CAT His	TGG Trp	AGC Ser	TTC Phe	CAA Gln	CAA Gln	CTA Leu	GGG Gly	ATC Ile	AAC Asn	GCT Ala	TTA Leu	AGC Ser	ATT Ile	GAT Asp	446	
110115120																	
GAA Glu	TTG Leu	AAT Asn	CTT Leu	TAT Tyr	CAG Gln	CTC Leu	GCT Ala	TTA Leu	GTA Val	ACC Thr	TTT Phe	CTC Leu	ATT Ile	CAA Gln	GGC Gly	494	
125130135																	
ATT Ile	CTT Leu	TAT Tyr	AAT Asn	CTT Leu	GTC Val	TTA Leu	GGC Gly	GTT Val	TTC Phe	AAT Asn	AGC Ser	CTC Leu	CCT Pro	ATC Ile	CCG Pro	542	
140145150155																	
CCC Pro	TTA Leu	GAC Asp	GGC Gly	TCC Ser	AAA Lys	GCG Ala	TTA Leu	GGC Gly	TTT Phe	TTA Leu	GCG Ala	TTG Leu	CAT His	TTT Phe	AAA Lys	590	
160165170																	
AGT Ser	GCG Ala	TTT Phe	TTA Leu	TTG Leu	GAA Glu	TGG Trp	TTT Phe	TCT Ser	AAA Lys	ATG Met	GAA Glu	CGC Arg	TAC Tyr	GGC Gly	TTG Leu	638	
175180185																	
TTG Leu	GTA Val	GTG Val	TTT Phe	ATT Ile	TTT Phe	TTG Leu	TTT Phe	ATC Ile	CCC Pro	CCT Pro	TTA Leu	TCG Ser	GAG Glu	TTT Phe	TTT Phe	686	
190195200																	
ATC Ile	CAT His	GCG Ala	CCC Pro	ACA Thr	AGA Arg	TTT Phe	TTA Leu	TTT Phe	TCT Ser	TTA Leu	CTC Leu	CTC Leu	TCT Ser	TAATCTTTT		737	
205210215																	
ATCAAGGAGA GTTTATGAAT AAGCTCTTAA AGTTTTCTCA A																	
778																	

(2) INFORMATION FOR SEQ ID NO:10:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys Ile Leu Ala Leu Leu Ile Ala Ile Ile Gly His Glu Ile Met
1 5 10 15
His Gly Leu Ser Ala Phe Leu Phe Gly Asp Arg Ser Thr Lys Asp Ala
20 25 30
Arg Arg Leu Ser Leu Asn Pro Ile Arg His Leu Asp Met Met Gly Ser
35 40 45
Val Leu Leu Pro Ala Leu Leu Ile Phe Gln Ala Pro Phe Leu Phe
50 55 60
Gly Trp Ala Lys Pro Val Pro Val Asp Met Arg Tyr Ile Val Ser Gln
65 70 75 80
Lys Gly Ser Leu Ala Cys Val Val Val Ser Leu Ala Gly Val Ala Tyr
85 90 95
Asn Phe Thr Leu Ala Val Leu Leu Ala Phe Ile Thr His Trp Ser Phe
100 105 110
Gln Gln Leu Gly Ile Asn Ala Leu Ser Ile Asp Glu Leu Asn Leu Tyr
115 120 125
Gln Leu Ala Leu Val Thr Phe Leu Ile Gln Gly Ile Leu Tyr Asn Leu
130 135 140
Val Leu Gly Val Phe Asn Ser Leu Pro Ile Pro Pro Leu Asp Gly Ser
145 150 155 160
Lys Ala Leu Gly Phe Leu Ala Leu His Phe Lys Ser Ala Phe Leu Leu
165 170 175
Glu Trp Phe Ser Lys Met Glu Arg Tyr Gly Leu Leu Val Val Phe Ile
180 185 190
Phe Leu Phe Ile Pro Pro Leu Ser Glu Phe Phe Ile His Ala Pro Thr
195 200 205
Arg Phe Leu Phe Ser Leu Leu Ser
210 215

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...336
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATCAGATAT TATCCAAGCG CCTTTTAAAA TCTTGCGCCG TATTTTCACA CCTATTGACA 60
TCATCGTGG ATG AAG TCA AAA AAA ACA TTG ATT CAA AAA GGA AGT AAA ATG 111
Met Lys Ser Lys Lys Thr Leu Ile Gln Lys Gly Ser Lys Met
1 5 10
ACG CTC AAT GAA GCC ATT AAA GAC AAA GTT TAT GAA ATC GTA GAA ATC 159
Thr Leu Asn Glu Ala Ile Lys Asp Lys Val Tyr Glu Ile Val Glu Ile

15	20	25	30	
GCT AAC TGC GAT GAA GCC CTT AAA AAA CGC TTT CTC TCT TTT GGT ATC	207			
Ala Asn Cys Asp Glu Ala Leu Lys Lys Arg Phe Leu Ser Phe Gly Ile				
35 40 45				
CAT GAA GGG GTT CAA TGC ATT CTT TTG CAT TAT TCC ATG AAA AAA GCC	255			
His Glu Gly Val Gln Cys Ile Leu Leu His Tyr Ser Met Lys Lys Ala				
50 55 60				
ACG CTT TCG GTT AAA ATC AAC CGC ATT CAA GTG GCT TTA AGA TCC CAT	303			
Thr Leu Ser Val Lys Ile Asn Arg Ile Gln Val Ala Leu Arg Ser His				
65 70 75				
GAA GCA CAA TAC CTT GTC ATC AAA GAA AGC GTG TGAAAATGGG TTTAAAACGC	356			
Glu Ala Gln Tyr Leu Val Ile Lys Glu Ser Val				
80 85				
GCTAAACGCT ATAATAA	373			

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Lys	Ser	Lys	Lys	Thr	Leu	Ile	Gln	Lys	Gly	Ser	Lys	Met	Thr	Leu
1				5					10				15		
Asn	Glu	Ala	Ile	Lys	Asp	Lys	Val	Tyr	Glu	Ile	Val	Glu	Ile	Ala	Asn
			20					25				30			
Cys	Asp	Glu	Ala	Leu	Lys	Lys	Arg	Phe	Leu	Ser	Phe	Gly	Ile	His	Glu
		35					40					45			
Gly	Val	Gln	Cys	Ile	Leu	Leu	His	Tyr	Ser	Met	Lys	Lys	Ala	Thr	Leu
	50				55					60					
Ser	Val	Lys	Ile	Asn	Arg	Ile	Gln	Val	Ala	Leu	Arg	Ser	His	Glu	Ala
65				70					75					80	
Gln	Tyr	Leu	Val	Ile	Lys	Glu	Ser	Val							
				85											

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...375

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGTTA ATTCCATGGT TTCATAAGTG ATTTTTTGGG GCTGT ATG AGG AGC TGT	57
Met Arg Ser Cys	
1	
TTG TTT TTG AAA ACT AAT TCG GTT TTA TCC ATT TTA ATG GGC GAT AAG	105
Leu Phe Leu Lys Thr Asn Ser Val Leu Ser Ile Leu Met Gly Asp Lys	
5 10 15 20	
CCA TCA TTA AAA ACG ACT GAA GGC TTC ATC AAA GTG GCT TTA ATT ACA	153
Pro Ser Leu Lys Thr Thr Glu Gly Phe Ile Lys Val Ala Leu Ile Thr	
25 30 35	
GAA TTT TTT AAA AGC GAT GGG ACA AAC TCG CTA GGA GTG AAA TTG GCT	201
Glu Phe Phe Lys Ser Asp Gly Thr Asn Ser Leu Gly Val Lys Leu Ala	
40 45 50	
TTG ATT GAA GCG TTA TCA ATC TTA AAG CTA GCG AAT TGG ATC TTA TCA	249
Leu Ile Glu Ala Leu Ser Ile Leu Lys Leu Ala Asn Trp Ile Leu Ser	
55 60 65	
AAA ATC CAT GTT TTT AAA TTT TTT TGC GAT TGG CGT TGG AAA AGA GGC	297
Lys Ile His Val Phe Lys Phe Phe Cys Asp Trp Arg Trp Lys Arg Gly	
70 75 80	
TTT AAA AAC GCC AGG CTT TTC ATT ACA GAA GTG TTA ATT TTT AAT TCT	345
Phe Lys Asn Ala Arg Leu Phe Ile Thr Glu Val Leu Ile Phe Asn Ser	
85 90 95 100	
ATG GTT TTT AAA TCG GTT AGC CCT TGC AAA TAAATTGCAG CGCTGGGTTC GAT	398
Met Val Phe Lys Ser Val Ser Pro Cys Lys	
105 110	
TAAGGGCTTG ACAATCAAAT TAAACGCCAT TTCCTAGCT TTGGGTGAAT AG	450

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Arg Ser Cys Leu Phe Leu Lys Thr Asn Ser Val Leu Ser Ile Leu	
1 5 10 15	
Met Gly Asp Lys Pro Ser Leu Lys Thr Thr Glu Gly Phe Ile Lys Val	
20 25 30	
Ala Leu Ile Thr Glu Phe Phe Lys Ser Asp Gly Thr Asn Ser Leu Gly	
35 40 45	
Val Lys Leu Ala Leu Ile Glu Ala Leu Ser Ile Leu Lys Leu Ala Asn	

AATGCGTGAG ATTATTTCTG ATGGGAATGA ATTAGTCGCT AAAGCGGCGA TTGAA

450

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Ala Lys Met Ser Ala Pro Asp Gly Val Ala Val Trp Val Asn Glu
 1           5           10           15
Asp Arg Cys Lys Gly Cys Asp Ile Cys Val Ser Val Cys Pro Ala Gly
          20           25           30
Val Leu Gly Met Gly Ile Glu Lys Glu Arg Val Leu Gly Lys Val Ala
          35           40           45
Lys Val Ala Tyr Pro Glu Ser Cys Ile Gly Cys Val Gln Cys Glu Leu
          50           55           60
His Cys Pro Asp Phe Ala Ile Tyr Val Ala Asp Arg Lys Asp Phe Lys
          65           70           75           80
Phe Ala Lys Val Ser Lys Glu Ala Gln Glu Arg Ser Glu Lys Val Lys
          85           90           95
Ala Asn Lys Tyr Met Leu Leu Glu Glu Thr Ile Leu Glu Gly Arg Asp
          100          105          110
Lys

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 127...1251
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

TGTGGCTGAC AGGAAGGATT TCAAATTCGC TAAAGTTTCT AAAGAAGCCC AAGAAAGAAG      60
CGAAAAGGTT AAGGCCAATA AATACATGCT CTTAGAAGAG ACTATTTTAG AAGGGAGAGA      120
CAAATA ATG CGT GAG ATT ATT TCT GAT GGG AAT GAA TTA GTC GCT AAA      168
      Met Arg Glu Ile Ile Ser Asp Gly Asn Glu Leu Val Ala Lys
          1           5           10

GCG GCG ATT GAA GTG GGG TGT CGG TTT TTT GGG GGC TAT CCT ATC ACG      216
Ala Ala Ile Glu Val Gly Cys Arg Phe Phe Gly Gly Tyr Pro Ile Thr
          15           20           25           30

```


CCA Pro	AGT Ser	TCG Ser	GAT Asp	ATT Ile 35	ATG Met	CAT His	GCG Ala	ATG Met	AGC Ser 40	GTG Val	GCT Ala	TTA Leu	CCC Pro	AAA Lys 45	TGC Cys	264
GGC Gly	GGT Gly	CAT His	TTT Phe 50	ATC Ile	CAA Gln	ATG Met	GAA Glu	GAT Asp 55	GAA Glu	ATC Ile	AGC Ser	GGG Gly	ATT Ile 60	AGC Ser	GTG Val	312
TCT Ser	TTA Leu	GGA Gly 65	GCG Ala	AGC Ser	ATG Met	AGC Ser	GGG Gly 70	ACG Thr	AAG Lys	TCT Ser	ATG Met	ACA Thr 75	GCA Ala	AGC Ser	TCT Ser	360
GGG Gly	CCT Pro 80	GGT Gly	ATT Ile	TCA Ser	TTG Leu	AAA Lys 85	GTG Val	GAG Glu	CAA Gln	ATC Ile	GGT Gly 90	TAT Tyr	TCT Ser	TTC Phe	ATG Met	408
GCG Ala 95	GAA Glu	ATC Ile	CCT Pro	TTA Leu 100	GTG Val	ATC Ile	GCT Ala	GAT Asp	GTG Val 105	ATG Met	CGT Arg	TCA Ser	GGC Gly	CCA Pro	TCA Ser 110	456
ACC Thr	GGA Gly	ATG Met	CCC Pro	ACT Thr 115	CGT Arg	GTG Val	GCT Ala	CAA Gln	GGC Gly 120	GAT Asp	GTG Val	AAT Asn	TTC Phe	TTA Leu 125	AGA Arg	504
CAC His	CCC Pro	ATA Ile	CAT His 130	GGG Gly	GAT Asp	TTT Phe	AAA Lys 135	GCC Ala	GTC Val	GCG Ala	CTC Leu	GCT Ala 140	CCT Pro	GCG Ala	AAT Asn	552
TTA Leu	GAA Glu 145	GAA Glu Ala	GCT Ala Tyr	TAC Tyr Thr	ACC Thr	GAA Glu	ACC Thr 150	GTT Val	CGC Arg	GCG Ala	TTC Phe	AAT Asn 155	TTG Leu	GCT Ala	GAA Glu	600
ATG Met 160	CTC Leu	ATG Met	ACT Thr	CCT Pro	GTA Val	TTC Phe 165	TTG Leu	CTC Leu	ATG Met	GAT Asp 170	GAA Glu	ACC Thr	GTG Val	GGG Gly	CAT His	648
ATG Met 175	TAT Tyr	GGC Gly	AAG Lys	GTG Val 180	CAA Gln	ATC Ile	CCA Pro	GAT Asp	TTA Leu 185	GAA Glu	GAA Glu	GTG Val	CAA Gln	AAG Lys	ATG Met 190	696
ACT Thr	ATT Ile	AAT Asn	CGT Arg 195	AAG Lys	GAA Glu	TTT Phe	CTG Leu	GGC Gly	GAT Asp 200	AAA Lys	AAA Lys	GAC Asp	TAC Tyr	AAG Lys 205	CCT Pro	744
TAT Tyr	GGG Gly	GTC Val	GCA Ala 210	CAA Gln	GAC Asp	GAG Glu	CCG Pro	GCT Ala 215	GTT Val	TTG Leu	AAC Asn	CCT Pro 220	TTC Phe	TTT Phe	AAA Lys	792
GGT Gly	TAT Tyr	CGC Arg 225	TAC Tyr	CAT His	GTT Val	TCA Ser	GGC Gly 230	TTG Leu	CAC His	CAT His	GGG Gly	CCT Pro 235	ATT Ile	GGC Gly	TTT Phe	840
CCT Pro 240	ACT Thr	GAA Glu	GAC Asp	GCT Ala	AAA Lys	ATT Ile 245	GGT Gly	GGG Gly	GAT Asp	TTG Leu 250	ATT Ile	GAC Asp	AGA Arg	TTA Leu	TTT Phe	888
AAT Asn	AAG Lys	ATT Ile	GAA Glu	TCC Ser	AAG Lys	CAA Gln	GAC Asp	ATT Ile	ATC Ile	AAC Asn	GAA Glu	AAT Asn	GAG Glu	GAA Glu	ATG Met	936

255						260						265						270	
GAT	TTA	GAG	GGT	GCT	GAA	ATC	GTT	GTT	ATC	GCT	TAC	GGT	TCG	GTT	TCT	984			
Asp	Leu	Glu	Gly	Ala	Glu	Ile	Val	Val	Ile	Ala	Tyr	Gly	Ser	Val	Ser				
				275					280					285					
TTG	GCG	GTT	AAA	GAG	GCC	TTG	AAA	GAT	TAC	CAT	AAA	GAA	AGC	AAG	CAA	1032			
Leu	Ala	Val	Lys	Glu	Ala	Leu	Lys	Asp	Tyr	His	Lys	Glu	Ser	Lys	Gln				
				290					295					300					
AAA	GTC	GGC	TTT	TTC	AGG	CCT	AAA	ACC	TTA	TGG	CCA	AGC	CCG	GCT	AAA	1080			
Lys	Val	Gly	Phe	Phe	Arg	Pro	Lys	Thr	Leu	Trp	Pro	Ser	Pro	Ala	Lys				
				305					310					315					
CGC	TTG	AAA	GAA	ATA	GGG	GAT	AAA	TAC	GAA	AAA	ATC	CTT	GTG	ATT	GAA	1128			
Arg	Leu	Lys	Glu	Ile	Gly	Asp	Lys	Tyr	Glu	Lys	Ile	Leu	Val	Ile	Glu				
				320					325					330					
TTG	AAT	AAA	GGG	CAG	TAT	TTA	GAA	GAA	ATT	GAA	AGG	GCT	ATG	CAA	AGA	1176			
Leu	Asn	Lys	Gly	Gln	Tyr	Leu	Glu	Glu	Ile	Glu	Arg	Ala	Met	Gln	Arg				
335					340					345					350				
AAG	GTG	CAT	TTC	TTG	GGG	CAA	GCC	AAT	GGG	CGC	ACG	ATT	TCG	CCT	AAA	1224			
Lys	Val	His	Phe	Leu	Gly	Gln	Ala	Asn	Gly	Arg	Thr	Ile	Ser	Pro	Lys				
				355					360					365					
CAA	ATC	ATC	GCA	AAA	TTG	AAG	GAG	CTT	TAAAATGGCG	TTTAATTATG	ATGAATA					1278			
Gln	Ile	Ile	Ala	Lys	Leu	Lys	Glu	Leu											
				370					375										
TTTGC	GTG	GATA	AAATAC	CCACT	TTTGTG	GTG	TTGGGGC	TGTGGCGATG	GCGTGATTTT							1338			
GAAATCCATT	AT															1350			

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met 1	Arg	Glu	Ile	Ile 5	Ser	Asp	Gly	Asn	Glu 10	Leu	Val	Ala	Lys	Ala 15	Ala
Ile	Glu	Val	Gly 20	Cys	Arg	Phe	Phe	Gly 25	Gly	Tyr	Pro	Ile	Thr 30	Pro	Ser
Ser	Asp	Ile 35	Met	His	Ala	Met	Ser	Val 40	Ala	Leu	Pro	Lys 45	Cys	Gly	Gly
His 50	Phe	Ile	Gln	Met	Glu	Asp 55	Glu	Ile	Ser	Gly	Ile 60	Ser	Val	Ser	Leu
Gly 65	Ala	Ser	Met	Ser	Gly 70	Thr	Lys	Ser	Met	Thr 75	Ala	Ser	Ser	Gly	Pro 80
Gly	Ile	Ser	Leu	Lys 85	Val	Glu	Gln	Ile	Gly 90	Tyr	Ser	Phe	Met	Ala 95	Glu
Ile	Pro	Leu	Val	Ile	Ala	Asp	Val	Met	Arg	Ser	Gly	Pro	Ser	Thr	Gly

TAT	TTA	GGC	TTA	AAC	CCA	AAA	CGC	ACC	ACC	AAA	AGC	GCC	ACA	GCC	CCT	104
Tyr	Leu	Gly	Leu	Asn	Pro	Lys	Arg	Thr	Thr	Lys	Ser	Ala	Thr	Ala	Pro	
			5					10					15			
ATT	AAA	ATC	ATG	TTG	ATG	CGT	TGC	GCC	CAG	CAA	AAA	ATA	CAA	GGC	GAA	152
Ile	Lys	Ile	Met	Leu	Met	Arg	Cys	Ala	Gln	Gln	Lys	Ile	Gln	Gly	Glu	
		20					25					30				
TCT	TTC	AAA	ACA	TAGCCAAAAT AACCTTAAAA AACGCTTT										192		
Ser	Phe	Lys	Thr													
																35

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Tyr	Leu	Gly	Leu	Asn	Pro	Lys	Arg	Thr	Thr	Lys	Ser	Ala	Thr	Ala		
1				5					10					15			
Pro	Ile	Lys	Ile	Met	Leu	Met	Arg	Cys	Ala	Gln	Gln	Lys	Ile	Gln	Gly		
			20					25					30				
Glu	Ser	Phe	Lys	Thr													
																	35

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...1049
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACCATAATTA	GACAAACCTT	TAAGGATTT	ATG	ATG	ATT	TTC	ATT	GAT	GCA	TGT	53					
			Met	Met	Ile	Phe	Ile	Asp	Ala	Cys						
			1				5									
TTT	AGA	AAG	GAA	ACG	CCT	TAC	ACG	CCC	ATT	TGG	ATG	ATG	AGG	CAA	GCG	101
Phe	Arg	Lys	Glu	Thr	Pro	Tyr	Thr	Pro	Ile	Trp	Met	Met	Arg	Gln	Ala	
	10					15					20					

GGG Gly 25	CGT Arg	TAC Tyr	CTT Leu	AGC Ser	GAA Glu 30	TAC Tyr	CAA Gln	GAG Glu	AGC Ser	CGT Arg 35	AAA Lys	AAA Lys	GCG Ala	GGG Gly	AGT Ser 40	149
TTC Phe	TTG Leu	GAA Glu	TTG Leu	TGT Cys 45	AAA Lys	AAT Asn	AGC Ser	GAT Asp	CTA Leu 50	GCC Ala	ACA Thr	GAA Glu	GTT Val	ACC Thr 55	TTA Leu	197
CAG Gln	CCG Pro	GTA Val	GAG Glu 60	ATT Ile	TTA Leu	GGC Gly	GTG Val	GAT Asp 65	GCG Ala	GCT Ala	ATT Ile	TTG Leu	TTT Phe 70	AGC Ser	GAT Asp	245
ATT Ile	TTA Leu	GTA Val 75	GTG Val	CCT Pro	TTG Leu	GAA Glu	ATG Met 80	GGC Gly	TTG Leu	AAT Asn	TTG Leu	GAG Glu 85	TTT Phe	ATC Ile	CCC Pro	293
AAA Lys	AAG Lys 90	GGG Gly	CCG Pro	CAT His	TTT Phe	TTA Leu 95	GAG Glu	ACG Thr	ATT Ile	ACG Thr	GAT Asp 100	TTA Leu	AAA Lys	AGC Ser	GTG Val	341
GAA Glu 105	AGC Ser	CTA Leu	AAA Lys	GTA Val	GGG Gly 110	GCT Ala	TAT Tyr	AAA Lys	CAA Gln	CTA Leu 115	AAC Asn	TAT Tyr	GTC Val	TAT Tyr	GAT Asp 120	389
ACG Thr	ATT Ile	TCT Ser	CAA Gln	ACG Thr 125	CGC Arg	CAA Gln	AAG Lys	CTT Leu	TCT Ser 130	AGA Arg	GAG Glu	AAA Lys	GCG Ala	TTA Leu 135	ATC Ile	437
GGT Gly	TTT Phe	TGC Cys	GGA Gly 140	TCG Ser	CCT Pro	TGG Trp	ACT Thr	TTA Leu 145	GCG Ala	ACT Thr	TAC Tyr	ATG Met	ATA Ile 150	GAA Glu	GGC Gly	485
GAG Glu	GGG Gly	AGC Ser 155	AAA Lys	TCG Ser	TAT Tyr	GCC Ala	AAA Lys 160	AGC Ser	AAG Lys	AAA Lys	ATG Met	CTT Leu 165	TAT Tyr	AGC Ser	GAG Glu	533
CCT Pro	GAA Glu 170	GTT Val	TTA Leu	AAA Lys	GCG Ala	CTT Leu 175	TTA Leu	GAA Glu	AAA Lys	TTA Leu 180	AGC Ser	CTT Leu	GAA Glu	TTG Leu	ATA Ile	581
GAG Glu 185	TAT Tyr	TTG Leu	AGC Ser	CTT Leu	CAA Gln 190	ATC Ile	CAA Gln	GCA Ala	GGG Gly	GTC Val 195	AAT Asn	GCA Ala	GTG Val	ATG Met	ATC Ile 200	629
TTT Phe	GAC Asp	TCA Ser	TGG Trp	GCT Ala 205	AGC Ser	GCT Ala	TTA Leu	GAA Glu	AAA Lys 210	GAA Glu	GCG Ala	TAT Tyr	TTG Leu	AAA Lys 215	TTC Phe	677
AGT Ser	TGG Trp	GAT Asp	TAT Tyr 220	TTG Leu	AAA Lys	AAA Lys	ATC Ile	TCT Ser 225	AAA Lys	GAG Glu	CTT Leu	AAA Lys	AAA Lys 230	CGC Arg	TAT Tyr	725
GCG Ala	CAT His	ATC Ile 235	CCA Pro	GTT Val	ATC Ile	CTT Leu	TTC Phe 240	CCT Pro	AAA Lys	GGG Gly	ATT Ile	GGC Gly 245	GCT Ala	TAT Tyr	TTG Leu	773
GAT Asp	AGC Ser	ATA Ile	GAT Asp	GGG Gly	GAA Glu	TTT Phe	GAT Asp	GTG Val	TTT Phe	GGC Gly	GTG Val	GAT Asp	TGG Trp	GGC Gly	ACG Thr	821

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Met	Ile	Phe	Ile	Asp	Ala	Cys	Phe	Arg	Lys	Glu	Thr	Pro	Tyr	Thr
1				5					10					15	
Pro	Ile	Trp	Met	Met	Arg	Gln	Ala	Gly	Arg	Tyr	Leu	Ser	Glu	Tyr	Gln
			20					25					30		
Glu	Ser	Arg	Lys	Lys	Ala	Gly	Ser	Phe	Leu	Glu	Leu	Cys	Lys	Asn	Ser
			35				40					45			
Asp	Leu	Ala	Thr	Glu	Val	Thr	Leu	Gln	Pro	Val	Glu	Ile	Leu	Gly	Val
			50			55				60					
Asp	Ala	Ala	Ile	Leu	Phe	Ser	Asp	Ile	Leu	Val	Val	Pro	Leu	Glu	Met
65					70				75					80	
Gly	Leu	Asn	Leu	Glu	Phe	Ile	Pro	Lys	Lys	Gly	Pro	His	Phe	Leu	Glu
				85				90					95		
Thr	Ile	Thr	Asp	Leu	Lys	Ser	Val	Glu	Ser	Leu	Lys	Val	Gly	Ala	Tyr
			100					105					110		
Lys	Gln	Leu	Asn	Tyr	Val	Tyr	Asp	Thr	Ile	Ser	Gln	Thr	Arg	Gln	Lys
			115				120					125			
Leu	Ser	Arg	Glu	Lys	Ala	Leu	Ile	Gly	Phe	Cys	Gly	Ser	Pro	Trp	Thr
			130			135				140					
Leu	Ala	Thr	Tyr	Met	Ile	Glu	Gly	Glu	Gly	Ser	Lys	Ser	Tyr	Ala	Lys
145					150				155						160
Ser	Lys	Lys	Met	Leu	Tyr	Ser	Glu	Pro	Glu	Val	Leu	Lys	Ala	Leu	Leu
				165				170					175		
Glu	Lys	Leu	Ser	Leu	Glu	Leu	Ile	Glu	Tyr	Leu	Ser	Leu	Gln	Ile	Gln
			180					185					190		
Ala	Gly	Val	Asn	Ala	Val	Met	Ile	Phe	Asp	Ser	Trp	Ala	Ser	Ala	Leu
			195			200						205			
Glu	Lys	Glu	Ala	Tyr	Leu	Lys	Phe	Ser	Trp	Asp	Tyr	Leu	Lys	Lys	Ile
			210			215					220				
Ser	Lys	Glu	Leu	Lys	Lys	Arg	Tyr	Ala	His	Ile	Pro	Val	Ile	Leu	Phe
225					230				235						240
Pro	Lys	Gly	Ile	Gly	Ala	Tyr	Leu	Asp	Ser	Ile	Asp	Gly	Glu	Phe	Asp
				245				250					255		
Val	Phe	Gly	Val	Asp	Trp	Gly	Thr	Pro	Leu	Thr	Ala	Ala	Lys	Lys	Ile
			260				265						270		
Leu	Gly	Gly	Lys	Tyr	Val	Leu	Gln	Gly	Asn	Leu	Glu	Pro	Thr	Arg	Leu
			275				280					285			
Tyr	Asp	Lys	Asn	Ala	Leu	Glu	Gly	Val	Glu	Thr	Ile	Leu	Lys	Val	
			290			295			300						
Met	Gly	Asn	Gln	Gly	His	Ile	Phe	Asn	Leu	Gly	His	Gly	Met	Leu	Pro
305					310				315						320
Asp	Leu	Pro	Arg	Glu	Asn	Ala	Lys	Tyr	Leu	Val	Gln	Leu	Val	His	Ala
				325					330					335	
Lys	Thr	Arg	Arg												
			340												

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...732
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAGACGACTA TGTGCATTAA GGGAATGAAA ATG ATA CGA AAA ATT TTA ATA GGA	54
Met Ile Arg Lys Ile Leu Ile Gly	
1 5	
CTT TTT TTG AGT TTT TTG AGC ATG GAA GCT GGC GAA AAA GTG TAT GCG	102
Leu Phe Leu Ser Phe Leu Ser Met Glu Ala Gly Glu Lys Val Tyr Ala	
10 15 20	
ATT TTC AAT GTG AAA GCG ACA CAA GAT TCC AAA CTC ACC TTA GAC AGC	150
Ile Phe Asn Val Lys Ala Thr Gln Asp Ser Lys Leu Thr Leu Asp Ser	
25 30 35 40	
ACA GGA ATT GTG GAT AGC ATT AAG GTT ACT GAG GGG AGC GTG GTC AAA	198
Thr Gly Ile Val Asp Ser Ile Lys Val Thr Glu Gly Ser Val Val Lys	
45 50 55	
AAG GGC GAT GTT TTG TTG CTT TTA TAT AAT CAA GAC AAA CAG GCT CAA	246
Lys Gly Asp Val Leu Leu Leu Leu Tyr Asn Gln Asp Lys Gln Ala Gln	
60 65 70	
AGC GAT TCC ACC GAA CAA CAA CTC ATT TTC GCT AAA AAG CAA TAC CAA	294
Ser Asp Ser Thr Glu Gln Gln Leu Ile Phe Ala Lys Lys Gln Tyr Gln	
75 80 85	
CGA TAC AGC AAA ATT GGG GGC GCT GTG GAT AAA AAC ACT CTA GAG GGT	342
Arg Tyr Ser Lys Ile Gly Gly Ala Val Asp Lys Asn Thr Leu Glu Gly	
90 95 100	
TAT GAG TTC ACT TAC AGG CGC TTG GAG TCT GAT TAC GCT TAT TCT ATT	390
Tyr Glu Phe Thr Tyr Arg Arg Leu Glu Ser Asp Tyr Ala Tyr Ser Ile	
105 110 115 120	
GCG GTA TTG AAT AAA ACC ATT TTA AGA GCC CCT TTT GAT GGC GTG ATA	438
Ala Val Leu Asn Lys Thr Ile Leu Arg Ala Pro Phe Asp Gly Val Ile	
125 130 135	
GCG AGT AAA AAC ATT CAA GTG GGC GAA GGG GTG AGC GCG AAT AAC ACG	486
Ala Ser Lys Asn Ile Gln Val Gly Glu Gly Val Ser Ala Asn Asn Thr	
140 145 150	
GTG TTA TTG AGA TTA GTC AGC CAT GCT AGG AAA TTA GTT ATT GAA TTT	534

Val	Leu	Leu	Arg	Leu	Val	Ser	His	Ala	Arg	Lys	Leu	Val	Ile	Glu	Phe		
	155						160					165					
GAT	TCT	AAA	TAT	ATT	AAT	GCG	GTC	AAA	GTA	GGG	GAC	ACT	TAC	ACC	TAT	582	
Asp	Ser	Lys	Tyr	Ile	Asn	Ala	Val	Lys	Val	Gly	Asp	Thr	Tyr	Thr	Tyr		
	170					175				180							
TCT	ATA	GAC	GGG	GAT	TCT	AAT	CAG	CAT	GAA	GCT	AAA	ATC	ACT	AAG	ATT	630	
Ser	Ile	Asp	Gly	Asp	Ser	Asn	Gln	His	Glu	Ala	Lys	Ile	Thr	Lys	Ile		
	185				190				195						200		
TAC	CCC	ACG	GTT	GAT	GAA	AAC	ACC	AGG	AAA	GTG	AGC	GCT	GAA	GCC	CTT	678	
Tyr	Pro	Thr	Val	Asp	Glu	Asn	Thr	Arg	Lys	Val	Ser	Ala	Glu	Ala	Leu		
				205					210					215			
TTA	TCT	AAG	CCT	ATG	GCA	GTG	GGG	CTT	TTT	GGC	GAT	GGG	TTT	ATC	CAA	726	
Leu	Ser	Lys	Pro	Met	Ala	Val	Gly	Leu	Phe	Gly	Asp	Gly	Phe	Ile	Gln		
			220				225						230				
ACG	AAA	TAATAGGATA	TTTTGATGTA	TAAAACAGCG	ATTA											766	
Thr	Lys																

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Ile	Arg	Lys	Ile	Leu	Ile	Gly	Leu	Phe	Leu	Ser	Phe	Leu	Ser	Met		
1				5					10					15			
Glu	Ala	Gly	Glu	Lys	Val	Tyr	Ala	Ile	Phe	Asn	Val	Lys	Ala	Thr	Gln		
			20					25				30					
Asp	Ser	Lys	Leu	Thr	Leu	Asp	Ser	Thr	Gly	Ile	Val	Asp	Ser	Ile	Lys		
		35				40					45						
Val	Thr	Glu	Gly	Ser	Val	Val	Lys	Lys	Gly	Asp	Val	Leu	Leu	Leu	Leu		
	50					55				60							
Tyr	Asn	Gln	Asp	Lys	Gln	Ala	Gln	Ser	Asp	Ser	Thr	Glu	Gln	Gln	Leu		
65				70					75					80			
Ile	Phe	Ala	Lys	Lys	Gln	Tyr	Gln	Arg	Tyr	Ser	Lys	Ile	Gly	Gly	Ala		
			85					90					95				
Val	Asp	Lys	Asn	Thr	Leu	Glu	Gly	Tyr	Glu	Phe	Thr	Tyr	Arg	Arg	Leu		
			100				105						110				
Glu	Ser	Asp	Tyr	Ala	Tyr	Ser	Ile	Ala	Val	Leu	Asn	Lys	Thr	Ile	Leu		
		115				120						125					
Arg	Ala	Pro	Phe	Asp	Gly	Val	Ile	Ala	Ser	Lys	Asn	Ile	Gln	Val	Gly		
	130				135						140						
Glu	Gly	Val	Ser	Ala	Asn	Asn	Thr	Val	Leu	Leu	Arg	Leu	Val	Ser	His		
145					150					155					160		
Ala	Arg	Lys	Leu	Val	Ile	Glu	Phe	Asp	Ser	Lys	Tyr	Ile	Asn	Ala	Val		
			165					170						175			

Lys Val Gly Asp Thr Tyr Thr Tyr Ser Ile Asp Gly Asp Ser Asn Gln
180 185 190
His Glu Ala Lys Ile Thr Lys Ile Tyr Pro Thr Val Asp Glu Asn Thr
195 200 205
Arg Lys Val Ser Ala Glu Ala Leu Leu Ser Lys Pro Met Ala Val Gly
210 215 220
Leu Phe Gly Asp Gly Phe Ile Gln Thr Lys
225 230

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 62...544
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ACGCCAAAGA GAGCAACGGG GAGTTTTTAG TCGCTTTAGC GNAGCGNTTG TGCTGATTTA	60
T ATG ATT TTA GCG GCG TTG TAT GAG TCC ATT TTA GAG CCT TTT ATC ATC	109
Met Ile Leu Ala Ala Leu Tyr Glu Ser Ile Leu Glu Pro Phe Ile Ile	
1 5 10 15	
ATG GTT ACC ATG CCT TTA AGT TTT TCA GGG GCG TTT TTT GCT CTA GGT	157
Met Val Thr Met Pro Leu Ser Phe Ser Gly Ala Phe Phe Ala Leu Gly	
20 25 30	
TTA GTC CAT CAG CCT TTG AGC ATG TTC TCT ATG ATA GGC TTG ATT TTG	205
Leu Val His Gln Pro Leu Ser Met Phe Ser Met Ile Gly Leu Ile Leu	
35 40 45	
CTC ATT GGT ATG GTG GGT AAA AAC GCC ACG CTT TTA ATT GAT GTG GCG	253
Leu Ile Gly Met Val Gly Lys Asn Ala Thr Leu Leu Ile Asp Val Ala	
50 55 60	
AAT GAA GAG CGT AAA AAA GGT TTG AAT ATC CAA GAG GCC ATT TTA TTT	301
Asn Glu Glu Arg Lys Lys Gly Leu Asn Ile Gln Glu Ala Ile Leu Phe	
65 70 75 80	
GCC GGC AAA ACC CGT CTA AGA CCG ATT TTA ATG ACG ACC ATT GCG ATG	349
Ala Gly Lys Thr Arg Leu Arg Pro Ile Leu Met Thr Thr Ile Ala Met	
85 90 95	
GTT TGC GGG ATG CTG CCT TTA GCG TTG GCG AGT GGG GAT GGA GCG GCG	397
Val Cys Gly Met Leu Pro Leu Ala Leu Ala Ser Gly Asp Gly Ala Ala	
100 105 110	
ATG AAA TCC CCT ATA GGG ATT GCG ATG AGT GGG GGC TTG ATG ATT TCT	445
Met Lys Ser Pro Ile Gly Ile Ala Met Ser Gly Gly Leu Met Ile Ser	

115	120	125	
ATG GTG TTA AGC TTA CTC ATT GTG CCG GTG TTT TAT CGT TTG CTC GCT	493		
Met Val Leu Ser Leu Leu Ile Val Pro Val Phe Tyr Arg Leu Leu Ala			
130 135 140			
CCC ATA GAC GAC AAA ATC AAG CGG TTT TAT CAA AAC CAA AAA ACT TTA	541		
Pro Ile Asp Asp Lys Ile Lys Arg Phe Tyr Gln Asn Gln Lys Thr Leu			
145 150 155 160			
GAA TGAAAAAAT TGCTTTCATT TTGGCTTTAT GGGTGGGCTT GTTAGGGGCG TTTGAG	600		
Glu			
CCTAAAAAAA GTCATATTTA TTTTGGGGCT	630		

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Ile	Leu	Ala	Ala	Leu	Tyr	Glu	Ser	Ile	Leu	Glu	Pro	Phe	Ile	Ile
1				5					10					15	
Met	Val	Thr	Met	Pro	Leu	Ser	Phe	Ser	Gly	Ala	Phe	Phe	Ala	Leu	Gly
			20					25					30		
Leu	Val	His	Gln	Pro	Leu	Ser	Met	Phe	Ser	Met	Ile	Gly	Leu	Ile	Leu
		35					40					45			
Leu	Ile	Gly	Met	Val	Gly	Lys	Asn	Ala	Thr	Leu	Leu	Ile	Asp	Val	Ala
	50					55				60					
Asn	Glu	Glu	Arg	Lys	Lys	Gly	Leu	Asn	Ile	Gln	Glu	Ala	Ile	Leu	Phe
65				70					75					80	
Ala	Gly	Lys	Thr	Arg	Leu	Arg	Pro	Ile	Leu	Met	Thr	Thr	Ile	Ala	Met
			85						90					95	
Val	Cys	Gly	Met	Leu	Pro	Leu	Ala	Leu	Ala	Ser	Gly	Asp	Gly	Ala	Ala
			100					105					110		
Met	Lys	Ser	Pro	Ile	Gly	Ile	Ala	Met	Ser	Gly	Gly	Leu	Met	Ile	Ser
		115					120					125			
Met	Val	Leu	Ser	Leu	Leu	Ile	Val	Pro	Val	Phe	Tyr	Arg	Leu	Leu	Ala
	130					135					140				
Pro	Ile	Asp	Asp	Lys	Ile	Lys	Arg	Phe	Tyr	Gln	Asn	Gln	Lys	Thr	Leu
145					150					155					160
Glu															

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 19...945
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TAAAAGGTTT TTACAAAC	ATG ATA AAA AGC CAA AAA GAA TAT TTA GAA AGA	51
	Met Ile Lys Ser Gln Lys Glu Tyr Leu Glu Arg	
	1 5 10	
ATT GCA TAT TTA AAC ACC CTA TCG CAC CAT TAT TAC AAC CTT GAT GAA	99	
Ile Ala Tyr Leu Asn Thr Leu Ser His His Tyr Tyr Asn Leu Asp Glu		
	15 20 25	
CCC ATC GTA AGC GAT GCG ATC TAT GAT GAA CTT TAC CAA GAA TTG AAA	147	
Pro Ile Val Ser Asp Ala Ile Tyr Asp Glu Leu Tyr Gln Glu Leu Lys		
	30 35 40	
GCT TAT GAA GAA AAA AAC CCT AAT GGC ATT CAA GCT AAT TCC CCT ACC	195	
Ala Tyr Glu Glu Lys Asn Pro Asn Gly Ile Gln Ala Asn Ser Pro Thr		
	45 50 55	
CAA AAA GTG GGG GCT ACT ACC ACC AAT TCG TTC AAT AAA AAC CCC CAT	243	
Gln Lys Val Gly Ala Thr Thr Thr Asn Ser Phe Asn Lys Asn Pro His		
	60 65 70 75	
TTA ATG CGG ATG TGG AGC TTA GAT GAT GTG TTC AAT CAA AGC GAA TTG	291	
Leu Met Arg Met Trp Ser Leu Asp Asp Val Phe Asn Gln Ser Glu Leu		
	80 85 90	
CAA GCG TGG TTG CAA CGC ATT TTA AAA GCC TAT CCT AGT GCT TCG TTC	339	
Gln Ala Trp Leu Gln Arg Ile Leu Lys Ala Tyr Pro Ser Ala Ser Phe		
	95 100 105	
GTG TGT TCG CCC AAA CTT GAT GGG GTT TCG CTC AAT CTT TTG TAT CAA	387	
Val Cys Ser Pro Lys Leu Asp Gly Val Ser Leu Asn Leu Leu Tyr Gln		
	110 115 120	
CAT GGC AAG CTA GTG AAG GCG ACC ACT AGG GGC AAC GGC TTA GAA GGA	435	
His Gly Lys Leu Val Lys Ala Thr Thr Arg Gly Asn Gly Leu Glu Gly		
	125 130 135	
GAA TTA GTT AGC GCA AAC GCT AAA CAC ATC GCT AAT ATC CCC CAC GCT	483	
Glu Leu Val Ser Ala Asn Ala Lys His Ile Ala Asn Ile Pro His Ala		
	140 145 150 155	
ATC GCT TAT AAT GGA GAA ATA GAA ATC AGG GGC GAA GTG ATC ATT TCT	531	
Ile Ala Tyr Asn Gly Glu Ile Glu Ile Arg Gly Glu Val Ile Ile Ser		
	160 165 170	
AAA AAG GAT TTT GAC GCT TTG AAT CAA GAG CGC TTA AAC GCT AAT GAA	579	
Lys Lys Asp Phe Asp Ala Leu Asn Gln Glu Arg Leu Asn Ala Asn Glu		
	175 180 185	

CCC Pro	CTA Leu	TTC Phe	GCT Ala	AAC Asn	CCC Pro	AGA Arg	AAC Asn	GCC Ala	GCA Ala	TCA Ser	GGG Gly	AGT Ser	TTG Leu	AGG Arg	CAA Gln	627	
190195200																	
CTT Leu	GAT Asp	AGC Ser	GAA Glu	ATC Ile	ACT Thr	AAA Lys	AAG Lys	CGT Arg	AAA Lys	TTG Leu	CAA Gln	TTC Phe	ATT Ile	CCT Pro	TGG Trp	675	
205210215																	
GGC Gly	GTG Val	GGC Gly	AAG Lys	CAT His	TCT Ser	TTA Leu	AAT Asn	TTT Phe	TTA Leu	AGC Ser	TTT Phe	AAG Lys	GAG Glu	TGT Cys	TTG Leu	723	
220225230235																	
GAT Asp	TTT Phe	ATC Ile	GTC Val	TCG Ser	TTA Leu	GGT Gly	TTT Phe	AGC Ser	GCC Ala	ATT Ile	CAA Gln	TAC Tyr	TTA Leu	AGC Ser	CTA Leu	771	
240245250																	
AAC Asn	AAA Lys	AAC Asn	CAC His	CAA Gln	GAA Glu	ATA Ile	GAA Glu	GAC Asp	AAT Asn	TAC Tyr	CAC His	ACC Thr	CTA Leu	ATT Ile	AGA Arg	819	
255260265																	
GAA Glu	AGG Arg	GAG Glu	GGC Gly	TTT Phe	TTT Phe	GCC Ala	CTT Leu	TTA Leu	GAC Asp	GGC Gly	ATG Met	GTG Val	ATC Ile	GTT Val	GTG Val	867	
270275280																	
AAT Asn	GAA Glu	TTA Leu	AAT Asn	ATT Ile	CAA Gln	AAG Lys	GAG Glu	CTA Leu	GGC Gly	TAC Tyr	ACG Thr	CAA Gln	AAA Lys	TCC Ser	CCT Pro	915	
285290295																	
AAA Lys	TNG Xaa	CTT Leu	GCG Ala	CTT Leu	ATA Ile	AAT Asn	TCC Ser	CGG Arg	CTT Leu	TAGAAAAACA				CACCAAAATT		GTA	968
300305																	
GGAGTCATTAACCAAGTGGGCGCASSGGGCGATCACAC																1007	

```

Arg Ile Leu Lys Ala Tyr Pro Ser Ala Ser Phe Val Cys Ser Pro Lys
      100      105      110
Leu Asp Gly Val Ser Leu Asn Leu Leu Tyr Gln His Gly Lys Leu Val
      115      120      125
Lys Ala Thr Thr Arg Gly Asn Gly Leu Glu Gly Glu Leu Val Ser Ala
      130      135      140
Asn Ala Lys His Ile Ala Asn Ile Pro His Ala Ile Ala Tyr Asn Gly
      145      150      155      160
Glu Ile Glu Ile Arg Gly Glu Val Ile Ile Ser Lys Lys Asp Phe Asp
      165      170      175
Ala Leu Asn Gln Glu Arg Leu Asn Ala Asn Glu Pro Leu Phe Ala Asn
      180      185      190
Pro Arg Asn Ala Ala Ser Gly Ser Leu Arg Gln Leu Asp Ser Glu Ile
      195      200      205
Thr Lys Lys Arg Lys Leu Gln Phe Ile Pro Trp Gly Val Gly Lys His
      210      215      220
Ser Leu Asn Phe Leu Ser Phe Lys Glu Cys Leu Asp Phe Ile Val Ser
      225      230      235      240
Leu Gly Phe Ser Ala Ile Gln Tyr Leu Ser Leu Asn Lys Asn His Gln
      245      250      255
Glu Ile Glu Asp Asn Tyr His Thr Leu Ile Arg Glu Arg Glu Gly Phe
      260      265      270
Phe Ala Leu Leu Asp Gly Met Val Ile Val Val Asn Glu Leu Asn Ile
      275      280      285
Gln Lys Glu Leu Gly Tyr Thr Gln Lys Ser Pro Lys Xaa Leu Ala Leu
      290      295      300
Ile Asn Ser Arg Leu
305

```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 44...880
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

GTGCTTTAGA TTAGATGCAG AAAAAGACGC CCAACTTTAT GGC ATG AAT ATT TTT      55
                               Met Asn Ile Phe
                               1

AAG ATC CGA GAA ATT ATC CAT TAT GAC GGG GAG GTT ACA GAG ATT CTT      103
Lys Ile Arg Glu Ile Ile His Tyr Asp Gly Glu Val Thr Glu Ile Leu
  5              10              15              20

GGG GGG AGC GAT GGC GTG ATG CTC GGG TTT CTT AGC GTT AGG GGC GAG      151
Gly Gly Ser Asp Gly Val Met Leu Gly Phe Leu Ser Val Arg Gly Glu
      25              30              35

```

TCT Ser	ATC Ile	CCT Pro	TTA Leu 40	GTG Val	GAT Asp	GTG Val	AAA Lys	AGG Arg 45	TGG Trp	TTG Leu	CAT His	TAT Tyr	AAC Asn 50	GCT Ala	AAT Asn	199
GAT Asp	CCG Pro	AGC Ser 55	CGT Arg	GAT Asp	CTA Leu	AAA Lys	GAA Glu 60	TGC Cys	AGC Ser	GTT Val	AAA Lys	GAT Asp 65	GAC Asp	CAT His	AAT Asn	247
TTG Leu	GTG Val 70	ATT Ile	GTG Val	TGC Cys	CAT His	TTT Phe 75	TCT Ser	AAC Asn	CAT His	TCC Ser	ATC Ile 80	GCT Ala	CTA Leu	AAG Lys	GTT Val	295
TTA Leu 85	AAA Lys	ATT Ile	GAA Glu	AGG Arg	ATC Ile 90	ATC Ile	CAT His	AAA Lys	AAT Asn	TGG Trp 95	ACT Thr	GAG Glu	ATT Ile	AGC Ser	GCT Ala 100	343
GGG Gly	GAC Asp	AAA Lys	CAA Gln	GGC Gly 105	ATT Ile	AAT Asn	GAA Glu	GAG Glu	GGT Gly 110	AAG Lys	CTT Leu	AGC Ser	GCT Ala	ATC Ile	ACT Thr 115	391
CGT Arg	TTT Phe	GAT Asp	GAA Glu 120	GAA Glu	CGA Arg	GTG Val	GTG Val	CAG Gln 125	ATC Ile	TTA Leu	GAT Asp	GTG Val	GAA Glu 130	AAA Lys	ATG Met	439
ATT Ile	AGC Ser	GAT Asp 135	GTT Val	TTC Phe	CCT Pro	AGC Ser	TTG Leu 140	AAA Lys	GAT Asp	TTA Leu	GAC Asp	GAT Asp 145	TTG Leu	ACT Thr	TTG Leu	487
CGT Arg	TGC Cys 150	ATA Ile	GAA Glu	GCC Ala	ATT Ile	CAA Gln 155	AGC Ser	CAA Gln	AAA Lys	CTC Leu	ATT Ile 160	TTA Leu	ATC Ile	GCT Ala	GAA Glu	535
GAC Asp 165	TCC Ser	CTA Leu	AGC Ser	GCT Ala	CTT Leu 170	AAA Lys	ACC Thr	TTA Leu	GAA Glu	AAG Lys 175	ATC Ile	GTT Val	CAA Gln	ACT Thr	TTA Leu 180	583
GAA Glu	TTG Leu	CGT Arg	TAT Tyr	TTA Leu 185	GCT Ala	TTT Phe	CCA Pro	AAC Asn	GGG Gly 190	AGG Arg	GAA Glu	TTG Leu	TTG Leu	GAT Asp 195	TAT Tyr	631
TTG Leu	TAT Tyr	GAA Glu	AAA Lys 200	GAA Glu	CAT His	TAC Tyr	CAA Gln	CAA Gln 205	GTT Val	GGC Gly	GTG Val	GTC Val	ATT Ile 210	ACG Thr	GAT Asp	679
TTA Leu	GAA Glu	ATG Met 215	CCT Pro	AAC Asn	ATT Ile	TCA Ser	GGG Gly 220	TTT Phe	GAA Glu	GTG Val	TTA Leu	AAA Lys 225	ACC Thr	ATT Ile	AAA Lys	727
GCT Ala	GAT Asp 230	CAT His	AGA Arg	ACT Thr	GAG Glu	CAT His 235	CTT Leu	CCT Pro	GTG Val	ATT Ile 240	ATC Ile	AAT Asn	TCG Ser	TCC Ser	ATG Met	775
AGC Ser 245	AGC Ser	GAT Asp	TCT Ser	AAC Asn	CGC Arg 250	CAG Gln	TTA Leu	GCC Ala	CAA Gln	TCT Ser 255	TTA Leu	GAA Glu	GCG Ala	GAT Asp	GGT Gly 260	823
TTT Phe	GTG Val	GTA Val	AAA Lys	TCT Ser	AAC Asn	ATT Ile	CTT Leu	GAA Glu	ATC Ile	CAT His	GAA Glu	ATG Met	CTT Leu	AAA Lys	AAA Lys	871

265

270

275

ACG CTT TCA TAAATTTAAT TTTTGTTTTA ATTTAAAGGG ATAAAACATG CGAAGTCAT 929
 Thr Leu Ser

TTTTGCAC

937

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Asn Ile Phe Lys Ile Arg Glu Ile Ile His Tyr Asp Gly Glu Val
 1 5 10 15
 Thr Glu Ile Leu Gly Gly Ser Asp Gly Val Met Leu Gly Phe Leu Ser
 20 25 30
 Val Arg Gly Glu Ser Ile Pro Leu Val Asp Val Lys Arg Trp Leu His
 35 40 45
 Tyr Asn Ala Asn Asp Pro Ser Arg Asp Leu Lys Glu Cys Ser Val Lys
 50 55 60
 Asp Asp His Asn Leu Val Ile Val Cys His Phe Ser Asn His Ser Ile
 65 70 75 80
 Ala Leu Lys Val Leu Lys Ile Glu Arg Ile Ile His Lys Asn Trp Thr
 85 90 95
 Glu Ile Ser Ala Gly Asp Lys Gln Gly Ile Asn Glu Glu Gly Lys Leu
 100 105 110
 Ser Ala Ile Thr Arg Phe Asp Glu Glu Arg Val Val Gln Ile Leu Asp
 115 120 125
 Val Glu Lys Met Ile Ser Asp Val Phe Pro Ser Leu Lys Asp Leu Asp
 130 135 140
 Asp Leu Thr Leu Arg Cys Ile Glu Ala Ile Gln Ser Gln Lys Leu Ile
 145 150 155 160
 Leu Ile Ala Glu Asp Ser Leu Ser Ala Leu Lys Thr Leu Glu Lys Ile
 165 170 175
 Val Gln Thr Leu Glu Leu Arg Tyr Leu Ala Phe Pro Asn Gly Arg Glu
 180 185 190
 Leu Leu Asp Tyr Leu Tyr Glu Lys Glu His Tyr Gln Gln Val Gly Val
 195 200 205
 Val Ile Thr Asp Leu Glu Met Pro Asn Ile Ser Gly Phe Glu Val Leu
 210 215 220
 Lys Thr Ile Lys Ala Asp His Arg Thr Glu His Leu Pro Val Ile Ile
 225 230 235 240
 Asn Ser Ser Met Ser Ser Asp Ser Asn Arg Gln Leu Ala Gln Ser Leu
 245 250 255
 Glu Ala Asp Gly Phe Val Val Lys Ser Asn Ile Leu Glu Ile His Glu
 260 265 270
 Met Leu Lys Lys Thr Leu Ser
 275

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 21...593
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATAATTAA	AGGATACGAT	ATG AAA CAA CTA TTT TTG ATC ATT GGA GCC	50
		Met Lys Gln Leu Phe Leu Ile Ile Gly Ala	
		1 5 10	
CCA GGG AGT GGT AAA ACC ACT GAT GCA GAG CTT ATC GCT AAA AAT AAC	98		
Pro Gly Ser Gly Lys Thr Thr Asp Ala Glu Leu Ile Ala Lys Asn Asn		15 20 25	
AGC GAA ACA ATC GCT CAT TTT TCT ACC GGG GAT TTA CTC AGG GCT GAG	146		
Ser Glu Thr Ile Ala His Phe Ser Thr Gly Asp Leu Leu Arg Ala Glu		30 35 40	
AGC GCT AAA AAG ACC GAG CGA GGC TTA TTG ATT GAA AAA TTC ACT TCT	194		
Ser Ala Lys Lys Thr Glu Arg Gly Leu Leu Ile Glu Lys Phe Thr Ser		45 50 55	
CAA GGC GAA TTA GTG CCT TTA GAA ATT GTG GTA GAA ACG ATC CTT TCA	242		
Gln Gly Glu Leu Val Pro Leu Glu Ile Val Val Glu Thr Ile Leu Ser		60 65 70	
GCG ATT AAA AGC TCT GGT AAA GGG ATC ATT TTA ATT GAT GGT TAT CCT	290		
Ala Ile Lys Ser Ser Gly Lys Gly Ile Ile Leu Ile Asp Gly Tyr Pro		75 80 85 90	
AGG AGC GTG GAA CAA ATG CAG GCT TTG GAT AAG GAA TTG AAC GCT CAA	338		
Arg Ser Val Glu Gln Met Gln Ala Leu Asp Lys Glu Leu Asn Ala Gln		95 100 105	
AAC GAA GTG ATC TTA AAA AGC GTG ATT GAA GTA GAA GTG AGT GAA AAC	386		
Asn Glu Val Ile Leu Lys Ser Val Ile Glu Val Glu Val Ser Glu Asn		110 115 120	
ACT GCT AAA GAA AGG GTT TTA GGG CGC TCT AGG GGG GCT GAT GAT AAT	434		
Thr Ala Lys Glu Arg Val Leu Gly Arg Ser Arg Gly Ala Asp Asp Asn		125 130 135	
GAA AAG GTG TTT CAT AAC CGC ATG CGG GTG TTT TTG GAT CCG TTG GGC	482		
Glu Lys Val Phe His Asn Arg Met Arg Val Phe Leu Asp Pro Leu Gly		140 145 150	
GAG ATC CAA AAT TTT TAC AAG AAT AAG AAG GTG TAT AAA GCG ATC GAT	530		
Glu Ile Gln Asn Phe Tyr Lys Asn Lys Lys Val Tyr Lys Ala Ile Asp			

155		160		165		170	
GGG GAG AGG AGC ATT GAA GAG ATT GTG GGC GAA ATG CAA GAG TAT ATC							578
Gly Glu Arg Ser Ile Glu Glu Ile Val Gly Glu Met Gln Glu Tyr Ile							
		175		180		185	
TTG TCT TTC GGT AAT TAAAATGCAC TCTCAAGGAG AATAGCTGTG ATTTCTG							630
Leu Ser Phe Gly Asn							
		190					

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Lys	Gln	Leu	Phe	Leu	Ile	Ile	Gly	Ala	Pro	Gly	Ser	Gly	Lys	Thr
1				5					10					15	
Thr	Asp	Ala	Glu	Leu	Ile	Ala	Lys	Asn	Asn	Ser	Glu	Thr	Ile	Ala	His
			20					25					30		
Phe	Ser	Thr	Gly	Asp	Leu	Leu	Arg	Ala	Glu	Ser	Ala	Lys	Lys	Thr	Glu
		35					40					45			
Arg	Gly	Leu	Leu	Ile	Glu	Lys	Phe	Thr	Ser	Gln	Gly	Glu	Leu	Val	Pro
	50					55					60				
Leu	Glu	Ile	Val	Val	Glu	Thr	Ile	Leu	Ser	Ala	Ile	Lys	Ser	Ser	Gly
65					70					75				80	
Lys	Gly	Ile	Ile	Leu	Ile	Asp	Gly	Tyr	Pro	Arg	Ser	Val	Glu	Gln	Met
				85					90					95	
Gln	Ala	Leu	Asp	Lys	Glu	Leu	Asn	Ala	Gln	Asn	Glu	Val	Ile	Leu	Lys
			100					105					110		
Ser	Val	Ile	Glu	Val	Glu	Val	Ser	Glu	Asn	Thr	Ala	Lys	Glu	Arg	Val
		115					120					125			
Leu	Gly	Arg	Ser	Arg	Gly	Ala	Asp	Asp	Asn	Glu	Lys	Val	Phe	His	Asn
	130					135					140				
Arg	Met	Arg	Val	Phe	Leu	Asp	Pro	Leu	Gly	Glu	Ile	Gln	Asn	Phe	Tyr
145					150					155					160
Lys	Asn	Lys	Lys	Val	Tyr	Lys	Ala	Ile	Asp	Gly	Glu	Arg	Ser	Ile	Glu
				165					170					175	
Glu	Ile	Val	Gly	Glu	Met	Gln	Glu	Tyr	Ile	Leu	Ser	Phe	Gly	Asn	
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...717
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGT	TAC	CCC	CCC	CCC	CCC	AAT	CCC	ACA	CAA	GAA	ACG	CAA	CAA	GAT	TTT	48
Ser	Tyr	Pro	Pro	Pro	Pro	Asn	Pro	Thr	Gln	Glu	Thr	Gln	Gln	Asp	Phe	
1				5					10					15		
ATT	ATT	GAA	GCA	CAA	CAA	GAT	TTG	ATT	ATT	GAA	ACG	CAA	CAA	GAC	CCC	96
Ile	Ile	Glu	Ala	Gln	Gln	Asp	Leu	Ile	Ile	Glu	Thr	Gln	Gln	Asp	Pro	
			20					25						30		
AAA	GAA	CTA	CCT	GAG	TCT	TGC	AAA	ATA	ACG	CCC	CAA	AAA	ATC	TCT	TTT	144
Lys	Glu	Leu	Pro	Glu	Ser	Cys	Lys	Ile	Thr	Pro	Gln	Lys	Ile	Ser	Phe	
			35				40						45			
AAC	CAA	GTG	GTT	TTT	AAA	AAA	ATT	AAA	AGA	AAA	CTC	AAC	CGC	TTC	ATT	192
Asn	Gln	Val	Val	Phe	Lys	Lys	Ile	Lys	Arg	Lys	Leu	Asn	Arg	Phe	Ile	
			50			55					60					
GGA	AGC	ATT	TTA	GCT	CGG	ACA	GAA	GTG	TAT	AAG	AAT	CTC	GTG	GCA	AAA	240
Gly	Ser	Ile	Leu	Ala	Arg	Thr	Glu	Val	Tyr	Lys	Asn	Leu	Val	Ala	Lys	
65					70					75					80	
TAC	GAT	GAA	CTC	ACA	GGA	AAA	TAC	GAA	TCA	TTA	TTG	GCA	AAA	GAG	GCA	288
Tyr	Asp	Glu	Leu	Thr	Gly	Lys	Tyr	Glu	Ser	Leu	Leu	Ala	Lys	Glu	Ala	
				85					90					95		
AAC	ATC	AAA	GAG	ACC	TTT	TGG	GAA	AGG	CGT	GCT	GAT	AGC	GAA	AAA	GAA	336
Asn	Ile	Lys	Glu	Thr	Phe	Trp	Glu	Arg	Arg	Ala	Asp	Ser	Glu	Lys	Glu	
				100				105						110		
GCC	TTT	TTT	TTA	GAG	CAT	TTT	TAC	CTC	ACT	AGC	GTG	TAT	GTG	GCT	TCT	384
Ala	Phe	Phe	Leu	Glu	His	Phe	Tyr	Leu	Thr	Ser	Val	Tyr	Val	Ala	Ser	
			115				120						125			
ACA	GCA	GGA	TAC	TAT	ATC	ACG	CCT	AAG	GGC	GCT	AAA	ACC	TTT	ATA	GAA	432
Thr	Ala	Gly	Tyr	Tyr	Ile	Thr	Pro	Lys	Gly	Ala	Lys	Thr	Phe	Ile	Glu	
			130				135					140				
GCC	ACG	GAG	CGT	TTT	AAA	ATC	ATA	GAG	CCG	GTG	GAT	ATG	TTC	ATA	AAC	480
Ala	Thr	Glu	Arg	Phe	Lys	Ile	Ile	Glu	Pro	Val	Asp	Met	Phe	Ile	Asn	
145					150					155					160	
AAC	CCC	ACT	TAC	CAT	GAT	GTG	GCT	AAT	TTT	ACC	TAT	TTG	CCT	TGC	CCT	528
Asn	Pro	Thr	Tyr	His	Asp	Val	Ala	Asn	Phe	Thr	Tyr	Leu	Pro	Cys	Pro	
				165					170					175		
GTT	TCT	TTA	AAC	AAG	CAT	GCT	TTC	AAT	AGC	ACC	ATT	CAA	AAT	GCA	AAA	576
Val	Ser	Leu	Asn	Lys	His	Ala	Phe	Asn	Ser	Thr	Ile	Gln	Asn	Ala	Lys	
			180					185					190			
AAG	CCT	GAC	ATT	TCA	TTA	AAA	CCC	CCT	AGA	AAA	TCC	TAT	TTT	GAT	AAT	624
Lys	Pro	Asp	Ile	Ser	Leu	Lys	Pro	Pro	Arg	Lys	Ser	Tyr	Phe	Asp	Asn	
			195				200						205			

CTT TTT TAT GAT CAA TTA AAC ACT AGA AAG TGC TTA AAA GCC TTT CAC 672
 Leu Phe Tyr Asp Gln Leu Asn Thr Arg Lys Cys Leu Lys Ala Phe His
 210 215 220

AAA TAC AGC AGA CGA TAC GCT CCT TTA AAA ACC CCT AAA GAG GTT TAAAA 722
 Lys Tyr Ser Arg Arg Tyr Ala Pro Leu Lys Thr Pro Lys Glu Val
 225 230 235

AGAGCGGGCT TTATGTTAGA ATAAGTCTTT TTATTCAAAG GAGATTGCAA TGAAT 777

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Tyr Pro Pro Pro Pro Asn Pro Thr Gln Glu Thr Gln Gln Asp Phe
 1 5 10 15
 Ile Ile Glu Ala Gln Gln Asp Leu Ile Ile Glu Thr Gln Gln Asp Pro
 20 25 30
 Lys Glu Leu Pro Glu Ser Cys Lys Ile Thr Pro Gln Lys Ile Ser Phe
 35 40 45
 Asn Gln Val Val Phe Lys Lys Ile Lys Arg Lys Leu Asn Arg Phe Ile
 50 55 60
 Gly Ser Ile Leu Ala Arg Thr Glu Val Tyr Lys Asn Leu Val Ala Lys
 65 70 75 80
 Tyr Asp Glu Leu Thr Gly Lys Tyr Glu Ser Leu Leu Ala Lys Glu Ala
 85 90 95
 Asn Ile Lys Glu Thr Phe Trp Glu Arg Arg Ala Asp Ser Glu Lys Glu
 100 105 110
 Ala Phe Phe Leu Glu His Phe Tyr Leu Thr Ser Val Tyr Val Ala Ser
 115 120 125
 Thr Ala Gly Tyr Tyr Ile Thr Pro Lys Gly Ala Lys Thr Phe Ile Glu
 130 135 140
 Ala Thr Glu Arg Phe Lys Ile Ile Glu Pro Val Asp Met Phe Ile Asn
 145 150 155 160
 Asn Pro Thr Tyr His Asp Val Ala Asn Phe Thr Tyr Leu Pro Cys Pro
 165 170 175
 Val Ser Leu Asn Lys His Ala Phe Asn Ser Thr Ile Gln Asn Ala Lys
 180 185 190
 Lys Pro Asp Ile Ser Leu Lys Pro Pro Arg Lys Ser Tyr Phe Asp Asn
 195 200 205
 Leu Phe Tyr Asp Gln Leu Asn Thr Arg Lys Cys Leu Lys Ala Phe His
 210 215 220
 Lys Tyr Ser Arg Arg Tyr Ala Pro Leu Lys Thr Pro Lys Glu Val
 225 230 235

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 50...1252
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGTGGAAAA	TTTAGCTAAA	GAAAGAGAAA	AAAGTTTAAA	GGATTAGGC	ATG	ATC	AAT	58								
					Met	Ile	Asn									
					1											
AAG	TTT	AAA	AAT	TTT	GTG	AGC	AAC	TAC	CAG	CAA	TCT	AAC	CAC	TAT	AAA	106
Lys	Phe	Lys	Asn	Phe	Val	Ser	Asn	Tyr	Gln	Gln	Ser	Asn	His	Tyr	Lys	
5						10					15					
GAG	CCT	TTA	GGT	TTT	GGC	ATT	GCC	AGA	GTG	GAT	ATT	GCC	CCT	ATT	TCC	154
Glu	Pro	Leu	Gly	Phe	Gly	Ile	Ala	Arg	Val	Asp	Ile	Ala	Pro	Ile	Ser	
20					25					30					35	
AAA	AAG	ATT	TTA	TGC	GCC	ACT	TAC	CCT	GTT	TTG	AAT	TGG	AAA	GAT	GAA	202
Lys	Lys	Ile	Leu	Cys	Ala	Thr	Tyr	Pro	Val	Leu	Asn	Trp	Lys	Asp	Glu	
				40					45					50		
AAT	TTA	GGC	TCT	TAT	GCG	GTG	TTT	TGC	AAC	TCG	CTT	TCA	AAA	GAA	AAA	250
Asn	Leu	Gly	Ser	Tyr	Ala	Val	Phe	Cys	Asn	Ser	Leu	Ser	Lys	Glu	Lys	
			55					60					65			
ATC	CTA	AAA	GAG	AGC	GCG	AGC	GAG	CGC	GTT	ATT	GAG	ATT	GAT	GAA	AGT	298
Ile	Leu	Lys	Glu	Ser	Ala	Ser	Glu	Arg	Val	Ile	Glu	Ile	Asp	Glu	Ser	
		70					75					80				
TTT	GTG	TTA	AAA	GCG	TTG	GAT	TTT	TAT	ACG	CCC	TTT	TTG	AAT	GAA	GCC	346
Phe	Val	Leu	Lys	Ala	Leu	Asp	Phe	Tyr	Thr	Pro	Phe	Leu	Asn	Glu	Ala	
85						90					95					
TAT	TCT	AAT	AAA	ATG	GCT	CAT	AAA	AAC	ATC	CAA	GTG	GTT	TTA	GAG	CTT	394
Tyr	Ser	Asn	Lys	Met	Ala	His	Lys	Asn	Ile	Gln	Val	Val	Leu	Glu	Leu	
100					105					110				115		
TTA	AAG	GCT	TTA	GAA	GAA	AAT	CGT	TTG	AAA	AAT	AGC	GAT	GGG	GAG	TCT	442
Leu	Lys	Ala	Leu	Glu	Glu	Asn	Arg	Leu	Lys	Asn	Ser	Asp	Gly	Glu	Ser	
				120				125						130		
CTT	TAT	CGC	TTG	GTG	ATC	TTG	TAT	GAA	GAT	AAG	CCT	TGC	GAG	AGC	GTG	490
Leu	Tyr	Arg	Leu	Val	Ile	Leu	Tyr	Glu	Asp	Lys	Pro	Cys	Glu	Ser	Val	
			135					140					145			
GAG	AGC	GCG	TAT	ATG	AAA	CTT	TTA	GCG	CTC	TCT	TTA	GGT	AAA	GCC	CCT	538
Glu	Ser	Ala	Tyr	Met	Lys	Leu	Leu	Ala	Leu	Ser	Leu	Gly	Lys	Ala	Pro	
		150				155						160				
TTG	AGG	AGT	TTG	AAT	TTA	GAG	GGT	ATT	TTT	AAC	CAG	CTT	TCT	AAT	GCG	586

Leu 165	Arg	Ser	Leu	Asn	Leu	Glu 170	Gly	Ile	Phe	Asn	Gln 175	Leu	Ser	Asn	Ala	
GCC Ala 180	TGG Trp	AGC Ser	GGT Gly	AAC Asn	AAG Lys 185	CCC Pro	TAT Tyr	GAA Glu	TTA Leu	GAA Glu 190	TGG Trp	CTT Leu	AGA Arg	ATG Met	AAC Asn 195	634
GAA Glu	GTG Val	GCT Ala	TTA Leu	AAA Lys 200	ATG Met	CGA Arg	GAC Asp	CAT His	TTC Phe 205	CCT Pro	AGC Ser	ATT Ile	GAT Asp	TTC Phe 210	ATA Ile	682
GAT Asp	AAA Lys	TTC Phe	CCA Pro 215	CGC Arg	TAT Tyr	TTG Leu	ATG Met	CAA Gln 220	TTA Leu	ATC Ile	CCT Pro	GAG Glu	TTT Phe 225	GAT Asp	AAT Asn	730
ATC Ile	CGC Arg	TTA Leu 230	TTG Leu	GAT Asp	AGC Ser	TCA Ser	AAA Lys 235	ACG Thr	CGC Arg	TTT Phe	GGG Gly 240	GCG Ala	TAT Tyr	TTA Leu	GGG Gly	778
ACT Thr	GGA Gly 245	GGT Gly	TAT Tyr	ACC Thr	CAA Gln	ATG Met 250	CCT Pro	GGG Gly	GCT Ala	AGT Ser	TAT Tyr 255	GTG Val	AAT Asn	TTT Phe	AAC Asn	826
GCA Ala 260	GGG Gly	GCT Ala	ATG Met	GGA Gly 265	GTG Val	TGC Cys	ATG Met	AAT Asn	GAG Glu	GGG Gly 270	CGT Arg	ATT Ile	TCT Ser	TCA Ser	TCG Ser 275	874
GTG Val	GTG Val	GTT Val	GGA Gly	GCA Ala 280	GGC Gly	ACT Thr	GAT Asp	ATT Ile	GGT Gly 285	GGG Gly	GGA Gly	GCG Ala	AGC Ser	GTG Val 290	TTA Leu	922
GGC Gly	GTT Val	TTA Leu	AGT Ser 295	GGA Gly	GGG Gly	AAT Asn	AAC Asn	AAC Asn 300	CCC Pro	ATT Ile	AGC Ser	ATC Ile	GGG Gly 305	AAA Lys	AAT Asn	970
TGT Cys	TTG Leu	CTA Leu 310	GGG Gly	GCT Ala	AAT Asn	AGC Ser	GTT Val 315	ACT Thr	GGA Gly	ATT Ile	AGT Ser	CTA Leu 320	GGC Gly	GAT Asp	GGC Gly	1018
TGT Cys	ATC Ile 325	GTG Val	GAT Asp	GCA Ala	GGC Gly	GTT Val 330	GCG Ala	ATA Ile	CTA Leu	GCC Ala	GGG Gly 335	AGC Ser	GTG Val	ATA Ile	GAA Glu	1066
ATT Ile 340	GAA Glu	GAA Glu	AAT Asn	GAG Glu 345	TTT Phe	AAA Lys	AAG Lys	CTT Leu	TTA Leu	GAA Glu 350	GTG Val	AAT Asn	AGC Ser	GCT Ala	TTA Leu 355	1114
GAA Glu	AAA Lys	CAT His	GCC Ala	AAC Asn 360	AAC Asn	CTT Leu	TAC Tyr	AAA Lys	GGC Gly 365	AAA Lys	GAA Glu	CTT Leu	TCC Ser	GGA Gly 370	AAA Lys	1162
AAT Asn	GGC Gly	GTG Val	CAT His 375	TTT Phe	CGT Arg	TCC Ser	AAT Asn	AGT Ser 380	CAG Gln	AAT Asn	GGC Gly	AAG Lys	CTG Leu 385	ATT Ile	GCT Ala	1210
TTT Phe	AGG Arg	AGC Ser 390	GTG Val	AAA Lys	AAA Lys	ATT Ile 395	GAG Glu	TTG Leu	AAT Asn	CAA Gln	AAC Asn 400	CTG Leu	CAT His	TAAGGATTA		1261

AAAGAATGCT CAAAAAAGT TTGTTATGTC TTGTTTTTTT AGTCTTACAG CTTAGCGGCG 1321
CTGAAGAAAA CAATCAAGCC CCAAAAAAC 1350

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Ile	Asn	Lys	Phe	Lys	Asn	Phe	Val	Ser	Asn	Tyr	Gln	Gln	Ser	Asn	1	5	10	15
His	Tyr	Lys	Glu	Pro	Leu	Gly	Phe	Gly	Ile	Ala	Arg	Val	Asp	Ile	Ala	20	25	30	
Pro	Ile	Ser	Lys	Lys	Ile	Leu	Cys	Ala	Thr	Tyr	Pro	Val	Leu	Asn	Trp	35	40	45	
Lys	Asp	Glu	Asn	Leu	Gly	Ser	Tyr	Ala	Val	Phe	Cys	Asn	Ser	Leu	Ser	50	55	60	
Lys	Glu	Lys	Ile	Leu	Lys	Glu	Ser	Ala	Ser	Glu	Arg	Val	Ile	Glu	Ile	65	70	75	80
Asp	Glu	Ser	Phe	Val	Leu	Lys	Ala	Leu	Asp	Phe	Tyr	Thr	Pro	Phe	Leu	85	90	95	
Asn	Glu	Ala	Tyr	Ser	Asn	Lys	Met	Ala	His	Lys	Asn	Ile	Gln	Val	Val	100	105	110	
Leu	Glu	Leu	Leu	Lys	Ala	Leu	Glu	Glu	Asn	Arg	Leu	Lys	Asn	Ser	Asp	115	120	125	
Gly	Glu	Ser	Leu	Tyr	Arg	Leu	Val	Ile	Leu	Tyr	Glu	Asp	Lys	Pro	Cys	130	135	140	
Glu	Ser	Val	Glu	Ser	Ala	Tyr	Met	Lys	Leu	Leu	Ala	Leu	Ser	Leu	Gly	145	150	155	160
Lys	Ala	Pro	Leu	Arg	Ser	Leu	Asn	Leu	Glu	Gly	Ile	Phe	Asn	Gln	Leu	165	170	175	
Ser	Asn	Ala	Ala	Trp	Ser	Gly	Asn	Lys	Pro	Tyr	Glu	Leu	Glu	Trp	Leu	180	185	190	
Arg	Met	Asn	Glu	Val	Ala	Leu	Lys	Met	Arg	Asp	His	Phe	Pro	Ser	Ile	195	200	205	
Asp	Phe	Ile	Asp	Lys	Phe	Pro	Arg	Tyr	Leu	Met	Gln	Leu	Ile	Pro	Glu	210	215	220	
Phe	Asp	Asn	Ile	Arg	Leu	Leu	Asp	Ser	Ser	Lys	Thr	Arg	Phe	Gly	Ala	225	230	235	240
Tyr	Leu	Gly	Thr	Gly	Gly	Tyr	Thr	Gln	Met	Pro	Gly	Ala	Ser	Tyr	Val	245	250	255	
Asn	Phe	Asn	Ala	Gly	Ala	Met	Gly	Val	Cys	Met	Asn	Glu	Gly	Arg	Ile	260	265	270	
Ser	Ser	Ser	Val	Val	Val	Gly	Ala	Gly	Thr	Asp	Ile	Gly	Gly	Gly	Ala	275	280	285	
Ser	Val	Leu	Gly	Val	Leu	Ser	Gly	Gly	Asn	Asn	Asn	Pro	Ile	Ser	Ile	290	295	300	
Gly	Lys	Asn	Cys	Leu	Leu	Gly	Ala	Asn	Ser	Val	Thr	Gly	Ile	Ser	Leu	305	310	315	320
Gly	Asp	Gly	Cys	Ile	Val	Asp	Ala	Gly	Val	Ala	Ile	Leu	Ala	Gly	Ser	325	330	335	
Val	Ile	Glu	Ile	Glu	Glu	Asn	Glu	Phe	Lys	Lys	Leu	Leu	Glu	Val	Asn				

100	105	110	115	
ACC ATC ATG GTA GCG AGC GGT TTT CAA GCT GAA AAA AGC TTG CAT GAC				442
Thr Ile Met Val Ala Ser Gly Phe Gln Ala Glu Lys Ser Leu His Asp	120	125	130	
GCC ATA GAA AAG CAT AAA AAC AAT TAC ATT TTA ATG GTA GAA GGG GGT				490
Ala Ile Glu Lys His Lys Asn Asn Tyr Ile Leu Met Val Glu Gly Gly	135	140	145	
ATC CCC CAA GGC ACG GAA TAC TTC CTC ACT CAA GGC CCA AAC GCT GAA				538
Ile Pro Gln Gly Thr Glu Tyr Phe Leu Thr Gln Gly Pro Asn Ala Glu	150	155	160	
ACG GGA GCT GAA GAG TGT AGG AAA GCC GCT CAA TAC GCA GCC GCT ATT				586
Thr Gly Ala Glu Glu Cys Arg Lys Ala Ala Gln Tyr Ala Ala Ala Ile	165	170	175	
TTT GCC ATA GGC ACA TGC TCA AGT TTT GGG GGC GTT CAA GCG GCT TAC				634
Phe Ala Ile Gly Thr Cys Ser Ser Phe Gly Gly Val Gln Ala Ala Tyr	180	185	190	195
CCT AAC CCC TCT AAC GCG CAA CCC TTG CAT AAA ATC ATT GAT AAA CCC				682
Pro Asn Pro Ser Asn Ala Gln Pro Leu His Lys Ile Ile Asp Lys Pro	200	205	210	
GTG ATC AAT GTT CCT GGT TGC CCG CCT AGT GAA AAA AAT ATC GTG GGT				730
Val Ile Asn Val Pro Gly Cys Pro Pro Ser Glu Lys Asn Ile Val Gly	215	220	225	
AAT GTG CTT TAT TAC TTG ATG TTT GGG GCT CTC CCT AAA TTG GAT GCG				778
Asn Val Leu Tyr Tyr Leu Met Phe Gly Ala Leu Pro Lys Leu Asp Ala	230	235	240	
TAT AAC CGC CCC TCT TGG GCT TAT GGG AAC AGG ATC CAT GAT TTG TGC				826
Tyr Asn Arg Pro Ser Trp Ala Tyr Gly Asn Arg Ile His Asp Leu Cys	245	250	255	
GAA AGG AGA GGG CAT TTT GAT GCG GGC GAA TTT GTG GAG CAT TTT GGC				874
Glu Arg Arg Gly His Phe Asp Ala Gly Glu Phe Val Glu His Phe Gly	260	265	270	275
GAT GAA AAC GCT AAA AGG GGC TTT TGT TTG TAT AAA ATG GGC TGT AAA				922
Asp Glu Asn Ala Lys Arg Gly Phe Cys Leu Tyr Lys Met Gly Cys Lys	280	285	290	
GGG CCT TAC ACT TTC AAC AAT TGC TCC AAA CTC CGC TTC AAT TCA CAC				970
Gly Pro Tyr Thr Phe Asn Asn Cys Ser Lys Leu Arg Phe Asn Ser His	295	300	305	
ACC TCT TGG CCC ATA GGT GCA GGG CAT GGG TGT ATA GGG TGT TCT GAG				1018
Thr Ser Trp Pro Ile Gly Ala Gly His Gly Cys Ile Gly Cys Ser Glu	310	315	320	
CCT AAT TTT TGG GAT ACG ATG AGT CCT TTT GAA GAG CCT TTA GCG AAT				1066
Pro Asn Phe Trp Asp Thr Met Ser Pro Phe Glu Glu Pro Leu Ala Asn	325	330	335	

CGT TCC ATT AAA ACC GCT TTT GAC GGA TTA GGG GCT GAT AAA GTA GCG 1114
 Arg Ser Ile Lys Thr Ala Phe Asp Gly Leu Gly Ala Asp Lys Val Ala
 340 345 350 355

GAT AAA GTA GGC ACG ACT TTG CTG AGC GCA ACC GCT ATT GGC ATT GTT 1162
 Asp Lys Val Gly Thr Thr Leu Leu Ser Ala Thr Ala Ile Gly Ile Val
 360 365 370

GCG CAT GCG CTC CTT TCT AAA GCG ATC AAA AAC AAA GAG TAAGGGATTA AC 1213
 Ala His Ala Leu Leu Ser Lys Ala Ile Lys Asn Lys Glu
 375 380

ATGTCAAAAA AAATCGTAGT CGATCCTATC ACTAGGATTG AGGGGCATTT AAGGATTGAA 1273
 GTGATCGTAG ATGATGATAA CGTGATCACT G 1304

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Phe Tyr Asp Glu Lys Lys Thr Tyr Gln Lys Ile Glu Glu Arg Leu
 1 5 10 15
 Asp Ile Val Arg Ser Phe Asn Ala His Asn Glu His Lys Asn Leu Gln
 20 25 30
 Asp Glu Phe Lys Gly Ala Gly Ile Ser Arg Arg Asp Leu Leu Lys Trp
 35 40 45
 Ala Gly Met Met Ser Thr Ala Leu Ala Leu Pro Ala Ser Phe Ala Pro
 50 55 60
 Leu Thr Leu Lys Ala Val Glu Val Ala Asn Arg Leu Pro Val Ile Trp
 65 70 75 80
 Leu His Met Ala Glu Cys Thr Gly Cys Ser Glu Ser Leu Leu Arg Ser
 85 90 95
 Ala Asp Pro Thr Ile Asp Ser Ile Ile Phe Asp Tyr Ile Asn Leu Glu
 100 105 110
 Tyr His Glu Thr Ile Met Val Ala Ser Gly Phe Gln Ala Glu Lys Ser
 115 120 125
 Leu His Asp Ala Ile Glu Lys His Lys Asn Asn Tyr Ile Leu Met Val
 130 135 140
 Glu Gly Gly Ile Pro Gln Gly Thr Glu Tyr Phe Leu Thr Gln Gly Pro
 145 150 155 160
 Asn Ala Glu Thr Gly Ala Glu Glu Cys Arg Lys Ala Ala Gln Tyr Ala
 165 170 175
 Ala Ala Ile Phe Ala Ile Gly Thr Cys Ser Ser Phe Gly Gly Val Gln
 180 185 190
 Ala Ala Tyr Pro Asn Pro Ser Asn Ala Gln Pro Leu His Lys Ile Ile
 195 200 205
 Asp Lys Pro Val Ile Asn Val Pro Gly Cys Pro Pro Ser Glu Lys Asn
 210 215 220
 Ile Val Gly Asn Val Leu Tyr Tyr Leu Met Phe Gly Ala Leu Pro Lys
 225 230 235 240
 Leu Asp Ala Tyr Asn Arg Pro Ser Trp Ala Tyr Gly Asn Arg Ile His

(A) LENGTH: 488 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ala	Cys	Asn	Leu	Gln	Ala	Arg	Phe	Tyr	Ser	Val	Tyr	Lys	Asp	Asn
1				5					10					15	
Thr	Thr	Ser	Phe	Tyr	Leu	Gln	Ala	Ser	Ala	Glu	Thr	Thr	Leu	Glu	Phe
		20						25					30		
Ala	Gln	Lys	Leu	Ser	Glu	Ile	Leu	Pro	Phe	Ser	Leu	Asp	Phe	Ser	Phe
		35					40					45			
Leu	Ser	Leu	Lys	Glu	Ile	Thr	Glu	Pro	Leu	Asp	Glu	Asn	Leu	Phe	Gln
	50					55					60				
Thr	Ala	Ser	Leu	Ser	Lys	Pro	Leu	Phe	Met	Asn	Ala	Lys	Glu	His	Gln
65					70					75				80	
Asp	Phe	Leu	Asp	Lys	Asn	Ser	Ser	Leu	Tyr	Ala	Asp	Thr	Leu	Gly	Leu
			85						90					95	
Ile	Lys	Asn	Thr	Ala	Phe	Lys	Gly	Asp	Ile	Ile	His	Ser	Pro	Lys	Glu
		100						105					110		
Leu	Ile	Asp	Cys	Leu	Thr	Gln	Leu	Lys	Gly	Met	Leu	Lys	Thr	Gln	Asp
		115					120					125			
Phe	Ile	Pro	Ile	Phe	Thr	Ser	Arg	Glu	Ala	Leu	Ser	Leu	Ser	Leu	Lys
	130					135					140				
Asn	Pro	Ser	Pro	Ser	Val	Ile	Phe	Ser	Asp	Leu	Ser	Ser	Val	Leu	Ser
145					150					155				160	
Cys	Thr	Lys	Leu	Pro	Leu	Glu	Asp	Ala	Lys	Tyr	Leu	Ala	Ser	Leu	Glu
			165						170					175	
Lys	Pro	Ser	Ile	Lys	Ala	Pro	Leu	Lys	Ser	Val	Phe	Lys	Asp	Thr	Phe
			180					185					190		
Lys	Asn	Asp	Glu	Ile	Ile	Ala	Gln	Leu	Pro	Tyr	Asp	Pro	Ile	Leu	Asn
		195					200					205			
Leu	Leu	Cys	His	Ile	Leu	Gln	Asp	Glu	Gly	Ile	Glu	Phe	Val	Phe	Met
	210					215					220				
His	Glu	Ser	Arg	Ser	Cys	Glu	Ala	Leu	Leu	Tyr	Tyr	Glu	Ala	Leu	Phe
225					230					235				240	
Lys	Thr	Pro	Lys	Arg	Leu	Ile	Thr	Pro	Thr	Lys	Lys	Phe	Val	Leu	Glu
			245						250					255	
Asn	Asn	Phe	Ser	Thr	Phe	Pro	Phe	Lys	Asp	Glu	Leu	Glu	Phe	Leu	Ser
		260						265					270		
Ala	Thr	Pro	Asn	Ser	Ile	Val	Leu	Tyr	Leu	Ser	Phe	Lys	Arg	Pro	Thr
		275					280					285			
Arg	Leu	Leu	Leu	His	Ala	Asn	Gly	Ser	Leu	Lys	Thr	Leu	Leu	Ser	Val
	290					295					300				
Ser	Phe	Asp	Phe	Asn	Lys	Met	Phe	Asn	Ala	Leu	Lys	Gln	Asp	Glu	Lys
305					310					315				320	
Ala	Ser	Arg	Met	Leu	Gln	Asn	Tyr	Ala	Thr	Lys	Phe	Pro	Asp	Phe	Tyr
			325						330					335	
Ala	Arg	Ile	Val	Glu	Leu	Ser	Lys	Tyr	Asp	Leu	Gly	Gly	Ala	Asn	Leu
		340						345					350		
Leu	Asp	Phe	Phe	Cys	Ile	Leu	Gly	Phe	Val	Leu	Gly	Tyr	Ser	Glu	Asp
	355					360					365				
Phe	Cys	Thr	Gln	Ser	Val	Ile	Pro	Leu	Ala	Lys	Glu	Cys	Leu	Arg	Pro
370					375						380				
Lys	Gly	Pro	Arg	Ile	Asp	Tyr	Lys	Ile	Leu	Lys	Asp	Asn	Ser	Leu	Lys

385		390		395		400									
Met	Ala	Leu	Asn	Phe	Ser	Lys	Ile	Met	His	Ser	Ala	Met	Ser	Phe	Arg
			405						410					415	
Leu	Ala	Gly	Val	Glu	Asn	Glu	Ile	Leu	Ser	Leu	Gly	Ile	Leu	Asp	Ser
		420						425					430		
Leu	Ala	Glu	Phe	Leu	Gly	Asn	Phe	Ile	Trp	Asp	Asn	Ala	Gln	Asn	Phe
		435					440					445			
Ser	Val	Gln	Glu	Val	Thr	Ile	Ala	Gly	Asp	Phe	Phe	Gly	Glu	Lys	Val
	450					455					460				
Phe	Leu	Asp	Leu	Phe	Val	Arg	Tyr	Phe	Pro	Lys	Thr	Leu	Ala	Leu	Lys
465					470					475				480	
Thr	His	Ala	Phe	Leu	Asp	Tyr	Glu								
			485												

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 17...694
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTTTTAAGGA	ATTTTG	ATG	GAA	CAA	AAA	ATT	TGC	GTG	ATC	GGT	TTT	AGC	GGC	52		
	Met	Glu	Gln	Lys	Ile	Cys	Val	Ile	Gly	Phe	Ser	Gly				
	1				5						10					
GGG	CAA	GAC	AGC	ACC	ACT	TTA	GCC	GTG	TGG	GCG	AAA	AAG	CGT	TTT	AAA	100
Gly	Gln	Asp	Ser	Thr	Thr	Leu	Ala	Val	Trp	Ala	Lys	Lys	Arg	Phe	Lys	
	15					20					25					
AAA	GTC	TGT	TTA	GTG	GGG	TTT	GAT	TAT	GCG	CAA	AAA	CAC	TCT	GTG	GAA	148
Lys	Val	Cys	Leu	Val	Gly	Phe	Asp	Tyr	Ala	Gln	Lys	His	Ser	Val	Glu	
	30				35				40							
TTA	GAA	TGC	GCT	CAA	AAA	ATC	GCT	TCT	CTT	TTA	CAA	CTC	CCT	TAT	GAA	196
Leu	Glu	Cys	Ala	Gln	Lys	Ile	Ala	Ser	Leu	Leu	Gln	Leu	Pro	Tyr	Glu	
45				50				55						60		
ATC	ATC	CCA	TTA	GAT	TTT	TTA	GAA	AAT	ATC	ACC	CGC	TCT	GCG	CTT	TTT	244
Ile	Ile	Pro	Leu	Asp	Phe	Leu	Glu	Asn	Ile	Thr	Arg	Ser	Ala	Leu	Phe	
			65					70					75			
AAA	AAC	TCT	AAC	GAT	TTA	ATA	GGG	CAT	TCG	CAT	GCG	CAA	AAT	AAA	GAT	292
Lys	Asn	Ser	Asn	Asp	Leu	Ile	Gly	His	Ser	His	Ala	Gln	Asn	Lys	Asp	
			80				85					90				
TTA	CCC	AAT	TCT	TTT	GTG	CCT	AAT	CGT	AAC	GCT	ATT	TTT	ATC	ACC	CTT	340
Leu	Pro	Asn	Ser	Phe	Val	Pro	Asn	Arg	Asn	Ala	Ile	Phe	Ile	Thr	Leu	

				85					90					95			
Phe	Val	Pro	Asn	Arg	Asn	Ala	Ile	Phe	Ile	Thr	Leu	Leu	His	Ser	Tyr		
			100					105					110				
Ala	Gln	Lys	Leu	Gly	Ala	Ser	Asn	Ile	Ala	Leu	Gly	Val	Ser	Gln	Ala		
		115					120					125					
Asp	Phe	Ser	Gly	Tyr	Pro	Asp	Cys	Lys	Glu	Asp	Phe	Ile	Lys	Ser	Ile		
	130					135					140						
Glu	His	Ala	Leu	Asn	Leu	Gly	Ser	Asn	Thr	Ala	Ile	Lys	Ile	Leu	Thr		
145					150					155					160		
Pro	Leu	Met	Phe	Leu	Asn	Lys	Ala	Gln	Glu	Phe	Gln	Met	Ala	Lys	Asp		
			165					170						175			
Leu	Gly	Val	Leu	Asp	Leu	Val	Ile	Lys	Glu	Thr	His	Thr	Cys	Tyr	Gln		
		180					185						190				
Gly	Glu	Arg	Lys	Ile	Leu	His	Ala	Tyr	Gly	Tyr	Gly	Cys	Asp	Lys	Cys		
	195					200					205						
Pro	Ala	Cys	Gln	Leu	Arg	Lys	Lys	Gly	Phe	Glu	Glu	Phe	Gln	Ala	Asn		
	210					215					220						
Lys	Lys																
225																	

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...1155
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCCTCTCATG AGCTTTACTT GGTAGGGGGG TGC GTGCGCG ATTATTTA ATG GGC ATT	57
Met Gly Ile	
1	
ACC CCA AAA GAT TAC GAT TTA ACC TCA AAC GCT TTA GTC AAT GAA AGC	105
Thr Pro Lys Asp Tyr Asp Leu Thr Ser Asn Ala Leu Val Asn Glu Ser	
5 10 15	
AAA GAG CTT CTT TTA AAG CGC CAT TTT AGG GTG CTA GAA ACC GGT ATC	153
Lys Glu Leu Leu Leu Lys Arg His Phe Arg Val Leu Glu Thr Gly Ile	
20 25 30 35	
AAA CAT GGT ACG ATC ACG GCT CTT AAA AAC CAT CAA AGC TAT GAA ATC	201
Lys His Gly Thr Ile Thr Ala Leu Lys Asn His Gln Ser Tyr Glu Ile	
40 45 50	
ACA ACT TTT AGA ATT GAA AAG GGG CAT ATC AAA CAC CGA AAG CCT AAA	249
Thr Thr Phe Arg Ile Glu Lys Gly His Ile Lys His Arg Lys Pro Lys	
55 60 65	

295	300	305	
CTT AAG GGC GGT GCG CTT CAA AGC TTG GGT TAC CAG CAC CAA AAA ATC			1017
Leu Lys Gly Gly Ala Leu Gln Ser Leu Gly Tyr Gln His Gln Lys Ile			
310	315	320	
GGC GAA ATT TTA AAC GCA TGC TTA GAT TTA GTC ATC GCT AAC CCT AAA			1065
Gly Glu Ile Leu Asn Ala Cys Leu Asp Leu Val Ile Ala Asn Pro Lys			
325	330	335	
AAT AAC GCT TTA GAA TGG CTG ATT GAA TGG GTT AAG GGT CAT TAT TTA			1113
Asn Asn Ala Leu Glu Trp Leu Ile Glu Trp Val Lys Gly His Tyr Leu			
340	345	350	355
CCT AAT GAT ACT ATA AAT CTT TCG CCA ATA GGC AGA AGA AAT TAAAAACAG			1164
Pro Asn Asp Thr Ile Asn Leu Ser Pro Ile Gly Arg Arg Asn			
360	365		
AGAAAACATG ATAACGATGA ATGCGATTCA ATGGCCT			1201

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Gly	Ile	Thr	Pro	Lys	Asp	Tyr	Asp	Leu	Thr	Ser	Asn	Ala	Leu	Val
1				5				10						15	
Asn	Glu	Ser	Lys	Glu	Leu	Leu	Leu	Lys	Arg	His	Phe	Arg	Val	Leu	Glu
			20					25					30		
Thr	Gly	Ile	Lys	His	Gly	Thr	Ile	Thr	Ala	Leu	Lys	Asn	His	Gln	Ser
			35				40					45			
Tyr	Glu	Ile	Thr	Thr	Phe	Arg	Ile	Glu	Lys	Gly	His	Ile	Lys	His	Arg
	50					55					60				
Lys	Pro	Lys	Glu	Leu	Val	Phe	Ser	Val	His	Leu	Thr	Asp	Asp	Leu	Lys
65				70						75				80	
Arg	Arg	Asp	Phe	Ser	Met	Asn	Ala	Ile	Ala	Tyr	Ser	Pro	Thr	Lys	Gly
				85				90						95	
Leu	Ile	Asp	Pro	Phe	Lys	Gly	Gln	Asn	Ala	Ile	Glu	Asn	Gln	Met	Ile
			100					105					110		
Glu	Cys	Val	Gly	Glu	Ala	Arg	Leu	Arg	Phe	Phe	Glu	Asp	Ala	Leu	Arg
		115					120					125			
Ile	Leu	Arg	Ser	Leu	Arg	Phe	Ser	Ala	Thr	Leu	Gly	Phe	Lys	Ile	Ala
	130					135					140				
Pro	Asn	Thr	Lys	Glu	Ala	Val	Phe	Ala	Cys	Lys	Asp	Leu	Leu	Lys	His
145				150						155				160	
Leu	Ser	Lys	Glu	Arg	Leu	Gln	Ser	Glu	Leu	Asn	Lys	Leu	Leu	Met	Gly
				165				170						175	
Lys	Asn	Ala	Tyr	Glu	Val	Ala	Lys	Glu	Tyr	Gln	Glu	Ile	Leu	Glu	Leu
		180						185					190		
Val	Ile	Gln	Glu	Lys	Ile	Glu	Asn	Leu	Gly	Phe	Leu	Lys	Asn	Ala	Pro
		195					200					205			

Phe Asn Leu Glu Leu Arg Leu Leu Gly Phe Phe Lys His Gln Lys Ser
 210 215 220
 Leu Glu Ser Leu Arg Tyr Pro Lys Lys Thr Ile Val Leu Phe Ser Lys
 225 230 235 240
 Ala Lys Glu Cys His Lys Ser Phe Leu Asn Ile His Asn Lys Thr Glu
 245 250 255
 Leu Lys Phe Leu Leu Lys Asn Tyr Asp Leu Glu Pro Phe Asn Leu Ala
 260 265 270
 Leu Asp Phe Tyr Ala Leu Lys Asn Pro Lys His Ala Leu Lys Ile Lys
 275 280 285
 Gly Leu Leu Lys Glu Ile Phe Asp Ser Asn Glu Pro Phe Lys Lys Glu
 290 295 300
 His Leu Ala Leu Lys Gly Gly Ala Leu Gln Ser Leu Gly Tyr Gln His
 305 310 315 320
 Gln Lys Ile Gly Glu Ile Leu Asn Ala Cys Leu Asp Leu Val Ile Ala
 325 330 335
 Asn Pro Lys Asn Asn Ala Leu Glu Trp Leu Ile Glu Trp Val Lys Gly
 340 345 350
 His Tyr Leu Pro Asn Asp Thr Ile Asn Leu Ser Pro Ile Gly Arg Arg
 355 360 365
 Asn

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...340
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TTTTCCCCTA TATCCAAAGC CATCATCAAG AAGTTTTAAG GCTCAAAGC ATG ATT TTT	58
Met Ile Phe	
1	
TCC ACT CTT ATT AAT GCG ATA GCG GTG ATT TTA AGC TCG CTC ATT ACG	106
Ser Thr Leu Ile Asn Ala Ile Ala Val Ile Leu Ser Ser Leu Ile Thr	
5 10 15	
ATT TAT ATG TGG ATA GTA ATC ATT TAT TCG CTT ATC AGT TTC GTG CAG	154
Ile Tyr Met Trp Ile Val Ile Ile Tyr Ser Leu Ile Ser Phe Val Gln	
20 25 30 35	
CCT AAC CCC AAT AAC CCC ATC ATG CAA ATT CTC GCT CGC TTG TGT GAG	202
Pro Asn Pro Asn Asn Pro Ile Met Gln Ile Leu Ala Arg Leu Cys Glu	
40 45 50	
CCG GTG TTT TAT TTT TTA CGC TCT AGA TTC AAG CTG GTG TTT AAC GGG	250

Pro Val Phe Tyr Phe Leu Arg Ser Arg Phe Lys Leu Val Phe Asn Gly
55 60 65

TTG GAT TTC TCT CCT TTA GTG GTG GTC ATT GTT TTG AAA TTC TTG GAT 298
Leu Asp Phe Ser Pro Leu Val Val Val Ile Val Leu Lys Phe Leu Asp
70 75 80

CTC ACG CTC ATT CAG TGG CTT TTC ATG CTC GCT AAA AAC CTT TAAAGAAAA 349
Leu Thr Leu Ile Gln Trp Leu Phe Met Leu Ala Lys Asn Leu
85 90 95

TCATGCGTTT T 360

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Ile Phe Ser Thr Leu Ile Asn Ala Ile Ala Val Ile Leu Ser Ser
1 5 10 15
Leu Ile Thr Ile Tyr Met Trp Ile Val Ile Ile Tyr Ser Leu Ile Ser
20 25 30
Phe Val Gln Pro Asn Pro Asn Asn Pro Ile Met Gln Ile Leu Ala Arg
35 40 45
Leu Cys Glu Pro Val Phe Tyr Phe Leu Arg Ser Arg Phe Lys Leu Val
50 55 60
Phe Asn Gly Leu Asp Phe Ser Pro Leu Val Val Val Ile Val Leu Lys
65 70 75 80
Phe Leu Asp Leu Thr Leu Ile Gln Trp Leu Phe Met Leu Ala Lys Asn
85 90 95
Leu

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...1701
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

220				225				230								
AAC Asn 235	GCG Ala	CAA Gln	ACC Thr	TTT Phe	TTT Phe 240	ATT Ile	CTA Leu	GGG Gly	ATT Ile	AAT Asn 245	GAA Glu	ATC Ile	TTG Leu	CGC Arg	AAA Lys 250	771
AAA Lys	CCC Pro	TCT Ser	AAA Lys	GCG Ala 255	CTC Leu	AAG Lys	TAT Tyr	TTT Phe	GAA Glu 260	CGA Arg	TCA Ser	GAA Glu	GCG Ala	GTT Val 265	GTC Val	819
AAA Lys	GAC Asp	GAT Asp	GAT Asp 270	TTT Phe	TCA Ser	AAA Lys	GAC Asp	AGA Arg 275	GCG Ala	ATT Ile	TTT Phe	TGG Trp	CAG Gln 280	TAT Tyr	TTA Leu	867
GTT Val	TCT Ser	AAA Lys 285	AAG Lys	AAA Lys	AAA Lys	ACT Thr	TTA Leu 290	GAA Glu	CGC Arg	CTT Leu	TCA Ser	CAA Gln 295	AGC Ser	CCA Pro	GCT Ala	915
TTA Leu 300	AAT Asn	CTC Leu	TAT Tyr	AGT Ser	CTT Leu	TAT Tyr 305	GCG Ala	AGC Ser	CGC Arg	AAA Lys	CTC Leu 310	AAA Lys	ACC Thr	ACG Thr	CCC Pro	963
AGT Ser 315	TAC Tyr	CGC Arg	ATC Ile	ATT Ile	TCA Ser 320	CGC Arg	ATC Ile	CAG Gln	AAT Asn	TTA Leu 325	AGC Ser	CAA Gln	GAA Glu	GAT Asp	CCT Pro 330	1011
CCT Pro	TTT Phe	AAC Asn	ACT Thr	TAT Tyr 335	GAC Asp	CCT Pro	TTT Phe	TCG Ser	TGG Trp 340	CAA Gln	ATT Ile	TTT Phe	AAG Lys	GAA Glu 345	AAA Lys	1059
ACC Thr	TTG Leu	AGT Ser	TTG Leu 350	AAA Lys	GAT Asp	GAG Glu	GGC Gly	GCG Ala 355	TTT Phe	AAT Asn	GCG Ala	ATG Met	CTA Leu 360	AAA Lys	AGC Ser	1107
CTG Leu	TAT Tyr	TAT Tyr 365	GAA Glu	AAA Lys	AGC Ser	GCT Ala	CCT Pro 370	GAA Glu	TTG Leu	ACC Thr	TAT Tyr	CTT Leu 375	TTA Leu	AGC Ser	CAA Gln	1155
CGC Arg 380	AAT Asn	AAA Lys	GAC Asp	AAG Lys	ATT Ile	TAT Tyr 385	TAT Tyr	TAT Tyr	TTA Leu	TCC Ser	CCT Pro 390	TAT Tyr	GAG Glu	GGC Gly	ATT Ile	1203
ATT Ile 395	GAA Glu	TGG Trp	CAA Gln	AAT Asn	ACT Thr 400	GAT Asp	GAA Glu	AAG Lys	GCT Ala	ATG Met 405	GCG Ala	TAT Tyr	GCG Ala	ATC Ile	GCT Ala 410	1251
AGG Arg	CAA Gln	GAA Glu	AGC Ser	TTT Phe 415	TTG Leu	CTC Leu	CCG Pro	GCA Ala	GTC Val 420	ATT Ile	TCG Ser	CGC Arg	TCG Ser	TTC Phe 425	GCT Ala	1299
CTG Leu	GGG Gly	CTT Leu	ATG Met 430	CAA Gln	ATC Ile	ATG Met	CCC Pro	TTT Phe 435	AAT Asn	GTA Val	GGG Gly	CCT Pro	TTC Phe 440	GCT Ala	AAA Lys	1347
AGC Ser	CTT Leu	GGC Gly 445	ATG Met	GAT Asp	AAC Asn	ATT Ile	GAT Asp 450	CTA Leu	AAC Asn	GAC Asp	ATG Met	TTT Phe 455	AAC Asn	CCC Pro	AAC Asn	1395

(A) LENGTH: 770 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 16...738
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TAAAAAGAAG GACAA ATG ATG CCA TTT GAA GCT GTA ATC GGG CTA GAA GTC	51
Met Met Pro Phe Glu Ala Val Ile Gly Leu Glu Val	
1 5 10	
CAT GTC CAA CTC AAC ACC AAA ACC AAA ATC TTT TGC TCT TGC TCT ACA	99
His Val Gln Leu Asn Thr Lys Thr Lys Ile Phe Cys Ser Cys Ser Thr	
15 20 25	
AGC TTT GGA GAA TCC CCT AAT TCT AAC ACC TGC CCT GTG TGT TTG GGT	147
Ser Phe Gly Glu Ser Pro Asn Ser Asn Thr Cys Pro Val Cys Leu Gly	
30 35 40	
TTA CCG GGA GCT TTG CCG GTA TTG AAT AAA GAA GTG GTT AAA AAA GCC	195
Leu Pro Gly Ala Leu Pro Val Leu Asn Lys Glu Val Val Lys Lys Ala	
45 50 55 60	
ATC CAA TTA GGC ACA GCC ATT GAA GCC AAT ATC AAC CAA TAT TCT ATT	243
Ile Gln Leu Gly Thr Ala Ile Glu Ala Asn Ile Asn Gln Tyr Ser Ile	
65 70 75	
TTT GCG AGG AAA AAT TAT TTT TAC CCT GAT TTG CCT AAG GCT TAT CAA	291
Phe Ala Arg Lys Asn Tyr Phe Tyr Pro Asp Leu Pro Lys Ala Tyr Gln	
80 85 90	
ATT TCG CAG TTT GAA GTC CCT ATT GTG AGC GAT GGG AAA TTA GAG ATT	339
Ile Ser Gln Phe Glu Val Pro Ile Val Ser Asp Gly Lys Leu Glu Ile	
95 100 105	
GAC ACT AAA GAG GGT GCA AAA ATC GTG CGT ATT GAA AGG GCC CAC ATG	387
Asp Thr Lys Glu Gly Ala Lys Ile Val Arg Ile Glu Arg Ala His Met	
110 115 120	
GAA GAA GAC GCC GGT AAA AAT ATC CAT GAG GGC AGT TAT TCT TTA GTG	435
Glu Glu Asp Ala Gly Lys Asn Ile His Glu Gly Ser Tyr Ser Leu Val	
125 130 135 140	
GAT TTG AAC CGC GCT TGC ACC CCT TTA TTA GAA ATT GTC AGT AAG CCG	483
Asp Leu Asn Arg Ala Cys Thr Pro Leu Leu Glu Ile Val Ser Lys Pro	
145 150 155	
GAC ATG CGA AAT AGT GAA GAA GCT ATA GCG TAT TTG AAA AAG CTC CAT	531
Asp Met Arg Asn Ser Glu Glu Ala Ile Ala Tyr Leu Lys Lys Leu His	
160 165 170	

GCT ATC GTG CGT TTT ATA GGG ATT TCT GAT GCG AAC ATG CAA GAG GGG	579
Ala Ile Val Arg Phe Ile Gly Ile Ser Asp Ala Asn Met Gln Glu Gly	
175 180 185	
AAT TTC AGG TGC GAT GCG AAC GTG TCC ATT AGA CCC AAA GGC GAT GAA	627
Asn Phe Arg Cys Asp Ala Asn Val Ser Ile Arg Pro Lys Gly Asp Glu	
190 195 200	
AAG CTT TAT ACG AGA GTA GAG ATT AAA AAT CTA AAT AGC TTT AGA TTC	675
Lys Leu Tyr Thr Arg Val Glu Ile Lys Asn Leu Asn Ser Phe Arg Phe	
205 210 215 220	
ATT GCT AAA GCG ATT GAA TAC GAG ATA GAG CGC CAA AGC GCG GAC GTG	723
Ile Ala Lys Ala Ile Glu Tyr Glu Ile Glu Arg Gln Ser Ala Asp Val	
225 230 235	
GGA GAA CGG GCG CTA TAATGAAGAG GTGGTTCAAG AAACGCGCCT TT	770
Gly Glu Arg Ala Leu	
240	

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Met Pro Phe Glu Ala Val Ile Gly Leu Glu Val His Val Gln Leu	
1 5 10 15	
Asn Thr Lys Thr Lys Ile Phe Cys Ser Cys Ser Thr Ser Phe Gly Glu	
20 25 30	
Ser Pro Asn Ser Asn Thr Cys Pro Val Cys Leu Gly Leu Pro Gly Ala	
35 40 45	
Leu Pro Val Leu Asn Lys Glu Val Val Lys Lys Ala Ile Gln Leu Gly	
50 55 60	
Thr Ala Ile Glu Ala Asn Ile Asn Gln Tyr Ser Ile Phe Ala Arg Lys	
65 70 75 80	
Asn Tyr Phe Tyr Pro Asp Leu Pro Lys Ala Tyr Gln Ile Ser Gln Phe	
85 90 95	
Glu Val Pro Ile Val Ser Asp Gly Lys Leu Glu Ile Asp Thr Lys Glu	
100 105 110	
Gly Ala Lys Ile Val Arg Ile Glu Arg Ala His Met Glu Glu Asp Ala	
115 120 125	
Gly Lys Asn Ile His Glu Gly Ser Tyr Ser Leu Val Asp Leu Asn Arg	
130 135 140	
Ala Cys Thr Pro Leu Leu Glu Ile Val Ser Lys Pro Asp Met Arg Asn	
145 150 155 160	
Ser Glu Glu Ala Ile Ala Tyr Leu Lys Lys Leu His Ala Ile Val Arg	
165 170 175	
Phe Ile Gly Ile Ser Asp Ala Asn Met Gln Glu Gly Asn Phe Arg Cys	
180 185 190	
Asp Ala Asn Val Ser Ile Arg Pro Lys Gly Asp Glu Lys Leu Tyr Thr	

	195		200		205
Arg	Val	Glu	Ile	Lys	Asn
	210		215		220
Ile	Glu	Tyr	Glu	Ile	Glu
225			230		235
Leu					

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...444
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATGGGAGTGG ATTGA ATG CAA GAA ATT GAA ATT TTT TGC GAT GGC TCT TCT	51
Met Gln Glu Ile Glu Ile Phe Cys Asp Gly Ser Ser	
1 5 10	
TTA GGC AAT CCC GGG CCA GGC GGT TAT GCG GCG ATT TTA CGC TAT AAA	99
Leu Gly Asn Pro Gly Pro Gly Gly Tyr Ala Ala Ile Leu Arg Tyr Lys	
15 20 25	
GAT AAA GAA AAA ACC ATC AGT GGG GGC GAA GAA TTC ACC ACG AAT AAC	147
Asp Lys Glu Lys Thr Ile Ser Gly Gly Glu Glu Phe Thr Thr Asn Asn	
30 35 40	
CGC ATG GAA TTA AGA GCG CTC AAT GAA GCG TTA AAA ATT TTG AAA CGC	195
Arg Met Glu Leu Arg Ala Leu Asn Glu Ala Leu Lys Ile Leu Lys Arg	
45 50 55 60	
CCA TGC CGT ATC ACG CTT TAT AGC GAT TCG CAA TAC GTG TGC CAA GCG	243
Pro Cys Arg Ile Thr Leu Tyr Ser Asp Ser Gln Tyr Val Cys Gln Ala	
65 70 75	
ATC AAT GTG TGG CTA GCT AAC TGG CAA AAA AAG AAT TTT TCT AAA GTT	291
Ile Asn Val Trp Leu Ala Asn Trp Gln Lys Lys Asn Phe Ser Lys Val	
80 85 90	
AAA AAT GTG GAT TTA TGG AAA GAA TTT TTA GAA GTC TCT AAA GGG CAT	339
Lys Asn Val Asp Leu Trp Lys Glu Phe Leu Glu Val Ser Lys Gly His	
95 100 105	
TCT ATT GTG GCT GTT TGG ATC AAG GGG CAT AAC GGG CAT GCC GAG AAT	387
Ser Ile Val Ala Val Trp Ile Lys Gly His Asn Gly His Ala Glu Asn	
110 115 120	

GAA CGA TGC GAT AGC CTC GCT AAA TTA GAG GCG CAA AAA CGG GTC AAA 435
 Glu Arg Cys Asp Ser Leu Ala Lys Leu Glu Ala Gln Lys Arg Val Lys
 125 130 135 140

ACG ACC ACT TAAAGGGAAA AATGATGAAA AACAAACGCT CTCAAAACAG CCC 487
 Thr Thr Thr

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Gln	Glu	Ile	Glu	Ile	Phe	Cys	Asp	Gly	Ser	Ser	Leu	Gly	Asn	Pro
1				5					10					15	
Gly	Pro	Gly	Gly	Tyr	Ala	Ala	Ile	Leu	Arg	Tyr	Lys	Asp	Lys	Glu	Lys
			20					25					30		
Thr	Ile	Ser	Gly	Gly	Glu	Glu	Phe	Thr	Thr	Asn	Asn	Arg	Met	Glu	Leu
		35					40					45			
Arg	Ala	Leu	Asn	Glu	Ala	Leu	Lys	Ile	Leu	Lys	Arg	Pro	Cys	Arg	Ile
		50				55					60				
Thr	Leu	Tyr	Ser	Asp	Ser	Gln	Tyr	Val	Cys	Gln	Ala	Ile	Asn	Val	Trp
65				70					75					80	
Leu	Ala	Asn	Trp	Gln	Lys	Lys	Asn	Phe	Ser	Lys	Val	Lys	Asn	Val	Asp
			85					90					95		
Leu	Trp	Lys	Glu	Phe	Leu	Glu	Val	Ser	Lys	Gly	His	Ser	Ile	Val	Ala
			100					105					110		
Val	Trp	Ile	Lys	Gly	His	Asn	Gly	His	Ala	Glu	Asn	Glu	Arg	Cys	Asp
		115				120						125			
Ser	Leu	Ala	Lys	Leu	Glu	Ala	Gln	Lys	Arg	Val	Lys	Thr	Thr	Thr	
		130				135					140				

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 48...1181
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

215										220					225					
CAA	AAG	CTC	CCC	ATT	GGC	TTA	GGT	CAA	GGG	CTA	TAC	GCT	AAA	TTA	GAC	776				
Gln	Lys	Leu	Pro	Ile	Gly	Leu	Gly	Gln	Gly	Leu	Tyr	Ala	Lys	Leu	Asp					
230					235					240										
GCT	AAA	ATC	GCT	GAA	GCG	ATG	ATG	GGG	CTT	AAT	GGG	GTG	AAA	GCG	GTT	824				
Ala	Lys	Ile	Ala	Glu	Ala	Met	Met	Gly	Leu	Asn	Gly	Val	Lys	Ala	Val					
245					250					255										
GAA	ATA	GGC	AAG	GGG	GTA	GAA	AGC	TCT	TTA	TTA	AAA	GGC	TCA	GAG	TAT	872				
Glu	Ile	Gly	Lys	Gly	Val	Glu	Ser	Ser	Leu	Leu	Lys	Gly	Ser	Glu	Tyr					
260					265					270					275					
AAT	GAT	TTA	ATG	GAT	CAA	AAG	GGG	TTT	TTG	AGC	AAT	CGT	AGC	GGA	GGG	920				
Asn	Asp	Leu	Met	Asp	Gln	Lys	Gly	Phe	Leu	Ser	Asn	Arg	Ser	Gly	Gly					
280					285					290										
GTT	TTA	GGG	GGC	ATG	AGC	AAT	GGG	GAA	GAA	ATC	ATT	GTT	AGA	GTG	CAT	968				
Val	Leu	Gly	Gly	Met	Ser	Asn	Gly	Glu	Glu	Ile	Ile	Val	Arg	Val	His					
295					300					305										
TTC	AAA	CCC	ACG	CCA	AGC	ATT	TTC	CAA	CCT	CAA	CGA	ACC	ATA	GAC	ATT	1016				
Phe	Lys	Pro	Thr	Pro	Ser	Ile	Phe	Gln	Pro	Gln	Arg	Thr	Ile	Asp	Ile					
310					315					320										
AAT	GGC	AAT	GAG	TGC	GAA	TGC	TTG	TTA	AAG	GGC	AGG	CAT	GAT	CCT	TGC	1064				
Asn	Gly	Asn	Glu	Cys	Glu	Cys	Leu	Leu	Lys	Gly	Arg	His	Asp	Pro	Cys					
325					330					335										
ATT	GCG	ATT	AGA	GGG	AGC	GTG	GTG	TGC	GAG	AGT	TTG	TTA	GCG	TTG	GTG	1112				
Ile	Ala	Ile	Arg	Gly	Ser	Val	Val	Cys	Glu	Ser	Leu	Leu	Ala	Leu	Val					
340					345					350					355					
TTG	GCT	GAT	ATG	GTA	TTA	CTC	AAT	TTG	ACT	TCA	AAA	ATA	GAG	TAT	TTA	1160				
Leu	Ala	Asp	Met	Val	Leu	Leu	Asn	Leu	Thr	Ser	Lys	Ile	Glu	Tyr	Leu					
360					365					370										
AAA	ACG	ATT	TAT	AAT	GAG	AAT	TAAACGAAAT	TGGATACAAT	CAGCTTAAAA	AGGA	1215									
Lys	Thr	Ile	Tyr	Asn	Glu	Asn														
375																				
TA															1217					

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Arg	Leu	Ser	Ser	Ala	Ser	Lys	Thr	Glu	Gly	Ser	Gln	Met	Asn	Thr
1				5					10					15	

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 20...535
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TCATTGTGCC	TGAAGCCAC	ATG	CGC	TAC	ATG	CTC	ATC	AAC	GAT	TAT	TAC	AAG	52			
		Met	Arg	Tyr	Met	Leu	Ile	Asn	Asp	Tyr	Tyr	Lys				
		1				5					10					
GTG	TTT	TTG	GGC	GAA	AAA	GAT	AAG	GAT	TTG	TAT	GTG	AAG	CGC	TTG	GAA	100
Val	Phe	Leu	Gly	Glu	Lys	Asp	Lys	Asp	Leu	Tyr	Val	Lys	Arg	Leu	Glu	
			15				20					25				
AAA	ATC	ACG	CCT	AAA	ATC	TAT	CTG	GCG	AGC	GTG	TTT	TTA	GAG	AAA	CAC	148
Lys	Ile	Thr	Pro	Lys	Ile	Tyr	Leu	Ala	Ser	Val	Phe	Leu	Glu	Lys	His	
		30					35					40				
ACC	CCT	TTA	AAA	AGT	CTT	TTA	GAA	AAA	ATC	CCT	AAG	GGA	AAA	AAA	GAG	196
Thr	Pro	Leu	Lys	Ser	Leu	Leu	Glu	Lys	Ile	Pro	Lys	Gly	Lys	Lys	Glu	
	45					50					55					
ACT	ATC	ACC	TAT	CAT	AAC	CCT	TGT	CAT	GCC	AAA	AAA	ACC	CTA	AAC	GCT	244
Thr	Ile	Thr	Tyr	His	Asn	Pro	Cys	His	Ala	Lys	Lys	Thr	Leu	Asn	Ala	
60					65				70						75	
CAC	AAA	GAA	GTG	CGC	AAC	TTG	CTC	AAT	TTG	CAT	TAT	GAA	ATT	AAA	GAA	292
His	Lys	Glu	Val	Arg	Asn	Leu	Leu	Asn	Leu	His	Tyr	Glu	Ile	Lys	Glu	
			80					85					90			
ATG	CCG	GAC	AAT	TGT	TGC	GGT	TTT	GGG	GGG	ATT	ACG	ATG	CAA	ACA	CAA	340
Met	Pro	Asp	Asn	Cys	Cys	Gly	Phe	Gly	Gly	Ile	Thr	Met	Gln	Thr	Gln	
			95					100					105			
AAG	GCG	GGA	TTT	TCT	TTA	AAA	GTG	GGG	CTT	CTT	AGG	GCT	AAA	GAA	ATC	388
Lys	Ala	Gly	Phe	Ser	Leu	Lys	Val	Gly	Leu	Leu	Arg	Ala	Lys	Glu	Ile	
		110					115					120				
ATA	GAC	ACC	AAA	GCT	GCA	ATT	TTG	AGC	GCT	GAA	TGC	GGG	GCA	TGC	CAT	436
Ile	Asp	Thr	Lys	Ala	Ala	Ile	Leu	Ser	Ala	Glu	Cys	Gly	Ala	Cys	His	
	125					130					135					
ATG	CAA	TTA	AAC	AAC	GCT	TTA	AAG	TCT	TTA	GAC	GAC	CCT	AAC	ACT	CCG	484
Met	Gln	Leu	Asn	Asn	Ala	Leu	Lys	Ser	Leu	Asp	Asp	Pro	Asn	Thr	Pro	
140					145				150						155	
CCA	TTT	TTG	CAC	CCT	TTA	GAA	CTC	ATC	GCT	AAA	GCC	TTA	AAA	AGC	GCT	532
Pro	Phe	Leu	His	Pro	Leu	Glu	Leu	Ile	Ala	Lys	Ala	Leu	Lys	Ser	Ala	
				160					165					170		
GAA	TAAAAAGCCT	TTTTAACCCC	ATTCTCCAAC	ATCTTTTAT	ATAATACAGA	GCT										588
Glu																

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

Met Arg Tyr Met Leu Ile Asn Asp Tyr Tyr Lys Val Phe Leu Gly Glu
 1      5      10      15
Lys Asp Lys Asp Leu Tyr Val Lys Arg Leu Glu Lys Ile Thr Pro Lys
 20      25      30
Ile Tyr Leu Ala Ser Val Phe Leu Glu Lys His Thr Pro Leu Lys Ser
 35      40      45
Leu Leu Glu Lys Ile Pro Lys Gly Lys Lys Glu Thr Ile Thr Tyr His
 50      55      60
Asn Pro Cys His Ala Lys Lys Thr Leu Asn Ala His Lys Glu Val Arg
 65      70      75      80
Asn Leu Leu Asn Leu His Tyr Glu Ile Lys Glu Met Pro Asp Asn Cys
 85      90      95
Cys Gly Phe Gly Gly Ile Thr Met Gln Thr Gln Lys Ala Gly Phe Ser
100      105      110
Leu Lys Val Gly Leu Leu Arg Ala Lys Glu Ile Ile Asp Thr Lys Ala
115      120      125
Ala Ile Leu Ser Ala Glu Cys Gly Ala Cys His Met Gln Leu Asn Asn
130      135      140
Ala Leu Lys Ser Leu Asp Asp Pro Asn Thr Pro Pro Phe Leu His Pro
145      150      155      160
Leu Glu Leu Ile Ala Lys Ala Leu Lys Ser Ala Glu
      165      170

```

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 30...317
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

GGCGTTAAAG CTCTGTATTA TATAAAAAG ATG TTG GAG AAT GGG GTT AAA AAG      53
      Met Leu Glu Asn Gly Val Lys Lys
      1      5

GCT TTT TAT TCA GCG CTT TTT AAG GCT TTA GCG ATG AGT TCT AAA GGG      101
Ala Phe Tyr Ser Ala Leu Phe Lys Ala Leu Ala Met Ser Ser Lys Gly
 10      15      20

```


(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Met	Ile	Phe	Ile	Asp	Ala	Cys	Phe	Arg	Lys	Glu	Thr	Pro	Tyr	Thr
1				5					10					15	
Pro	Ile	Trp	Met	Met	Arg	Gln	Ala	Gly	Arg	Tyr	Leu	Ser	Glu	Tyr	Gln
			20					25					30		
Glu	Ser	Arg	Lys	Lys	Ala	Gly	Ser	Phe	Leu	Glu	Leu	Cys	Lys	Asn	Ser
			35				40					45			
Asp	Leu	Ala	Thr	Glu	Val	Thr	Leu	Gln	Pro	Val	Glu	Ile	Leu	Gly	Val
			50			55					60				
Asp	Ala	Ala	Ile	Leu	Phe	Ser	Asp	Ile	Leu	Val	Val	Pro	Leu	Glu	Met
65					70				75						80
Gly	Leu	Asn	Leu	Glu	Phe	Ile	Pro	Lys	Lys	Gly	Pro	His	Phe	Leu	Glu
			85					90						95	
Thr	Ile	Thr	Asp	Leu	Lys	Ser	Val	Glu	Ser	Leu	Lys	Val	Gly	Ala	Tyr
			100					105					110		
Lys	Gln	Leu	Asn	Tyr	Val	Tyr	Asp	Thr	Ile	Ser	Gln	Thr	Arg	Gln	Lys
			115				120					125			
Leu	Ser	Arg	Glu	Lys	Ala	Leu	Ile	Gly	Phe	Cys	Gly	Ser	Pro	Trp	Thr
			130			135					140				
Leu	Ala	Thr	Tyr	Met	Ile	Glu	Gly	Glu	Gly	Ser	Lys	Ser	Tyr	Ala	Lys
145					150					155					160
Ser	Lys	Lys	Met	Leu	Tyr	Ser	Glu	Pro	Glu	Val	Leu	Lys	Ala	Leu	Leu
			165					170						175	
Glu	Lys	Leu	Ser	Leu	Glu	Leu	Ile	Glu	Tyr	Leu	Ser	Leu	Gln	Ile	Gln
			180					185					190		
Ala	Gly	Val	Asn	Ala	Val	Met	Ile	Phe	Asp	Ser	Trp	Ala	Ser	Ala	Leu
			195			200						205			
Glu	Lys	Glu	Ala	Tyr	Leu	Lys	Phe	Ser	Trp	Asp	Tyr	Leu	Lys	Lys	Ile
			210			215				220					
Ser	Lys	Glu	Leu	Lys	Lys	Arg	Tyr	Ala	His	Ile	Pro	Val	Ile	Leu	Phe
225					230					235					240
Pro	Lys	Gly	Ile	Gly	Ala	Tyr	Leu	Asp	Ser	Ile	Asp	Gly	Glu	Phe	Asp
			245					250						255	
Val	Phe	Gly	Val	Asp	Trp	Gly	Thr	Pro	Leu	Thr	Ala	Ala	Lys	Lys	Ile
			260					265					270		
Leu	Gly	Gly	Lys	Tyr	Val	Leu	Gln	Gly	Asn	Leu	Glu	Pro	Thr	Arg	Leu
			275				280					285			
Tyr	Asp	Lys	Asn	Ala	Leu	Glu	Gly	Val	Glu	Thr	Ile	Leu	Lys	Val	
			290			295				300					
Met	Gly	Asn	Gln	Gly	His	Ile	Phe	Asn	Leu	Gly	His	Gly	Met	Leu	Pro
305					310					315					320
Asp	Leu	Pro	Arg	Glu	Asn	Ala	Lys	Tyr	Leu	Val	Gln	Leu	Val	His	Ala
			325					330						335	
Lys	Thr	Arg	Arg												
			340												

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...732
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAGACGACTA	TGTGCATTAA	GGAATGAAA	ATG ATA CGA AAA ATT TTA ATA GGA	54
			Met Ile Arg Lys Ile Leu Ile Gly	
			1 5	
CTT TTT TTG AGT TTT TTG AGC ATG GAA GCT GGC GAA AAA GTG TAT GCG	102			
Leu Phe Leu Ser Phe Leu Ser Met Glu Ala Gly Glu Lys Val Tyr Ala				
10 15 20				
ATT TTC AAT GTG AAA GCG ACA CAA GAT TCC AAA CTC ACC TTA GAC AGC	150			
Ile Phe Asn Val Lys Ala Thr Gln Asp Ser Lys Leu Thr Leu Asp Ser				
25 30 35 40				
ACA GGA ATT GTG GAT AGC ATT AAG GTT ACT GAG GGG AGC GTG GTC AAA	198			
Thr Gly Ile Val Asp Ser Ile Lys Val Thr Glu Gly Ser Val Val Lys				
45 50 55				
AAG GGC GAT GTT TTG TTG CTT TTA TAT AAT CAA GAC AAA CAG GCT CAA	246			
Lys Gly Asp Val Leu Leu Leu Leu Tyr Asn Gln Asp Lys Gln Ala Gln				
60 65 70				
AGC GAT TCC ACC GAA CAA CAA CTC ATT TTC GCT AAA AAG CAA TAC CAA	294			
Ser Asp Ser Thr Glu Gln Gln Leu Ile Phe Ala Lys Lys Gln Tyr Gln				
75 80 85				
CGA TAC AGC AAA ATT GGG GGC GCT GTG GAT AAA AAC ACT CTA GAG GGT	342			
Arg Tyr Ser Lys Ile Gly Gly Ala Val Asp Lys Asn Thr Leu Glu Gly				
90 95 100				
TAT GAG TTC ACT TAC AGG CGC TTG GAG TCT GAT TAC GCT TAT TCT ATT	390			
Tyr Glu Phe Thr Tyr Arg Arg Leu Glu Ser Asp Tyr Ala Tyr Ser Ile				
105 110 115 120				
GCG GTA TTG AAT AAA ACC ATT TTA AGA GCC CCT TTT GAT GGC GTG ATA	438			
Ala Val Leu Asn Lys Thr Ile Leu Arg Ala Pro Phe Asp Gly Val Ile				
125 130 135				
GCG AGT AAA AAC ATT CAA GTG GGC GAA GGG GTG AGC GCG AAT AAC ACG	486			
Ala Ser Lys Asn Ile Gln Val Gly Glu Gly Val Ser Ala Asn Asn Thr				
140 145 150				
GTG TTA TTG AGA TTA GTC AGC CAT GCT AGG AAA TTA GTT ATT GAA TTT	534			
Val Leu Leu Arg Leu Val Ser His Ala Arg Lys Leu Val Ile Glu Phe				

155	160	165	
GAT TCT AAA TAT ATT AAT GCG GTC AAA GTA GGG GAC ACT TAC ACC TAT			582
Asp Ser Lys Tyr Ile Asn Ala Val Lys Val Gly Asp Thr Tyr Thr Tyr			
170	175	180	
TCT ATA GAC GGG GAT TCT AAT CAG CAT GAA GCT AAA ATC ACT AAG ATT			630
Ser Ile Asp Gly Asp Ser Asn Gln His Glu Ala Lys Ile Thr Lys Ile			
185	190	195	200
TAC CCC ACG GTT GAT GAA AAC ACC AGG AAA GTG AGC GCT GAA GCC CTT			678
Tyr Pro Thr Val Asp Glu Asn Thr Arg Lys Val Ser Ala Glu Ala Leu			
205	210	215	
TTA TCT AAG CCT ATG GCA GTG GGG CTT TTT GGC GAT GGG TTT ATC CAA			726
Leu Ser Lys Pro Met Ala Val Gly Leu Phe Gly Asp Gly Phe Ile Gln			
220	225	230	
ACG AAA TAATAGGATA TTTTGATGTA TAAAACAGCG ATTA			766
Thr Lys			

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Ile	Arg	Lys	Ile	Leu	Ile	Gly	Leu	Phe	Leu	Ser	Phe	Leu	Ser	Met
1				5					10					15	
Glu	Ala	Gly	Glu	Lys	Val	Tyr	Ala	Ile	Phe	Asn	Val	Lys	Ala	Thr	Gln
			20					25					30		
Asp	Ser	Lys	Leu	Thr	Leu	Asp	Ser	Thr	Gly	Ile	Val	Asp	Ser	Ile	Lys
		35					40					45			
Val	Thr	Glu	Gly	Ser	Val	Val	Lys	Lys	Gly	Asp	Val	Leu	Leu	Leu	Leu
		50				55					60				
Tyr	Asn	Gln	Asp	Lys	Gln	Ala	Gln	Ser	Asp	Ser	Thr	Glu	Gln	Gln	Leu
65					70					75					80
Ile	Phe	Ala	Lys	Lys	Gln	Tyr	Gln	Arg	Tyr	Ser	Lys	Ile	Gly	Gly	Ala
			85						90				95		
Val	Asp	Lys	Asn	Thr	Leu	Glu	Gly	Tyr	Glu	Phe	Thr	Tyr	Arg	Arg	Leu
			100					105					110		
Glu	Ser	Asp	Tyr	Ala	Tyr	Ser	Ile	Ala	Val	Leu	Asn	Lys	Thr	Ile	Leu
		115					120					125			
Arg	Ala	Pro	Phe	Asp	Gly	Val	Ile	Ala	Ser	Lys	Asn	Ile	Gln	Val	Gly
		130				135					140				
Glu	Gly	Val	Ser	Ala	Asn	Asn	Thr	Val	Leu	Leu	Arg	Leu	Val	Ser	His
145					150					155					160
Ala	Arg	Lys	Leu	Val	Ile	Glu	Phe	Asp	Ser	Lys	Tyr	Ile	Asn	Ala	Val
			165						170				175		
Lys	Val	Gly	Asp	Thr	Tyr	Thr	Tyr	Ser	Ile	Asp	Gly	Asp	Ser	Asn	Gln

ATG GTG TTA AGC TTA CTC ATT GTG CCG GTG TTT TAT CGT TTG CTC GCT 493
Met Val Leu Ser Leu Leu Ile Val Pro Val Phe Tyr Arg Leu Leu Ala
130 135 140

CCC ATA GAC GAC AAA ATC AAG CGG TTT TAT CAA AAC CAA AAA ACT TTA 541
Pro Ile Asp Asp Lys Ile Lys Arg Phe Tyr Gln Asn Gln Lys Thr Leu
145 150 155 160

GAA TGAAAAAAT TGCTTTCATT TTGGCTTTAT GGGTGGGCTT GTTAGGGGCG TTTGAG 600
Glu

CCTAAAAAAA GTCATATTTA TTTTGGGGCT 630

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ile Leu Ala Ala Leu Tyr Glu Ser Ile Leu Glu Pro Phe Ile Ile
1 5 10 15
Met Val Thr Met Pro Leu Ser Phe Ser Gly Ala Phe Phe Ala Leu Gly
20 25 30
Leu Val His Gln Pro Leu Ser Met Phe Ser Met Ile Gly Leu Ile Leu
35 40 45
Leu Ile Gly Met Val Gly Lys Asn Ala Thr Leu Leu Ile Asp Val Ala
50 55 60
Asn Glu Glu Arg Lys Lys Gly Leu Asn Ile Gln Glu Ala Ile Leu Phe
65 70 75 80
Ala Gly Lys Thr Arg Leu Arg Pro Ile Leu Met Thr Thr Ile Ala Met
85 90 95
Val Cys Gly Met Leu Pro Leu Ala Leu Ala Ser Gly Asp Gly Ala Ala
100 105 110
Met Lys Ser Pro Ile Gly Ile Ala Met Ser Gly Gly Leu Met Ile Ser
115 120 125
Met Val Leu Ser Leu Leu Ile Val Pro Val Phe Tyr Arg Leu Leu Ala
130 135 140
Pro Ile Asp Asp Lys Ile Lys Arg Phe Tyr Gln Asn Gln Lys Thr Leu
145 150 155 160
Glu

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 19...945

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TAAAAGGTTT TTACAAAC	ATG ATA AAA AGC CAA AAA GAA TAT TTA GAA AGA	51
	Met Ile Lys Ser Gln Lys Glu Tyr Leu Glu Arg	
	1 5 10	
ATT GCA TAT TTA AAC ACC CTA TCG CAC CAT TAT TAC AAC CTT GAT GAA	99	
Ile Ala Tyr Leu Asn Thr Leu Ser His His Tyr Tyr Asn Leu Asp Glu		
	15 20 25	
CCC ATC GTA AGC GAT GCG ATC TAT GAT GAA CTT TAC CAA GAA TTG AAA	147	
Pro Ile Val Ser Asp Ala Ile Tyr Asp Glu Leu Tyr Gln Glu Leu Lys		
	30 35 40	
GCT TAT GAA GAA AAA AAC CCT AAT GGC ATT CAA GCT AAT TCC CCT ACC	195	
Ala Tyr Glu Glu Lys Asn Pro Asn Gly Ile Gln Ala Asn Ser Pro Thr		
	45 50 55	
CAA AAA GTG GGG GCT ACT ACC ACC AAT TCG TTC AAT AAA AAC CCC CAT	243	
Gln Lys Val Gly Ala Thr Thr Thr Asn Ser Phe Asn Lys Asn Pro His		
	60 65 70 75	
TTA ATG CGG ATG TGG AGC TTA GAT GAT GTG TTC AAT CAA AGC GAA TTG	291	
Leu Met Arg Met Trp Ser Leu Asp Asp Val Phe Asn Gln Ser Glu Leu		
	80 85 90	
CAA GCG TGG TTG CAA CGC ATT TTA AAA GCC TAT CCT AGT GCT TCG TTC	339	
Gln Ala Trp Leu Gln Arg Ile Leu Lys Ala Tyr Pro Ser Ala Ser Phe		
	95 100 105	
GTG TGT TCG CCC AAA CTT GAT GGG GTT TCG CTC AAT CTT TTG TAT CAA	387	
Val Cys Ser Pro Lys Leu Asp Gly Val Ser Leu Asn Leu Leu Tyr Gln		
	110 115 120	
CAT GGC AAG CTA GTG AAG GCG ACC ACT AGG GGC AAC GGC TTA GAA GGA	435	
His Gly Lys Leu Val Lys Ala Thr Thr Arg Gly Asn Gly Leu Glu Gly		
	125 130 135	
GAA TTA GTT AGC GCA AAC GCT AAA CAC ATC GCT AAT ATC CCC CAC GCT	483	
Glu Leu Val Ser Ala Asn Ala Lys His Ile Ala Asn Ile Pro His Ala		
	140 145 150 155	
ATC GCT TAT AAT GGA GAA ATA GAA ATC AGG GGC GAA GTG ATC ATT TCT	531	
Ile Ala Tyr Asn Gly Glu Ile Glu Ile Arg Gly Glu Val Ile Ile Ser		
	160 165 170	
AAA AAG GAT TTT GAC GCT TTG AAT CAA GAG CGC TTA AAC GCT AAT GAA	579	
Lys Lys Asp Phe Asp Ala Leu Asn Gln Glu Arg Leu Asn Ala Asn Glu		
	175 180 185	
CCC CTA TTC GCT AAC CCC AGA AAC GCC GCA TCA GGG AGT TTG AGG CAA	627	

Pro	Leu	Phe	Ala	Asn	Pro	Arg	Asn	Ala	Ala	Ser	Gly	Ser	Leu	Arg	Gln		
		190					195					200					
CTT	GAT	AGC	GAA	ATC	ACT	AAA	AAG	CGT	AAA	TTG	CAA	TTC	ATT	CCT	TGG	675	
Leu	Asp	Ser	Glu	Ile	Thr	Lys	Lys	Arg	Lys	Leu	Gln	Phe	Ile	Pro	Trp		
	205					210				215							
GGC	GTG	GGC	AAG	CAT	TCT	TTA	AAT	TTT	TTA	AGC	TTT	AAG	GAG	TGT	TTG	723	
Gly	Val	Gly	Lys	His	Ser	Leu	Asn	Phe	Leu	Ser	Phe	Lys	Glu	Cys	Leu		
	220				225					230					235		
GAT	TTT	ATC	GTC	TCG	TTA	GGT	TTT	AGC	GCC	ATT	CAA	TAC	TTA	AGC	CTA	771	
Asp	Phe	Ile	Val	Ser	Leu	Gly	Phe	Ser	Ala	Ile	Gln	Tyr	Leu	Ser	Leu		
			240						245					250			
AAC	AAA	AAC	CAC	CAA	GAA	ATA	GAA	GAC	AAT	TAC	CAC	ACC	CTA	ATT	AGA	819	
Asn	Lys	Asn	His	Gln	Glu	Ile	Glu	Asp	Asn	Tyr	His	Thr	Leu	Ile	Arg		
			255					260					265				
GAA	AGG	GAG	GGC	TTT	TTT	GCC	CTT	TTA	GAC	GGC	ATG	GTG	ATC	GTT	GTG	867	
Glu	Arg	Glu	Gly	Phe	Phe	Ala	Leu	Leu	Asp	Gly	Met	Val	Ile	Val	Val		
	270					275					280						
AAT	GAA	TTA	AAT	ATT	CAA	AAG	GAG	CTA	GGC	TAC	ACG	CAA	AAA	TCC	CCT	915	
Asn	Glu	Leu	Asn	Ile	Gln	Lys	Glu	Leu	Gly	Tyr	Thr	Gln	Lys	Ser	Pro		
	285					290				295							
AAA	TNG	CTT	GCG	CTT	ATA	AAT	TCC	CGG	CTT	TAGAAAAACA	CACCAAAATT	GTA				968	
Lys	Xaa	Leu	Ala	Leu	Ile	Asn	Ser	Arg	Leu								
	300				305												
GGAGTCATTA	ACCAAGTGGG	GCGCASSGGG	CGATCACAC													1007	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Ile	Lys	Ser	Gln	Lys	Glu	Tyr	Leu	Glu	Arg	Ile	Ala	Tyr	Leu	Asn		
1				5				10						15			
Thr	Leu	Ser	His	His	Tyr	Tyr	Asn	Leu	Asp	Glu	Pro	Ile	Val	Ser	Asp		
		20					25						30				
Ala	Ile	Tyr	Asp	Glu	Leu	Tyr	Gln	Glu	Leu	Lys	Ala	Tyr	Glu	Glu	Lys		
	35					40					45						
Asn	Pro	Asn	Gly	Ile	Gln	Ala	Asn	Ser	Pro	Thr	Gln	Lys	Val	Gly	Ala		
	50				55				60								
Thr	Thr	Thr	Asn	Ser	Phe	Asn	Lys	Asn	Pro	His	Leu	Met	Arg	Met	Trp		
	65			70				75						80			
Ser	Leu	Asp	Asp	Val	Phe	Asn	Gln	Ser	Glu	Leu	Gln	Ala	Trp	Leu	Gln		
			85					90					95				
Arg	Ile	Leu	Lys	Ala	Tyr	Pro	Ser	Ala	Ser	Phe	Val	Cys	Ser	Pro	Lys		

Leu	Asp	Gly	Val	Ser	Leu	Asn	Leu	Tyr	Gln	His	Gly	Lys	Leu	Val	
		115					120				125				
Lys	Ala	Thr	Thr	Arg	Gly	Asn	Gly	Leu	Glu	Gly	Glu	Leu	Val	Ser	Ala
		130				135				140					
Asn	Ala	Lys	His	Ile	Ala	Asn	Ile	Pro	His	Ala	Ile	Ala	Tyr	Asn	Gly
					150					155					160
Glu	Ile	Glu	Ile	Arg	Gly	Glu	Val	Ile	Ile	Ser	Lys	Lys	Asp	Phe	Asp
					165				170						175
Ala	Leu	Asn	Gln	Glu	Arg	Leu	Asn	Ala	Asn	Glu	Pro	Leu	Phe	Ala	Asn
			180					185					190		
Pro	Arg	Asn	Ala	Ala	Ser	Gly	Ser	Leu	Arg	Gln	Leu	Asp	Ser	Glu	Ile
		195					200					205			
Thr	Lys	Lys	Arg	Lys	Leu	Gln	Phe	Ile	Pro	Trp	Gly	Val	Gly	Lys	His
		210				215					220				
Ser	Leu	Asn	Phe	Leu	Ser	Phe	Lys	Glu	Cys	Leu	Asp	Phe	Ile	Val	Ser
					230					235					240
Leu	Gly	Phe	Ser	Ala	Ile	Gln	Tyr	Leu	Ser	Leu	Asn	Lys	Asn	His	Gln
					245					250					255
Glu	Ile	Glu	Asp	Asn	Tyr	His	Thr	Leu	Ile	Arg	Glu	Arg	Glu	Gly	Phe
			260					265					270		
Phe	Ala	Leu	Leu	Asp	Gly	Met	Val	Ile	Val	Val	Asn	Glu	Leu	Asn	Ile
		275					280					285			
Gln	Lys	Glu	Leu	Gly	Tyr	Thr	Gln	Lys	Ser	Pro	Lys	Xaa	Leu	Ala	Leu
		290				295					300				
Ile	Asn	Ser	Arg	Leu											
															305

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 44...880
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGCTTTAGA	TTAGATGCAG	AAAAAGACGC	CCAACTTTAT	GGC	ATG	AAT	ATT	TTT		55
					Met	Asn	Ile	Phe		
					1					
AAG ATC CGA	GAA ATT ATC	CAT TAT GAC	GGG GAG GTT	ACA GAG ATT	CTT					103
Lys Ile Arg	Glu Ile Ile	His Tyr Asp	Gly Glu Val	Thr Glu Ile	Leu					
5		10		15	20					
GGG GGG AGC	GAT GGC GTG	ATG CTC GGG	TTT CTT AGC	GTT AGG GGC	GAG					151
Gly Gly Ser	Asp Gly Val	Met Leu Gly	Phe Leu Ser	Val Arg Gly	Glu					
	25		30		35					

TCT Ser	ATC Ile	CCT Pro	TTA Leu 40	GTG Val	GAT Asp	GTG Val	AAA Lys	AGG Arg 45	TGG Trp	TTG Leu	CAT His	TAT Tyr	AAC Asn 50	GCT Ala	AAT Asn	199
GAT Asp	CCG Pro	AGC Ser 55	CGT Arg	GAT Asp	CTA Leu	AAA Lys 60	GAA Glu	TGC Cys	AGC Ser	GTT Val	AAA Lys 65	GAT Asp	GAC Asp	CAT His	AAT Asn	247
TTG Leu	GTG Val 70	ATT Ile	GTG Val	TGC Cys	CAT His	TTT Phe 75	TCT Ser	AAC Asn	CAT His	TCC Ser	ATC Ile 80	GCT Ala	CTA Leu	AAG Lys	GTT Val	295
TTA Leu 85	AAA Lys	ATT Ile	GAA Glu	AGG Arg	ATC Ile 90	ATC Ile	CAT His	AAA Lys	AAT Asn	TGG Trp 95	ACT Thr	GAG Glu	ATT Ile	AGC Ser	GCT Ala 100	343
GGG Gly	GAC Asp	AAA Lys	CAA Gln	GGC Gly 105	ATT Ile	AAT Asn	GAA Glu	GAG Glu	GGT Gly 110	AAG Lys	CTT Leu	AGC Ser	GCT Ala	ATC Ile 115	ACT Thr	391
CGT Arg	TTT Phe	GAT Asp	GAA Glu 120	GAA Glu	CGA Arg	GTG Val	GTG Val	CAG Gln 125	ATC Ile	TTA Leu	GAT Asp	GTG Val	GAA Glu 130	AAA Lys	ATG Met	439
ATT Ile	AGC Ser	GAT Asp 135	GTT Val	TTC Phe	CCT Pro	AGC Ser	TTG Leu 140	AAA Lys	GAT Asp	TTA Leu	GAC Asp	GAT Asp 145	TTG Leu	ACT Thr	TTG Leu	487
CGT Arg	TGC Cys 150	ATA Ile	GAA Glu	GCC Ala	ATT Ile	CAA Gln 155	AGC Ser	CAA Gln	AAA Lys	CTC Leu	ATT Ile 160	TTA Leu	ATC Ile	GCT Ala	GAA Glu	535
GAC Asp 165	TCC Ser	CTA Leu	AGC Ser	GCT Ala	CTT Leu 170	AAA Lys	ACC Thr	TTA Leu	GAA Glu	AAG Lys 175	ATC Ile	GTT Val	CAA Gln	ACT Thr	TTA Leu 180	583
GAA Glu	TTG Leu	CGT Arg	TAT Tyr	TTA Leu 185	GCT Ala	TTT Phe	CCA Pro	AAC Asn	GGG Gly 190	AGG Arg	GAA Glu	TTG Leu	TTG Leu	GAT Asp 195	TAT Tyr	631
TTG Leu	TAT Tyr	GAA Glu	AAA Lys 200	GAA Glu	CAT His	TAC Tyr	CAA Gln	CAA Gln 205	GTT Val	GGC Gly	GTG Val	GTC Val	ATT Ile 210	ACG Thr	GAT Asp	679
TTA Leu	GAA Glu	ATG Met 215	CCT Pro	AAC Asn	ATT Ile	TCA Ser	GGG Gly 220	TTT Phe	GAA Glu	GTG Val	TTA Leu	AAA Lys 225	ACC Thr	ATT Ile	AAA Lys	727
GCT Ala	GAT Asp 230	CAT His	AGA Arg	ACT Thr	GAG Glu	CAT His	CTT Leu 235	CCT Pro	GTG Val	ATT Ile	ATC Ile 240	AAT Asn	TCG Ser	TCC Ser	ATG Met	775
AGC Ser 245	AGC Ser	GAT Asp	TCT Ser	AAC Asn	CGC Arg 250	CAG Gln	TTA Leu	GCC Ala	CAA Gln	TCT Ser 255	TTA Leu	GAA Glu	GCG Ala	GAT Asp	GGT Gly 260	823
TTT Phe	GTG Val	GTA Val	AAA Lys	TCT Ser	AAC Asn	ATT Ile	CTT Leu	GAA Glu	ATC Ile	CAT His	GAA Glu	ATG Met	CTT Leu	AAA Lys	AAA Lys	871

265

270

275

ACG CTT TCA TAAATTTAAT TTTTGTTTTA ATTTAAAGGG ATAAAACATG CGAAGTCAT 929
 Thr Leu Ser

TTTTGCAC

937

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Asn Ile Phe Lys Ile Arg Glu Ile Ile His Tyr Asp Gly Glu Val
 1 5 10 15
 Thr Glu Ile Leu Gly Gly Ser Asp Gly Val Met Leu Gly Phe Leu Ser
 20 25 30
 Val Arg Gly Glu Ser Ile Pro Leu Val Asp Val Lys Arg Trp Leu His
 35 40 45
 Tyr Asn Ala Asn Asp Pro Ser Arg Asp Leu Lys Glu Cys Ser Val Lys
 50 55 60
 Asp Asp His Asn Leu Val Ile Val Cys His Phe Ser Asn His Ser Ile
 65 70 75 80
 Ala Leu Lys Val Leu Lys Ile Glu Arg Ile Ile His Lys Asn Trp Thr
 85 90 95
 Glu Ile Ser Ala Gly Asp Lys Gln Gly Ile Asn Glu Glu Gly Lys Leu
 100 105 110
 Ser Ala Ile Thr Arg Phe Asp Glu Glu Arg Val Val Gln Ile Leu Asp
 115 120 125
 Val Glu Lys Met Ile Ser Asp Val Phe Pro Ser Leu Lys Asp Leu Asp
 130 135 140
 Asp Leu Thr Leu Arg Cys Ile Glu Ala Ile Gln Ser Gln Lys Leu Ile
 145 150 155 160
 Leu Ile Ala Glu Asp Ser Leu Ser Ala Leu Lys Thr Leu Glu Lys Ile
 165 170 175
 Val Gln Thr Leu Glu Leu Arg Tyr Leu Ala Phe Pro Asn Gly Arg Glu
 180 185 190
 Leu Leu Asp Tyr Leu Tyr Glu Lys Glu His Tyr Gln Gln Val Gly Val
 195 200 205
 Val Ile Thr Asp Leu Glu Met Pro Asn Ile Ser Gly Phe Glu Val Leu
 210 215 220
 Lys Thr Ile Lys Ala Asp His Arg Thr Glu His Leu Pro Val Ile Ile
 225 230 235 240
 Asn Ser Ser Met Ser Ser Asp Ser Asn Arg Gln Leu Ala Gln Ser Leu
 245 250 255
 Glu Ala Asp Gly Phe Val Val Lys Ser Asn Ile Leu Glu Ile His Glu
 260 265 270
 Met Leu Lys Lys Thr Leu Ser
 275

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 21...593
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATAATTTAAA AGGATACGAT	ATG AAA CAA CTA TTT TTG ATC ATT GGA GCC	50
	Met Lys Gln Leu Phe Leu Ile Ile Gly Ala	
	1 5 10	
CCA GGG AGT GGT AAA ACC ACT GAT GCA GAG CTT ATC GCT AAA AAT AAC		98
Pro Gly Ser Gly Lys Thr Thr Asp Ala Glu Leu Ile Ala Lys Asn Asn		
	15 20 25	
AGC GAA ACA ATC GCT CAT TTT TCT ACC GGG GAT TTA CTC AGG GCT GAG		146
Ser Glu Thr Ile Ala His Phe Ser Thr Gly Asp Leu Leu Arg Ala Glu		
	30 35 40	
AGC GCT AAA AAG ACC GAG CGA GGC TTA TTG ATT GAA AAA TTC ACT TCT		194
Ser Ala Lys Lys Thr Glu Arg Gly Leu Leu Ile Glu Lys Phe Thr Ser		
	45 50 55	
CAA GGC GAA TTA GTG CCT TTA GAA ATT GTG GTA GAA ACG ATC CTT TCA		242
Gln Gly Glu Leu Val Pro Leu Glu Ile Val Val Glu Thr Ile Leu Ser		
	60 65 70	
GCG ATT AAA AGC TCT GGT AAA GGG ATC ATT TTA ATT GAT GGT TAT CCT		290
Ala Ile Lys Ser Ser Gly Lys Gly Ile Ile Leu Ile Asp Gly Tyr Pro		
	75 80 85 90	
AGG AGC GTG GAA CAA ATG CAG GCT TTG GAT AAG GAA TTG AAC GCT CAA		338
Arg Ser Val Glu Gln Met Gln Ala Leu Asp Lys Glu Leu Asn Ala Gln		
	95 100 105	
AAC GAA GTG ATC TTA AAA AGC GTG ATT GAA GTA GAA GTG AGT GAA AAC		386
Asn Glu Val Ile Leu Lys Ser Val Ile Glu Val Glu Val Ser Glu Asn		
	110 115 120	
ACT GCT AAA GAA AGG GTT TTA GGG CGC TCT AGG GGG GCT GAT GAT AAT		434
Thr Ala Lys Glu Arg Val Leu Gly Arg Ser Arg Gly Ala Asp Asp Asn		
	125 130 135	
GAA AAG GTG TTT CAT AAC CGC ATG CGG GTG TTT TTG GAT CCG TTG GGC		482
Glu Lys Val Phe His Asn Arg Met Arg Val Phe Leu Asp Pro Leu Gly		
	140 145 150	
GAG ATC CAA AAT TTT TAC AAG AAT AAG AAG GTG TAT AAA GCG ATC GAT		530
Glu Ile Gln Asn Phe Tyr Lys Asn Lys Lys Val Tyr Lys Ala Ile Asp		

155	160	165	170	
GGG GAG AGG AGC ATT GAA GAG ATT GTG GGC GAA ATG CAA GAG TAT ATC				578
Gly Glu Arg Ser Ile Glu Glu Ile Val Gly Glu Met Gln Glu Tyr Ile				
	175	180	185	
TTG TCT TTC GGT AAT TAAAATGCAC TCTCAAGGAG AATAGCTGTG ATTTCTG				630
Leu Ser Phe Gly Asn				
	190			

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Lys	Gln	Leu	Phe	Leu	Ile	Ile	Gly	Ala	Pro	Gly	Ser	Gly	Lys	Thr
1				5				10					15		
Thr	Asp	Ala	Glu	Leu	Ile	Ala	Lys	Asn	Asn	Ser	Glu	Thr	Ile	Ala	His
			20					25					30		
Phe	Ser	Thr	Gly	Asp	Leu	Leu	Arg	Ala	Glu	Ser	Ala	Lys	Lys	Thr	Glu
		35					40					45			
Arg	Gly	Leu	Leu	Ile	Glu	Lys	Phe	Thr	Ser	Gln	Gly	Glu	Leu	Val	Pro
	50					55					60				
Leu	Glu	Ile	Val	Val	Glu	Thr	Ile	Leu	Ser	Ala	Ile	Lys	Ser	Ser	Gly
	65					70				75					80
Lys	Gly	Ile	Ile	Leu	Ile	Asp	Gly	Tyr	Pro	Arg	Ser	Val	Glu	Gln	Met
				85					90					95	
Gln	Ala	Leu	Asp	Lys	Glu	Leu	Asn	Ala	Gln	Asn	Glu	Val	Ile	Leu	Lys
			100					105					110		
Ser	Val	Ile	Glu	Val	Glu	Val	Ser	Glu	Asn	Thr	Ala	Lys	Glu	Arg	Val
		115						120				125			
Leu	Gly	Arg	Ser	Arg	Gly	Ala	Asp	Asp	Asn	Glu	Lys	Val	Phe	His	Asn
	130					135					140				
Arg	Met	Arg	Val	Phe	Leu	Asp	Pro	Leu	Gly	Glu	Ile	Gln	Asn	Phe	Tyr
	145				150					155					160
Lys	Asn	Lys	Lys	Val	Tyr	Lys	Ala	Ile	Asp	Gly	Glu	Arg	Ser	Ile	Glu
				165					170					175	
Glu	Ile	Val	Gly	Glu	Met	Gln	Glu	Tyr	Ile	Leu	Ser	Phe	Gly	Asn	
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...717
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGT	TAC	CCC	CCC	CCC	CCC	AAT	CCC	ACA	CAA	GAA	ACG	CAA	CAA	GAT	TTT	48
Ser	Tyr	Pro	Pro	Pro	Pro	Asn	Pro	Thr	Gln	Glu	Thr	Gln	Gln	Asp	Phe	
1				5					10					15		
ATT	ATT	GAA	GCA	CAA	CAA	GAT	TTG	ATT	ATT	GAA	ACG	CAA	CAA	GAC	CCC	96
Ile	Ile	Glu	Ala	Gln	Gln	Asp	Leu	Ile	Ile	Glu	Thr	Gln	Gln	Asp	Pro	
			20					25						30		
AAA	GAA	CTA	CCT	GAG	TCT	TGC	AAA	ATA	ACG	CCC	CAA	AAA	ATC	TCT	TTT	144
Lys	Glu	Leu	Pro	Glu	Ser	Cys	Lys	Ile	Thr	Pro	Gln	Lys	Ile	Ser	Phe	
			35				40					45				
AAC	CAA	GTG	GTT	TTT	AAA	AAA	ATT	AAA	AGA	AAA	CTC	AAC	CGC	TTC	ATT	192
Asn	Gln	Val	Val	Phe	Lys	Lys	Ile	Lys	Arg	Lys	Leu	Asn	Arg	Phe	Ile	
			50				55				60					
GGA	AGC	ATT	TTA	GCT	CGG	ACA	GAA	GTG	TAT	AAG	AAT	CTC	GTG	GCA	AAA	240
Gly	Ser	Ile	Leu	Ala	Arg	Thr	Glu	Val	Tyr	Lys	Asn	Leu	Val	Ala	Lys	
65					70					75					80	
TAC	GAT	GAA	CTC	ACA	GGA	AAA	TAC	GAA	TCA	TTA	TTG	GCA	AAA	GAG	GCA	288
Tyr	Asp	Glu	Leu	Thr	Gly	Lys	Tyr	Glu	Ser	Leu	Leu	Ala	Lys	Glu	Ala	
				85					90					95		
AAC	ATC	AAA	GAG	ACC	TTT	TGG	GAA	AGG	CGT	GCT	GAT	AGC	GAA	AAA	GAA	336
Asn	Ile	Lys	Glu	Thr	Phe	Trp	Glu	Arg	Arg	Ala	Asp	Ser	Glu	Lys	Glu	
			100					105					110			
GCC	TTT	TTT	TTA	GAG	CAT	TTT	TAC	CTC	ACT	AGC	GTG	TAT	GTG	GCT	TCT	384
Ala	Phe	Phe	Leu	Glu	His	Phe	Tyr	Leu	Thr	Ser	Val	Tyr	Val	Ala	Ser	
			115				120					125				
ACA	GCA	GGA	TAC	TAT	ATC	ACG	CCT	AAG	GGC	GCT	AAA	ACC	TTT	ATA	GAA	432
Thr	Ala	Gly	Tyr	Tyr	Ile	Thr	Pro	Lys	Gly	Ala	Lys	Thr	Phe	Ile	Glu	
			130				135					140				
GCC	ACG	GAG	CGT	TTT	AAA	ATC	ATA	GAG	CCG	GTG	GAT	ATG	TTC	ATA	AAC	480
Ala	Thr	Glu	Arg	Phe	Lys	Ile	Ile	Glu	Pro	Val	Asp	Met	Phe	Ile	Asn	
145					150					155					160	
AAC	CCC	ACT	TAC	CAT	GAT	GTG	GCT	AAT	TTT	ACC	TAT	TTG	CCT	TGC	CCT	528
Asn	Pro	Thr	Tyr	His	Asp	Val	Ala	Asn	Phe	Thr	Tyr	Leu	Pro	Cys	Pro	
				165					170					175		
GTT	TCT	TTA	AAC	AAG	CAT	GCT	TTC	AAT	AGC	ACC	ATT	CAA	AAT	GCA	AAA	576
Val	Ser	Leu	Asn	Lys	His	Ala	Phe	Asn	Ser	Thr	Ile	Gln	Asn	Ala	Lys	
			180					185					190			
AAG	CCT	GAC	ATT	TCA	TTA	AAA	CCC	CCT	AGA	AAA	TCC	TAT	TTT	GAT	AAT	624
Lys	Pro	Asp	Ile	Ser	Leu	Lys	Pro	Pro	Arg	Lys	Ser	Tyr	Phe	Asp	Asn	
			195				200					205				

CTT TTT TAT GAT CAA TTA AAC ACT AGA AAG TGC TTA AAA GCC TTT CAC 672
 Leu Phe Tyr Asp Gln Leu Asn Thr Arg Lys Cys Leu Lys Ala Phe His
 210 215 220

AAA TAC AGC AGA CGA TAC GCT CCT TTA AAA ACC CCT AAA GAG GTT TAAAA 722
 Lys Tyr Ser Arg Arg Tyr Ala Pro Leu Lys Thr Pro Lys Glu Val
 225 230 235

AGAGCGGGCT TTATGTTAGA ATAAGTCTTT TTATTCAAAG GAGATTGCAA TGAAT 777

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser	Tyr	Pro	Pro	Pro	Pro	Asn	Pro	Thr	Gln	Glu	Thr	Gln	Gln	Asp	Phe	1	5	10	15
Ile	Ile	Glu	Ala	Gln	Gln	Asp	Leu	Ile	Ile	Glu	Thr	Gln	Gln	Asp	Pro	20	25	30	
Lys	Glu	Leu	Pro	Glu	Ser	Cys	Lys	Ile	Thr	Pro	Gln	Lys	Ile	Ser	Phe	35	40	45	
Asn	Gln	Val	Val	Phe	Lys	Lys	Ile	Lys	Arg	Lys	Leu	Asn	Arg	Phe	Ile	50	55	60	
Gly	Ser	Ile	Leu	Ala	Arg	Thr	Glu	Val	Tyr	Lys	Asn	Leu	Val	Ala	Lys	65	70	75	80
Tyr	Asp	Glu	Leu	Thr	Gly	Lys	Tyr	Glu	Ser	Leu	Leu	Ala	Lys	Glu	Ala	85	90	95	
Asn	Ile	Lys	Glu	Thr	Phe	Trp	Glu	Arg	Arg	Ala	Asp	Ser	Glu	Lys	Glu	100	105	110	
Ala	Phe	Phe	Leu	Glu	His	Phe	Tyr	Leu	Thr	Ser	Val	Tyr	Val	Ala	Ser	115	120	125	
Thr	Ala	Gly	Tyr	Tyr	Ile	Thr	Pro	Lys	Gly	Ala	Lys	Thr	Phe	Ile	Glu	130	135	140	
Ala	Thr	Glu	Arg	Phe	Lys	Ile	Ile	Glu	Pro	Val	Asp	Met	Phe	Ile	Asn	145	150	155	160
Asn	Pro	Thr	Tyr	His	Asp	Val	Ala	Asn	Phe	Thr	Tyr	Leu	Pro	Cys	Pro	165	170	175	
Val	Ser	Leu	Asn	Lys	His	Ala	Phe	Asn	Ser	Thr	Ile	Gln	Asn	Ala	Lys	180	185	190	
Lys	Pro	Asp	Ile	Ser	Leu	Lys	Pro	Pro	Arg	Lys	Ser	Tyr	Phe	Asp	Asn	195	200	205	
Leu	Phe	Tyr	Asp	Gln	Leu	Asn	Thr	Arg	Lys	Cys	Leu	Lys	Ala	Phe	His	210	215	220	
Lys	Tyr	Ser	Arg	Arg	Tyr	Ala	Pro	Leu	Lys	Thr	Pro	Lys	Glu	Val		225	230	235	

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 50...1252
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGTGGAAAA TTTAGCTAAA GAAAGAGAAA AAAGTTTAAA GGATTAGGC ATG ATC AAT	58
Met Ile Asn	
1	
AAG TTT AAA AAT TTT GTG AGC AAC TAC CAG CAA TCT AAC CAC TAT AAA	106
Lys Phe Lys Asn Phe Val Ser Asn Tyr Gln Gln Ser Asn His Tyr Lys	
5 10 15	
GAG CCT TTA GGT TTT GGC ATT GCC AGA GTG GAT ATT GCC CCT ATT TCC	154
Glu Pro Leu Gly Phe Gly Ile Ala Arg Val Asp Ile Ala Pro Ile Ser	
20 25 30 35	
AAA AAG ATT TTA TGC GCC ACT TAC CCT GTT TTG AAT TGG AAA GAT GAA	202
Lys Lys Ile Leu Cys Ala Thr Tyr Pro Val Leu Asn Trp Lys Asp Glu	
40 45 50	
AAT TTA GGC TCT TAT GCG GTG TTT TGC AAC TCG CTT TCA AAA GAA AAA	250
Asn Leu Gly Ser Tyr Ala Val Phe Cys Asn Ser Leu Ser Lys Glu Lys	
55 60 65	
ATC CTA AAA GAG AGC GCG AGC GAG CGC GTT ATT GAG ATT GAT GAA AGT	298
Ile Leu Lys Glu Ser Ala Ser Glu Arg Val Ile Glu Ile Asp Glu Ser	
70 75 80	
TTT GTG TTA AAA GCG TTG GAT TTT TAT ACG CCC TTT TTG AAT GAA GCC	346
Phe Val Leu Lys Ala Leu Asp Phe Tyr Thr Pro Phe Leu Asn Glu Ala	
85 90 95	
TAT TCT AAT AAA ATG GCT CAT AAA AAC ATC CAA GTG GTT TTA GAG CTT	394
Tyr Ser Asn Lys Met Ala His Lys Asn Ile Gln Val Val Leu Glu Leu	
100 105 110 115	
TTA AAG GCT TTA GAA GAA AAT CGT TTG AAA AAT AGC GAT GGG GAG TCT	442
Leu Lys Ala Leu Glu Glu Asn Arg Leu Lys Asn Ser Asp Gly Glu Ser	
120 125 130	
CTT TAT CGC TTG GTG ATC TTG TAT GAA GAT AAG CCT TGC GAG AGC GTG	490
Leu Tyr Arg Leu Val Ile Leu Tyr Glu Asp Lys Pro Cys Glu Ser Val	
135 140 145	
GAG AGC GCG TAT ATG AAA CTT TTA GCG CTC TCT TTA GGT AAA GCC CCT	538
Glu Ser Ala Tyr Met Lys Leu Leu Ala Leu Ser Leu Gly Lys Ala Pro	
150 155 160	
TTG AGG AGT TTG AAT TTA GAG GGT ATT TTT AAC CAG CTT TCT AAT GCG	586

Leu 165	Arg	Ser	Leu	Asn	Leu	Glu 170	Gly	Ile	Phe	Asn	Gln 175	Leu	Ser	Asn	Ala	
GCC Ala 180	TGG Trp	AGC Ser	GGT Gly	AAC Asn	AAG Lys 185	CCC Pro	TAT Tyr	GAA Glu	TTA Leu	GAA Glu 190	TGG Trp	CTT Leu	AGA Arg	ATG Met	AAC Asn 195	634
GAA Glu	GTG Val	GCT Ala	TTA Leu	AAA Lys 200	ATG Met	CGA Arg	GAC Asp	CAT His	TTC Phe 205	CCT Pro	AGC Ser	ATT Ile	GAT Asp	TTC Phe 210	ATA Ile	682
GAT Asp	AAA Lys	TTC Phe	CCA Pro 215	CGC Arg	TAT Tyr	TTG Leu	ATG Met	CAA Gln 220	TTA Leu	ATC Ile	CCT Pro	GAG Glu	TTT Phe 225	GAT Asp	AAT Asn	730
ATC Ile	CGC Arg	TTA Leu 230	TTG Leu	GAT Asp	AGC Ser	TCA Ser	AAA Lys 235	ACG Thr	CGC Arg	TTT Phe	GGG Gly	GCG Ala 240	TAT Tyr	TTA Leu	GGG Gly	778
ACT Thr	GGA Gly 245	GGT Gly	TAT Tyr	ACC Thr	CAA Gln 250	ATG Met	CCT Pro	GGG Gly	GCT Ala	AGT Ser	TAT Tyr 255	GTG Val	AAT Asn	TTT Phe	AAC Asn	826
GCA Ala 260	GGG Gly	GCT Ala	ATG Met	GGA Gly	GTG Val 265	TGC Cys	ATG Met	AAT Asn	GAG Glu	GGG Gly 270	CGT Arg	ATT Ile	TCT Ser	TCA Ser	TCG Ser 275	874
GTG Val	GTG Val	GTT Val	GGA Gly	GCA Ala 280	GGC Gly	ACT Thr	GAT Asp	ATT Ile	GGT Gly 285	GGG Gly	GGA Gly	GCG Ala	AGC Ser	GTG Val 290	TTA Leu	922
GGC Gly	GTT Val	TTA Leu	AGT Ser 295	GGA Gly	GGG Gly	AAT Asn	AAC Asn	AAC Asn 300	CCC Pro	ATT Ile	AGC Ser	ATC Ile	GGG Gly 305	AAA Lys	AAT Asn	970
TGT Cys	TTG Leu	CTA Leu 310	GGG Gly	GCT Ala	AAT Asn	AGC Ser	GTT Val 315	ACT Thr	GGA Gly	ATT Ile	AGT Ser	CTA Leu 320	GGC Gly	GAT Asp	GGC Gly	1018
TGT Cys	ATC Ile 325	GTG Val	GAT Asp	GCA Ala	GGC Gly	GTT Val 330	GCG Ala	ATA Ile	CTA Leu	GCC Ala	GGG Gly 335	AGC Ser	GTG Val	ATA Ile	GAA Glu	1066
ATT Ile 340	GAA Glu	GAA Glu	AAT Asn	GAG Glu	TTT Phe 345	AAA Lys	AAG Lys	CTT Leu	TTA Leu	GAA Glu 350	GTG Val	AAT Asn	AGC Ser	GCT Ala	TTA Leu 355	1114
GAA Glu	AAA Lys	CAT His	GCC Ala	AAC Asn 360	AAC Asn	CTT Leu	TAC Tyr	AAA Lys	GGC Gly 365	AAA Lys	GAA Glu	CTT Leu	TCC Ser	GGA Gly 370	AAA Lys	1162
AAT Asn	GGC Gly	GTG Val	CAT His 375	TTT Phe	CGT Arg	TCC Ser	AAT Asn	AGT Ser 380	CAG Gln	AAT Asn	GGC Gly	AAG Lys	CTG Leu	ATT Ile	GCT Ala	1210
TTT Phe	AGG Arg	AGC Ser 390	GTG Val	AAA Lys	AAA Lys	ATT Ile	GAG Glu 395	TTG Leu	AAT Asn	CAA Gln	AAC Asn	CTG Leu 400	CAT His	TAAGGATTA		1261

	340		345		350										
Ser	Ala	Leu	Glu	Lys	His	Ala	Asn	Asn	Leu	Tyr	Lys	Gly	Lys	Glu	Leu
	355		360		365										
Ser	Gly	Lys	Asn	Gly	Val	His	Phe	Arg	Ser	Asn	Ser	Gln	Asn	Gly	Lys
	370		375		380										
Leu	Ile	Ala	Phe	Arg	Ser	Val	Lys	Lys	Ile	Glu	Leu	Asn	Gln	Asn	Leu
385			390		395									400	
His															

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...1201
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTATTTTAT	TATGTTAAGA	TAATGAAAAT	TTCTAATTAA	GGAGTGGTC	ATG	TTC	TAC	58								
					Met	Phe	Tyr									
					1											
GAT	GAA	AAA	AAG	ACC	TAT	CAA	AAG	ATT	GAA	GAA	CGC	CTT	GAT	ATA	GTC	106
Asp	Glu	Lys	Lys	Thr	Tyr	Gln	Lys	Ile	Glu	Glu	Arg	Leu	Asp	Ile	Val	
5					10				15							
CGT	TCG	TTT	AAC	GCT	CAC	AAC	GAG	CAT	AAA	AAC	TTG	CAA	GAC	GAG	TTT	154
Arg	Ser	Phe	Asn	Ala	His	Asn	Glu	His	Lys	Asn	Leu	Gln	Asp	Glu	Phe	
20			25			30			35							
AAA	GGG	GCG	GGC	ATT	TCT	AGG	CGC	GAT	TTA	TTG	AAG	TGG	GCG	GGC	ATG	202
Lys	Gly	Ala	Gly	Ile	Ser	Arg	Arg	Asp	Leu	Leu	Lys	Trp	Ala	Gly	Met	
			40			45			50							
ATG	AGC	ACA	GCG	TTA	GCC	TTG	CCG	GCT	AGT	TTT	GCT	CCC	TTG	ACT	TTG	250
Met	Ser	Thr	Ala	Leu	Ala	Leu	Pro	Ala	Ser	Phe	Ala	Pro	Leu	Thr	Leu	
			55			60			65							
AAG	GCG	GTG	GAA	GTG	GCT	AAC	AGA	TTG	CCC	GTG	ATT	TGG	TTG	CAC	ATG	298
Lys	Ala	Val	Glu	Val	Ala	Asn	Arg	Leu	Pro	Val	Ile	Trp	Leu	His	Met	
		70				75			80							
GCA	GAA	TGC	ACC	GGT	TGT	AGC	GAA	AGT	TTG	TTA	AGG	AGC	GCA	GAC	CCC	346
Ala	Glu	Cys	Thr	Gly	Cys	Ser	Glu	Ser	Leu	Leu	Arg	Ser	Ala	Asp	Pro	
85						90			95							
ACC	ATT	GAT	AGC	ATT	ATC	TTT	GAT	TAC	ATC	AAC	CTA	GAA	TAC	CAT	GAG	394
Thr	Ile	Asp	Ser	Ile	Ile	Phe	Asp	Tyr	Ile	Asn	Leu	Glu	Tyr	His	Glu	

100				105				110				115				
ACC Thr	ATC Ile	ATG Met	GTA Val	GCG Ala 120	AGC Ser	GGT Gly	TTT Phe	CAA Gln 125	GCT Ala 125	GAA Glu 125	AAA Lys	AGC Ser	TTG Leu	CAT His 130	GAC Asp	442
GCC Ala	ATA Ile	GAA Glu	AAG Lys 135	CAT His	AAA Lys	AAC Asn	AAT Asn 140	TAC Tyr 140	ATT Ile	TTA Leu	ATG Met	GTA Val	GAA Glu 145	GGG Gly	GGT Gly	490
ATC Ile	CCC Pro	CAA Gln 150	GGC Gly	ACG Thr	GAA Glu	TAC Tyr	TTC Phe 155	CTC Leu	ACT Thr	CAA Gln	GGC Gly	CCA Pro 160	AAC Asn	GCT Ala	GAA Glu	538
ACG Thr 165	GGA Gly	GCT Ala	GAA Glu	GAG Glu	TGT Cys	AGG Arg 170	AAA Lys	GCC Ala	GCT Ala	CAA Gln 175	TAC Tyr	GCA Ala	GCC Ala	GCT Ala	ATT Ile	586
TTT Phe 180	GCC Ala	ATA Ile	GGC Gly	ACA Thr 185	TGC Cys	TCA Ser	AGT Ser	TTT Phe	GGG Gly 190	GGC Gly	GTT Val	CAA Gln	GCG Ala	GCT Ala	TAC Tyr 195	634
CCT Pro	AAC Asn	CCC Pro	TCT Ser 200	AAC Asn	GCG Ala	CAA Gln	CCC Pro	TTG Leu 205	CAT His	AAA Lys	ATC Ile	ATT Ile	GAT Asp 210	AAA Lys	CCC Pro	682
GTG Val	ATC Ile	AAT Asn 215	GTT Val	CCT Pro	GGT Gly	TGC Cys	CCG Pro	CCT Pro 220	AGT Ser	GAA Glu	AAA Lys	AAT Asn 225	ATC Ile	GTG Val	GGT Gly	730
AAT Asn	GTG Val 230	CTT Leu	TAT Tyr	TAC Tyr	TTG Leu	ATG Met	TTT Phe 235	GGG Gly	GCT Ala	CTC Leu	CCT Pro	AAA Lys 240	TTG Leu	GAT Asp	GCG Ala	778
TAT Tyr 245	AAC Asn	CGC Arg	CCC Pro	TCT Ser	TGG Trp	GCT Ala 250	TAT Tyr	GGG Gly	AAC Asn	AGG Arg	ATC Ile 255	CAT His	GAT Asp	TTG Leu	TGC Cys	826
GAA Glu 260	AGG Arg	AGA Arg	GGG Gly	CAT His 265	TTT Phe	GAT Asp	GCG Ala	GGC Gly	GAA Glu	TTT Phe 270	GTG Val	GAG Glu	CAT His	TTT Phe	GGC Gly 275	874
GAT Asp	GAA Glu	AAC Asn	GCT Ala 280	AAA Lys	AGG Arg	GGC Gly	TTT Phe	TGT Cys 285	TTG Leu	TAT Tyr	AAA Lys	ATG Met	GGC Gly	TGT Cys 290	AAA Lys	922
GGG Gly	CCT Pro	TAC Tyr 295	ACT Thr	TTC Phe	AAC Asn	AAT Asn	TGC Cys 300	TCC Ser	AAA Lys	CTC Leu	CGC Arg	TTC Phe	AAT Asn 305	TCA Ser	CAC His	970
ACC Thr	TCT Ser 310	TGG Trp	CCC Pro	ATA Ile	GGT Gly	GCA Ala	GGG Gly 315	CAT His	GGG Gly	TGT Cys	ATA Ile	GGG Gly 320	TGT Cys	TCT Ser	GAG Glu	1018
CCT Pro	AAT Asn 325	TTT Phe	TGG Trp	GAT Asp	ACG Thr	ATG Met 330	AGT Ser	CCT Pro	TTT Phe	GAA Glu	GAG Glu	CCT Pro	TTA Leu	GCG Ala	AAT Asn	1066

CGT TCC ATT AAA ACC GCT TTT GAC GGA TTA GGG GCT GAT AAA GTA GCG	1114
Arg Ser Ile Lys Thr Ala Phe Asp Gly Leu Gly Ala Asp Lys Val Ala	
340 345 350 355	
GAT AAA GTA GGC ACG ACT TTG CTG AGC GCA ACC GCT ATT GGC ATT GTT	1162
Asp Lys Val Gly Thr Thr Leu Leu Ser Ala Thr Ala Ile Gly Ile Val	
360 365 370	
GCG CAT GCG CTC CTT TCT AAA GCG ATC AAA AAC AAA GAG TAAGGGATTA AC	1213
Ala His Ala Leu Leu Ser Lys Ala Ile Lys Asn Lys Glu	
375 380	
ATGTCAAAAA AAATCGTAGT CGATCCTATC ACTAGGATTG AGGGGCATTT AAGGATTGAA	1273
GTGATCGTAG ATGATGATAA CGTGATCACT G	1304

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Phe Tyr Asp Glu Lys Lys Thr Tyr Gln Lys Ile Glu Glu Arg Leu	
1 5 10 15	
Asp Ile Val Arg Ser Phe Asn Ala His Asn Glu His Lys Asn Leu Gln	
20 25 30	
Asp Glu Phe Lys Gly Ala Gly Ile Ser Arg Arg Asp Leu Leu Lys Trp	
35 40 45	
Ala Gly Met Met Ser Thr Ala Leu Ala Leu Pro Ala Ser Phe Ala Pro	
50 55 60	
Leu Thr Leu Lys Ala Val Glu Val Ala Asn Arg Leu Pro Val Ile Trp	
65 70 75 80	
Leu His Met Ala Glu Cys Thr Gly Cys Ser Glu Ser Leu Leu Arg Ser	
85 90 95	
Ala Asp Pro Thr Ile Asp Ser Ile Ile Phe Asp Tyr Ile Asn Leu Glu	
100 105 110	
Tyr His Glu Thr Ile Met Val Ala Ser Gly Phe Gln Ala Glu Lys Ser	
115 120 125	
Leu His Asp Ala Ile Glu Lys His Lys Asn Asn Tyr Ile Leu Met Val	
130 135 140	
Glu Gly Gly Ile Pro Gln Gly Thr Glu Tyr Phe Leu Thr Gln Gly Pro	
145 150 155 160	
Asn Ala Glu Thr Gly Ala Glu Glu Cys Arg Lys Ala Ala Gln Tyr Ala	
165 170 175	
Ala Ala Ile Phe Ala Ile Gly Thr Cys Ser Ser Phe Gly Gly Val Gln	
180 185 190	
Ala Ala Tyr Pro Asn Pro Ser Asn Ala Gln Pro Leu His Lys Ile Ile	
195 200 205	
Asp Lys Pro Val Ile Asn Val Pro Gly Cys Pro Pro Ser Glu Lys Asn	
210 215 220	
Ile Val Gly Asn Val Leu Tyr Tyr Leu Met Phe Gly Ala Leu Pro Lys	
225 230 235 240	
Leu Asp Ala Tyr Asn Arg Pro Ser Trp Ala Tyr Gly Asn Arg Ile His	

75								80				85					
AGC Ser	TTG Leu	ATG Met	GAA Glu 90	CGC Arg	AAG Lys	AGT Ser	TTT Phe	AGC Ser 95	CAA Gln	CTT Leu	TTA Leu	AGC Ser	CCA Pro 100	AAA Lys	GCC Ala	344	
TGG Trp	ATT Ile	GAT Asp 105	CAG Gln	ATG Met	AAA Lys	GCG Ala	TAT Tyr 110	TTT Phe	CTT Leu	ATC Ile	AGC Ser	GGC Gly 115	AAA Lys	CCC Pro	CAC His	392	
ACT Thr	AAA Lys 120	GGA Gly	GCG Ala	TAT Tyr	AAC Asn	CCT Pro 125	ATC Ile	CAA Gln	CTC Leu	GTG Val 130	GCT Ala	TAT Tyr	TCC Ser	ACT Thr	TTG Leu	440	
ATT Ile 135	GTT Val	TTG Leu	ATC Ile	GTG Val	TTG Leu 140	ATG Met	AGT Ser	TTG Leu	AGC Ser	GGG Gly 145	ATG Met	GTG Val	CTG Leu	TAT Tyr	TAT Tyr 150	488	
AAT Asn	GTC Val	TAT Tyr	CAT His 155	GCG Ala	GGG Gly	CTT Leu	GGA Gly	GCG Ala 160	TTT Phe	TTA Leu	GGA Gly	AGC Ser	GCT Ala 165	TTT Phe	AAG Lys	536	
TGG Trp	TTT Phe	GAA Glu 170	ACG Thr	CTT Leu	TGT Cys	GGA Gly	GGG Gly	TTA Leu 175	GCG Ala	AAT Asn	GTT Val	CGT Arg	TTC Phe 180	ATC Ile	CAC His	584	
CAC His	TTA Leu 185	GCG Ala	ACT Thr	TGG Trp	GGG Gly	TTT Phe	ATT Ile 190	TTG Leu	TTT Phe	GTC Val	CCT Pro 195	GTG Val	CAT His	GTT Val	TAT Tyr	632	
ATG Met 200	GTG Val	TTT Phe	TTC Phe	CAT His	TCT Ser	ATC Ile 205	AGG Arg	TAT Tyr	GAA Glu	AGT Ser	TCG Ser 210	GGG Gly	GCG Ala	GAT Asp	TCT Ser	680	
ATG Met 215	ATT Ile	AAT Asn	GGC Gly	TAT Tyr	GGT Gly 220	TAT Tyr	ACC Thr	AAA Lys	GAA Glu	TGAGTCAAAA				AATCCTAATT		CTA	733
GGTATTGGCA			ATATCCTTTT			TGGCGATGAA			GGGATTGGGG			TGCATTTAGC			CCACTACCTC		793
AAAAAAAAATT			TTTCTTT														810

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

-22-

GAG Glu	CCT Pro	TTA Leu	GAT Asp	GAA Glu 60	AAT Asn	CTT Leu	TTC Phe	CAA Gln 65	ACA Thr	GCA Ala	AGC Ser	CTT Leu	TCA Ser	AAG Lys 70	CCC Pro	244
CTT Leu	TTT Phe	ATG Met 75	AAC Asn	GCT Ala	AAA Lys	GAG Glu	CAT His 80	CAA Gln 85	GAT Asp	TTT Phe	TTA Leu	GAC Asp	AAA Lys 85	AAT Asn	TCA Ser	292
TCT Ser	TTG Leu	TAT Tyr 90	GCC Ala	GAT Asp	ACT Thr	CTG Leu	GGC Gly 95	TTG Leu	ATT Ile	AAA Lys	AAC Asn	ACC Thr 100	GCT Ala	TTT Phe	AAG Lys	340
GGG Gly	GAT Asp 105	ATA Ile	ATC Ile	CAT His	AGC Ser	CCT Pro 110	AAA Lys	GAG Glu	CTT Leu	ATA Ile	GAT Asp 115	TGC Cys	TTA Leu	ACC Thr	CAA Gln	388
TTA Leu 120	AAA Lys	GGC Gly	ATG Met	CTC Leu	AAA Lys 125	ACG Thr	CAA Gln	GAT Asp	TTT Phe 130	ATC Ile	CCT Pro	ATT Ile	TTC Phe	ACT Thr	TCT Ser 135	436
AGA Arg	GAG Glu	GCG Ala	TTA Leu	TCC Ser 140	CTT Leu	TCT Ser	TTA Leu	AAA Lys 145	AAT Asn	CCC Pro	TCT Ser	CCA Pro	AGC Ser	GTT Val 150	ATT Ile	484
TTT Phe	AGC Ser	GAT Asp	CTT Leu 155	TCT Ser	AGC Ser	GTT Val	TTG Leu	AGC Ser 160	TGC Cys	ACT Thr	AAA Lys	TTG Leu 165	CCT Pro	TTA Leu	GAG Glu	532
GAC Asp	GCT Ala	AAA Lys 170	TAT Tyr	TTG Leu	GCC Ala	AGT Ser	TTG Leu 175	GAA Glu	AAA Lys	CCC Pro	TCC Ser 180	ATC Ile	AAA Lys	GCC Ala	CCA Pro	580
TTA Leu 185	AAA Lys	AGC Ser	GTG Val	TTT Phe	AAA Lys 190	GAC Asp	ACT Thr	TTC Phe	AAA Lys	AAC Asn	GAT Asp 195	GAA Glu	ATC Ile	ATC Ile	GCC Ala	628
CAG Gln 200	CTA Leu	CCC Pro	TAT Tyr	GAC Asp 205	CCC Pro	ATA Ile	TTG Leu	AAT Asn	TTA Leu 210	TTG Leu	TGC Cys	CAT His	ATT Ile	TTA Leu	CAA Gln 215	676
GAT Asp	GAG Glu	GGG Gly	ATA Ile 220	GAA Glu	TTT Phe	GTT Val	TTT Phe	ATG Met 225	CAT His	GAA Glu	AGC Ser	CGT Arg	TCT Ser	TGT Cys 230	GAA Glu	724
GCG Ala	CTT Leu	TTG Leu	TAT Tyr 235	TAT Tyr	GAA Glu	GCG Ala	CTT Leu 240	TTT Phe	AAA Lys	ACC Thr	CCT Pro	AAA Lys	CGC Arg 245	TTG Leu	ATC Ile	772
ACA Thr	CCC Pro	ACT Thr 250	AAA Lys	AAA Lys	TTC Phe	GTG Val	CTA Leu 255	GAA Glu	AAT Asn	AAT Asn	TTT Phe 260	TCT Ser	ACC Thr	TTT Phe	CCC Pro	820
TTT Phe 265	AAA Lys	GAT Asp	GAA Glu	TTA Leu	GAG Glu	TTT Phe 270	TTA Leu	AGC Ser	GCA Ala	ACC Thr	CCC Pro 275	AAT Asn	TCT Ser	ATC Ile	GTT Val	868
TTG Leu	TAT Tyr	CTC Leu	AGT Ser	TTC Phe	AAG Lys	CGC Arg	CCT Pro	ACA Thr	AGG Arg	TTG Leu	TTA Leu	TTG Leu	CAT His	GCT Ala	AAT Asn	916

280	285	290	295	
GGT TCT TTA AAA ACG CTT TTA AGC GTC AGT TTT GAT TTT AAC AAA ATG				964
Gly Ser Leu Lys Thr Leu Leu Ser Val Ser Phe Asp Phe Asn Lys Met				
	300	305	310	
TTT AAC GCG CTC AAA CAA GAT GAA AAA GCC TCC AGA ATG CTA CAA AAC				1012
Phe Asn Ala Leu Lys Gln Asp Glu Lys Ala Ser Arg Met Leu Gln Asn				
	315	320	325	
TAC GCC ACT AAA TTC CCT GAT TTT TAC GCG CGC ATT GTA GAG CTT TCT				1060
Tyr Ala Thr Lys Phe Pro Asp Phe Tyr Ala Arg Ile Val Glu Leu Ser				
	330	335	340	
AAA TAC GAT CTA GGG GGC GCG AAT TTA TTG GAT TTT TTT TGC ATT TTA				1108
Lys Tyr Asp Leu Gly Gly Ala Asn Leu Leu Asp Phe Phe Cys Ile Leu				
	345	350	355	
GGG TTT GTT TTG GGC TAT AGC GAG GAT TTT TGC ACA CAG AGC GTT ATT				1156
Gly Phe Val Leu Gly Tyr Ser Glu Asp Phe Cys Thr Gln Ser Val Ile				
	360	365	370	
CCT TTG GCT AAA GAA TGC TTA CGC CCT AAA GGC CCT AGG ATT GAT TAT				1204
Pro Leu Ala Lys Glu Cys Leu Arg Pro Lys Gly Pro Arg Ile Asp Tyr				
	380	385	390	
AAA ATC CTT AAA GAC AAT TCT TTG AAA ATG GCT TTA AAC TTT TCA AAG				1252
Lys Ile Leu Lys Asp Asn Ser Leu Lys Met Ala Leu Asn Phe Ser Lys				
	395	400	405	
ATC ATG CAC AGT GCG ATG AGT TTC AGG CTC GCA GGC GTG GAA AAT GAA				1300
Ile Met His Ser Ala Met Ser Phe Arg Leu Ala Gly Val Glu Asn Glu				
	410	415	420	
ATT TTG AGT TTG GGG ATT TTG GAT TCT TTA GCG GAG TTT TTA GGG AAT				1348
Ile Leu Ser Leu Gly Ile Leu Asp Ser Leu Ala Glu Phe Leu Gly Asn				
	425	430	435	
TTC ATT TGG GAT AAC GCG CAA AAT TTT AGC GTT CAA GAA GTA ACG ATC				1396
Phe Ile Trp Asp Asn Ala Gln Asn Phe Ser Val Gln Glu Val Thr Ile				
	440	445	450	
GCT GGG GAT TTC TTT GGC GAA AAA GTG TTT TTG GAT TTG TTT GTG CGG				1444
Ala Gly Asp Phe Phe Gly Glu Lys Val Phe Leu Asp Leu Phe Val Arg				
	460	465	470	
TAT TTC CCT AAA ACC CTA GCC CTT AAA ACG CAT GCA TTT TTG GAT TAT				1492
Tyr Phe Pro Lys Thr Leu Ala Leu Lys Thr His Ala Phe Leu Asp Tyr				
	475	480	485	
GAA TAAGGGCTTA AAAGCGGATG TGCATCATCA GCCCGCCGTC CATGTATT				1543
Glu				

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 488 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ala	Cys	Asn	Leu	Gln	Ala	Arg	Phe	Tyr	Ser	Val	Tyr	Lys	Asp	Asn
1				5					10					15	
Thr	Thr	Ser	Phe	Tyr	Leu	Gln	Ala	Ser	Ala	Glu	Thr	Thr	Leu	Glu	Phe
			20					25					30		
Ala	Gln	Lys	Leu	Ser	Glu	Ile	Leu	Pro	Phe	Ser	Leu	Asp	Phe	Ser	Phe
		35					40					45			
Leu	Ser	Leu	Lys	Glu	Ile	Thr	Glu	Pro	Leu	Asp	Glu	Asn	Leu	Phe	Gln
	50					55				60					
Thr	Ala	Ser	Leu	Ser	Lys	Pro	Leu	Phe	Met	Asn	Ala	Lys	Glu	His	Gln
65					70				75						80
Asp	Phe	Leu	Asp	Lys	Asn	Ser	Ser	Leu	Tyr	Ala	Asp	Thr	Leu	Gly	Leu
			85					90					95		
Ile	Lys	Asn	Thr	Ala	Phe	Lys	Gly	Asp	Ile	Ile	His	Ser	Pro	Lys	Glu
			100				105						110		
Leu	Ile	Asp	Cys	Leu	Thr	Gln	Leu	Lys	Gly	Met	Leu	Lys	Thr	Gln	Asp
		115					120					125			
Phe	Ile	Pro	Ile	Phe	Thr	Ser	Arg	Glu	Ala	Leu	Ser	Leu	Ser	Leu	Lys
	130					135				140					
Asn	Pro	Ser	Pro	Ser	Val	Ile	Phe	Ser	Asp	Leu	Ser	Ser	Val	Leu	Ser
145					150				155					160	
Cys	Thr	Lys	Leu	Pro	Leu	Glu	Asp	Ala	Lys	Tyr	Leu	Ala	Ser	Leu	Glu
			165					170					175		
Lys	Pro	Ser	Ile	Lys	Ala	Pro	Leu	Lys	Ser	Val	Phe	Lys	Asp	Thr	Phe
			180				185						190		
Lys	Asn	Asp	Glu	Ile	Ile	Ala	Gln	Leu	Pro	Tyr	Asp	Pro	Ile	Leu	Asn
		195				200					205				
Leu	Leu	Cys	His	Ile	Leu	Gln	Asp	Glu	Gly	Ile	Glu	Phe	Val	Phe	Met
	210					215				220					
His	Glu	Ser	Arg	Ser	Cys	Glu	Ala	Leu	Leu	Tyr	Tyr	Glu	Ala	Leu	Phe
225					230					235					240
Lys	Thr	Pro	Lys	Arg	Leu	Ile	Thr	Pro	Thr	Lys	Lys	Phe	Val	Leu	Glu
			245					250						255	
Asn	Asn	Phe	Ser	Thr	Phe	Pro	Phe	Lys	Asp	Glu	Leu	Glu	Phe	Leu	Ser
		260					265						270		
Ala	Thr	Pro	Asn	Ser	Ile	Val	Leu	Tyr	Leu	Ser	Phe	Lys	Arg	Pro	Thr
		275					280					285			
Arg	Leu	Leu	Leu	His	Ala	Asn	Gly	Ser	Leu	Lys	Thr	Leu	Leu	Ser	Val
	290					295					300				
Ser	Phe	Asp	Phe	Asn	Lys	Met	Phe	Asn	Ala	Leu	Lys	Gln	Asp	Glu	Lys
305					310					315					320
Ala	Ser	Arg	Met	Leu	Gln	Asn	Tyr	Ala	Thr	Lys	Phe	Pro	Asp	Phe	Tyr
			325					330					335		
Ala	Arg	Ile	Val	Glu	Leu	Ser	Lys	Tyr	Asp	Leu	Gly	Gly	Ala	Asn	Leu
		340					345					350			
Leu	Asp	Phe	Phe	Cys	Ile	Leu	Gly	Phe	Val	Leu	Gly	Tyr	Ser	Glu	Asp
	355					360					365				
Phe	Cys	Thr	Gln	Ser	Val	Ile	Pro	Leu	Ala	Lys	Glu	Cys	Leu	Arg	Pro
	370					375				380					
Lys	Gly	Pro	Arg	Ile	Asp	Tyr	Lys	Ile	Leu	Lys	Asp	Asn	Ser	Leu	Lys

GAA Glu	TTG Leu	GTT Val 70	TTT Phe	AGC Ser	GTT Val	CAT His 75	TTA Leu 75	ACA Thr	GAC Asp	GAT Asp	TTA Leu 80	AAG Lys 80	CGG Arg	CGC Arg	GAT Asp	297
TTT Phe 85	AGC Ser 85	ATG Met	AAT Asn	GCG Ala	ATC Ile	GCT Ala 90	TAT Tyr	AGC Ser	CCT Pro	ACA Thr	AAA Lys 95	GGG Gly	CTG Leu	ATT Ile	GAT Asp	345
CCT Pro 100	TTT Phe	AAA Lys	GGG Gly	CAG Gln	AAT Asn 105	GCG Ala	ATT Ile	GAA Glu	AAT Asn 110	CAA Gln 110	ATG Met	ATT Ile	GAA Glu	TGC Cys	GTG Val 115	393
GGG Gly	GAA Glu	GCG Ala	CGA Arg 120	TTA Leu 120	AGG Arg	TTT Phe	TTT Phe	GAA Glu	GAC Asp 125	GCT Ala	TTA Leu	AGG Arg	ATT Ile	TTA Leu 130	AGA Arg	441
TCG Ser	CTG Leu	CGA Arg	TTC Phe 135	AGT Ser	GCA Ala	ACT Thr	TTA Leu	GGC Gly 140	TTT Phe	AAG Lys	ATA Ile	GCG Ala	CCA Pro 145	AAC Asn	ACC Thr	489
AAA Lys 150	GAA Glu 150	GCG Ala	GTT Val	TTT Phe	GCG Ala	TGT Cys 155	AAG Lys 155	GAT Asp	TTG Leu	TTA Leu	AAA Lys 160	CAC His 160	CTT Leu	TCT Ser	AAA Lys	537
GAA Glu 165	CGC Arg 165	TTA Leu	CAA Gln	AGT Ser	GAA Glu	TTG Leu 170	AAT Asn 170	AAG Lys	CTT Leu	CTT Leu	ATG Met 175	GGG Gly	AAA Lys	AAC Asn	GCC Ala	585
TAT Tyr 180	GAA Glu	GTG Val	GCT Ala	AAA Lys	GAA Glu 185	TAT Tyr	CAA Gln	GAA Glu	ATT Ile 190	TTA Leu 190	GAG Glu	TTG Leu	GTT Val	ATT Ile	CAA Gln 195	633
GAA Glu 200	AAA Lys	ATA Ile	GAA Glu	AAT Asn 200	TTA Leu	GGG Gly	TTT Phe	TTA Leu	AAA Lys 205	AAC Asn 205	GCG Ala	CCT Pro	TTC Phe	AAT Asn 210	CTG Leu	681
GAA Glu 215	TTA Leu	AGA Arg	TTG Leu 215	TTA Leu	GGG Gly	TTT Phe	TTT Phe	AAG Lys 220	CAT His	CAA Gln	AAA Lys	AGT Ser	TTA Leu 225	GAA Glu	AGT Ser	729
TTA Leu 230	CGC Arg	TAC Tyr 230	CCT Pro	AAA Lys	AAA Lys	ACG Thr	ATC Ile 235	GTT Val	TTA Leu	TTT Phe	TCC Ser 240	AAA Lys 240	GCT Ala	AAA Lys	GAA Glu	777
TGC Cys 245	CAT His 245	AAA Lys	TCT Ser	TTT Phe	TTA Leu	AAT Asn 250	ATT Ile	CAT His	AAC Asn	AAA Lys	ACA Thr 255	GAG Glu	TTA Leu	AAA Lys	TTT Phe	825
TTA Leu 260	TTG Leu	AAA Lys	AAC Asn	TAC Tyr	GAT Asp 265	TTA Leu	GAG Glu	CCT Pro	TTT Phe	AAT Asn 270	TTG Leu	GCT Ala	TTA Leu	GAT Asp	TTT Phe 275	873
TAT Tyr	GCG Ala	CTC Leu	AAA Lys	AAC Asn 280	CCC Pro	AAA Lys	CAT His	GCT Ala 285	TTA Leu 285	AAA Lys	ATT Ile	AAA Lys	GGC Gly	TTG Leu 290	TTA Leu	921
AAA Lys	GAA Glu	ATC Ile	TTT Phe	GAT Asp	TCT Ser	AAC Asn	GAG Glu	CCT Pro	TTT Phe	AAA Lys	AAA Lys	GAA Glu	CAC His	TTG Leu	GCC Ala	969

Phe Asn Leu Glu Leu Arg Leu Leu Gly Phe Phe Lys His Gln Lys Ser
 210 215 220
 Leu Glu Ser Leu Arg Tyr Pro Lys Lys Thr Ile Val Leu Phe Ser Lys
 225 230 235 240
 Ala Lys Glu Cys His Lys Ser Phe Leu Asn Ile His Asn Lys Thr Glu
 245 250 255
 Leu Lys Phe Leu Leu Lys Asn Tyr Asp Leu Glu Pro Phe Asn Leu Ala
 260 265 270
 Leu Asp Phe Tyr Ala Leu Lys Asn Pro Lys His Ala Leu Lys Ile Lys
 275 280 285
 Gly Leu Leu Lys Glu Ile Phe Asp Ser Asn Glu Pro Phe Lys Lys Glu
 290 295 300
 His Leu Ala Leu Lys Gly Gly Ala Leu Gln Ser Leu Gly Tyr Gln His
 305 310 315 320
 Gln Lys Ile Gly Glu Ile Leu Asn Ala Cys Leu Asp Leu Val Ile Ala
 325 330 335
 Asn Pro Lys Asn Asn Ala Leu Glu Trp Leu Ile Glu Trp Val Lys Gly
 340 345 350
 His Tyr Leu Pro Asn Asp Thr Ile Asn Leu Ser Pro Ile Gly Arg Arg
 355 360 365
 Asn

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...340
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TTTTCCCCTA TATCCAAAGC CATCATCAAG AAGTTTAAAG GCTCAAAGC ATG ATT TTT	58
Met Ile Phe	
1	
TCC ACT CTT ATT AAT GCG ATA GCG GTG ATT TTA AGC TCG CTC ATT ACG	106
Ser Thr Leu Ile Asn Ala Ile Ala Val Ile Leu Ser Ser Leu Ile Thr	
5 10 15	
ATT TAT ATG TGG ATA GTA ATC ATT TAT TCG CTT ATC AGT TTC GTG CAG	154
Ile Tyr Met Trp Ile Val Ile Ile Tyr Ser Leu Ile Ser Phe Val Gln	
20 25 30 35	
CCT AAC CCC AAT AAC CCC ATC ATG CAA ATT CTC GCT CGC TTG TGT GAG	202
Pro Asn Pro Asn Asn Pro Ile Met Gln Ile Leu Ala Arg Leu Cys Glu	
40 45 50	
CCG GTG TTT TAT TTT TTA CGC TCT AGA TTC AAG CTG GTG TTT AAC GGG	250

Pro Val Phe Tyr Phe Leu Arg Ser Arg Phe Lys Leu Val Phe Asn Gly
55 60 65

TTG GAT TTC TCT CCT TTA GTG GTG GTC ATT GTT TTG AAA TTC TTG GAT 298
Leu Asp Phe Ser Pro Leu Val Val Val Ile Val Leu Lys Phe Leu Asp
70 75 80

CTC ACG CTC ATT CAG TGG CTT TTC ATG CTC GCT AAA AAC CTT TAAAGAAAA 349
Leu Thr Leu Ile Gln Trp Leu Phe Met Leu Ala Lys Asn Leu
85 90 95

TCATGCGTTT T 360

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Ile Phe Ser Thr Leu Ile Asn Ala Ile Ala Val Ile Leu Ser Ser
1 5 10 15
Leu Ile Thr Ile Tyr Met Trp Ile Val Ile Ile Tyr Ser Leu Ile Ser
20 25 30
Phe Val Gln Pro Asn Pro Asn Asn Pro Ile Met Gln Ile Leu Ala Arg
35 40 45
Leu Cys Glu Pro Val Phe Tyr Phe Leu Arg Ser Arg Phe Lys Leu Val
50 55 60
Phe Asn Gly Leu Asp Phe Ser Pro Leu Val Val Val Ile Val Leu Lys
65 70 75 80
Phe Leu Asp Leu Thr Leu Ile Gln Trp Leu Phe Met Leu Ala Lys Asn
85 90 95
Leu

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...1701
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TAAAAACCTT TAAAGAAAAT C ATG CGT TTT Phe Thr Leu Phe Phe Ile GGT																51
Met 1 Arg 5																
ATG CTT GGC GTT GGT TTT TCT CAA ACC GAG TTA AAT TTA AAA GAT TTA	99															
Met Leu Gly Val Gly Phe Ser Gln Thr Glu Leu Asn Leu Lys Asp Leu	15 20 25															
GAA AAA AAG CCC GCC GGG ATC GTT AGG GAT TAT TAT TTG TGG CGT TAT																147
Glu Lys Lys Pro Ala Gly Ile Val Arg Asp Tyr Tyr Leu Trp Arg Tyr	30 35 40															
ATT AGC GAT AAA AAA ACC AGT TTA GAA AAC GCT AAA AAA GCC TAT GAA																195
Ile Ser Asp Lys Lys Thr Ser Leu Glu Asn Ala Lys Lys Ala Tyr Glu	45 50 55															
TTG ACT CAA AAT AAA AAC AAC GCC CTA CAA AAG GCC ATG CAA GAA AAA																243
Leu Thr Gln Asn Lys Asn Asn Ala Leu Gln Lys Ala Met Gln Glu Lys	60 65 70															
GGC TCA GAC AAT GCA GAA AAA AAC CCT GAT GTT AAA TTG CCT GAA GAT																291
Gly Ser Asp Asn Ala Glu Lys Asn Pro Asp Val Lys Leu Pro Glu Asp	75 80 85 90															
ATT TAT TGC AAG CAA ACG GCT TTA GAA AGC ATG CTA GAA ACA ACA GAC																339
Ile Tyr Cys Lys Gln Thr Ala Leu Glu Ser Met Leu Glu Thr Thr Asp	95 100 105															
ACT TTC CAA GCA AGC TGC ATC GCT ATC GCT TTA AAA TCA AAG ATC AGA																387
Thr Phe Gln Ala Ser Cys Ile Ala Ile Ala Leu Lys Ser Lys Ile Arg	110 115 120															
GAT TTT GAT AAA ATC CCT ATT GAA ACC CTT AAG CCC TTA CAA ATT AAA																435
Asp Phe Asp Lys Ile Pro Ile Glu Thr Leu Lys Pro Leu Gln Ile Lys	125 130 135															
ATC AAA GAG GCT TAC CCC GTT CTT TAT GAA GAA TTA GAA ATT TTG CAA																483
Ile Lys Glu Ala Tyr Pro Val Leu Tyr Glu Glu Leu Glu Ile Leu Gln	140 145 150															
AGT AAG CAT GTG AGC GCT TCT TTG TTT AAG GCT AAC GCG CAA GTG TTT																531
Ser Lys His Val Ser Ala Ser Leu Phe Lys Ala Asn Ala Gln Val Phe	155 160 165 170															
AGC GCG CTT TTC AAT CAT TTG AGT TAT GAA AAA AAG CTC CAA ATT TTT																579
Ser Ala Leu Phe Asn His Leu Ser Tyr Glu Lys Lys Leu Gln Ile Phe	175 180 185															
GAA AAG CAT ATC CCC ATT AAA GAG TTA AAC CGT CTT TTA GAC GAA AAT																627
Glu Lys His Ile Pro Ile Lys Glu Leu Asn Arg Leu Leu Asp Glu Asn	190 195 200															
TAT CCG GCG TTT AAC CGC TTG ATC TAT CAG GTT ATT TTA GAT CCT AAA																675
Tyr Pro Ala Phe Asn Arg Leu Ile Tyr Gln Val Ile Leu Asp Pro Lys	205 210 215															
TTG GAT CAT TTT AAA GAC GCT CTC ACT AAA AGT AAC GCT ACC CAC AGC																723
Leu Asp His Phe Lys Asp Ala Leu Thr Lys Ser Asn Ala Thr His Ser																

220				225				230								
AAC Asn 235	GCG Ala	CAA Gln	ACC Thr	TTT Phe	TTT Phe	ATT Ile	CTA Leu	GGG Gly	ATT Ile	AAT Asn	GAA Glu	ATC Ile	TTG Leu	CGC Arg	AAA Lys	771
				240				245				250				
AAA Lys	CCC Pro	TCT Ser	AAA Lys	GCG Ala	CTC Leu	AAG Lys	TAT Tyr	TTT Phe	GAA Glu	CGA Arg	TCA Ser	GAA Glu	GCG Ala	GTT Val	GTC Val	819
				255				260				265				
AAA Lys	GAC Asp	GAT Asp	GAT Asp	TTT Phe	TCA Ser	AAA Lys	GAC Asp	AGA Arg	GCG Ala	ATT Ile	TTT Phe	TGG Trp	CAG Gln	TAT Tyr	TTA Leu	867
				270				275				280				
GTT Val	TCT Ser	AAA Lys	AAG Lys	AAA Lys	AAA Lys	ACT Thr	TTA Leu	GAA Glu	CGC Arg	CTT Leu	TCA Ser	CAA Gln	AGC Ser	CCA Pro	GCT Ala	915
				285				290				295				
TTA Leu	AAT Asn	CTC Leu	TAT Tyr	AGT Ser	CTT Leu	TAT Tyr	GCG Ala	AGC Ser	CGC Arg	AAA Lys	CTC Leu	AAA Lys	ACC Thr	ACG Thr	CCC Pro	963
				300				305				310				
AGT Ser	TAC Tyr	CGC Arg	ATC Ile	ATT Ile	TCA Ser	CGC Arg	ATC Ile	CAG Gln	AAT Asn	TTA Leu	AGC Ser	CAA Gln	GAA Glu	GAT Asp	CCT Pro	1011
				315				320				325				
CCT Pro	TTT Phe	AAC Asn	ACT Thr	TAT Tyr	GAC Asp	CCT Pro	TTT Phe	TCG Ser	TGG Trp	CAA Gln	ATT Ile	TTT Phe	AAG Lys	GAA Glu	AAA Lys	1059
				335				340				345				
ACC Thr	TTG Leu	AGT Ser	TTG Leu	AAA Lys	GAT Asp	GAG Glu	GGC Gly	GCG Ala	TTT Phe	AAT Asn	GCG Ala	ATG Met	CTA Leu	AAA Lys	AGC Ser	1107
				350				355				360				
CTG Leu	TAT Tyr	TAT Tyr	GAA Glu	AAA Lys	AGC Ser	GCT Ala	CCT Pro	GAA Glu	TTG Leu	ACC Thr	TAT Tyr	CTT Leu	TTA Leu	AGC Ser	CAA Gln	1155
				365				370				375				
CGC Arg	AAT Asn	AAA Lys	GAC Asp	AAG Lys	ATT Ile	TAT Tyr	TAT Tyr	TAT Tyr	TTA Leu	TCC Ser	CCT Pro	TAT Tyr	GAG Glu	GGC Gly	ATT Ile	1203
				380				385				390				
ATT Ile	GAA Glu	TGG Trp	CAA Gln	AAT Asn	ACT Thr	GAT Asp	GAA Glu	AAG Lys	GCT Ala	ATG Met	GCG Ala	TAT Tyr	GCG Ala	ATC Ile	GCT Ala	1251
				400				405				410				
AGG Arg	CAA Gln	GAA Glu	AGC Ser	TTT Phe	TTG Leu	CTC Leu	CCG Pro	GCA Ala	GTC Val	ATT Ile	TCG Ser	CGC Arg	TCG Ser	TTC Phe	GCT Ala	1299
				415				420				425				
CTG Leu	GGG Gly	CTT Leu	ATG Met	CAA Gln	ATC Ile	ATG Met	CCC Pro	TTT Phe	AAT Asn	GTA Val	GGG Gly	CCT Pro	TTC Phe	GCT Ala	AAA Lys	1347
				430				435				440				
AGC Ser	CTT Leu	GGC Gly	ATG Met	GAT Asp	AAC Asn	ATT Ile	GAT Asp	CTA Leu	AAC Asn	GAC Asp	ATG Met	TTT Phe	AAC Asn	CCC Pro	AAC Asn	1395
				445				450				455				

(A) LENGTH: 770 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 16...738
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TAAAAAGAAG GACAA ATG ATG CCA TTT GAA GCT GTA ATC GGG CTA GAA GTC	51
Met Met Pro Phe Glu Ala Val Ile Gly Leu Glu Val	
1 5 10	
CAT GTC CAA CTC AAC ACC AAA ACC AAA ATC TTT TGC TCT TGC TCT ACA	99
His Val Gln Leu Asn Thr Lys Thr Lys Ile Phe Cys Ser Cys Ser Thr	
15 20 25	
AGC TTT GGA GAA TCC CCT AAT TCT AAC ACC TGC CCT GTG TGT TTG GGT	147
Ser Phe Gly Glu Ser Pro Asn Ser Asn Thr Cys Pro Val Cys Leu Gly	
30 35 40	
TTA CCG GGA GCT TTG CCG GTA TTG AAT AAA GAA GTG GTT AAA AAA GCC	195
Leu Pro Gly Ala Leu Pro Val Leu Asn Lys Glu Val Val Lys Lys Ala	
45 50 55 60	
ATC CAA TTA GGC ACA GCC ATT GAA GCC AAT ATC AAC CAA TAT TCT ATT	243
Ile Gln Leu Gly Thr Ala Ile Glu Ala Asn Ile Asn Gln Tyr Ser Ile	
65 70 75	
TTT GCG AGG AAA AAT TAT TTT TAC CCT GAT TTG CCT AAG GCT TAT CAA	291
Phe Ala Arg Lys Asn Tyr Phe Tyr Pro Asp Leu Pro Lys Ala Tyr Gln	
80 85 90	
ATT TCG CAG TTT GAA GTC CCT ATT GTG AGC GAT GGG AAA TTA GAG ATT	339
Ile Ser Gln Phe Glu Val Pro Ile Val Ser Asp Gly Lys Leu Glu Ile	
95 100 105	
GAC ACT AAA GAG GGT GCA AAA ATC GTG CGT ATT GAA AGG GCC CAC ATG	387
Asp Thr Lys Glu Gly Ala Lys Ile Val Arg Ile Glu Arg Ala His Met	
110 115 120	
GAA GAA GAC GCC GGT AAA AAT ATC CAT GAG GGC AGT TAT TCT TTA GTG	435
Glu Glu Asp Ala Gly Lys Asn Ile His Glu Gly Ser Tyr Ser Leu Val	
125 130 135 140	
GAT TTG AAC CGC GCT TGC ACC CCT TTA TTA GAA ATT GTC AGT AAG CCG	483
Asp Leu Asn Arg Ala Cys Thr Pro Leu Leu Glu Ile Val Ser Lys Pro	
145 150 155	
GAC ATG CGA AAT AGT GAA GAA GCT ATA GCG TAT TTG AAA AAG CTC CAT	531
Asp Met Arg Asn Ser Glu Glu Ala Ile Ala Tyr Leu Lys Lys Leu His	
160 165 170	

GCT ATC GTG CGT TTT ATA GGG ATT TCT GAT GCG AAC ATG CAA GAG GGG	579
Ala Ile Val Arg Phe Ile Gly Ile Ser Asp Ala Asn Met Gln Glu Gly	
175 180 185	
AAT TTC AGG TGC GAT GCG AAC GTG TCC ATT AGA CCC AAA GGC GAT GAA	627
Asn Phe Arg Cys Asp Ala Asn Val Ser Ile Arg Pro Lys Gly Asp Glu	
190 195 200	
AAG CTT TAT ACG AGA GTA GAG ATT AAA AAT CTA AAT AGC TTT AGA TTC	675
Lys Leu Tyr Thr Arg Val Glu Ile Lys Asn Leu Asn Ser Phe Arg Phe	
205 210 215 220	
ATT GCT AAA GCG ATT GAA TAC GAG ATA GAG CGC CAA AGC GCG GAC GTG	723
Ile Ala Lys Ala Ile Glu Tyr Glu Ile Glu Arg Gln Ser Ala Asp Val	
225 230 235	
GGA GAA CGG GCG CTA TAATGAAGAG GTGGTTCAAG AAACGCGCCT TT	770
Gly Glu Arg Ala Leu	
240	

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Met Pro Phe Glu Ala Val Ile Gly Leu Glu Val His Val Gln Leu	
1 5 10 15	
Asn Thr Lys Thr Lys Ile Phe Cys Ser Cys Ser Thr Ser Phe Gly Glu	
20 25 30	
Ser Pro Asn Ser Asn Thr Cys Pro Val Cys Leu Gly Leu Pro Gly Ala	
35 40 45	
Leu Pro Val Leu Asn Lys Glu Val Val Lys Lys Ala Ile Gln Leu Gly	
50 55 60	
Thr Ala Ile Glu Ala Asn Ile Asn Gln Tyr Ser Ile Phe Ala Arg Lys	
65 70 75 80	
Asn Tyr Phe Tyr Pro Asp Leu Pro Lys Ala Tyr Gln Ile Ser Gln Phe	
85 90 95	
Glu Val Pro Ile Val Ser Asp Gly Lys Leu Glu Ile Asp Thr Lys Glu	
100 105 110	
Gly Ala Lys Ile Val Arg Ile Glu Arg Ala His Met Glu Glu Asp Ala	
115 120 125	
Gly Lys Asn Ile His Glu Gly Ser Tyr Ser Leu Val Asp Leu Asn Arg	
130 135 140	
Ala Cys Thr Pro Leu Leu Glu Ile Val Ser Lys Pro Asp Met Arg Asn	
145 150 155 160	
Ser Glu Glu Ala Ile Ala Tyr Leu Lys Lys Leu His Ala Ile Val Arg	
165 170 175	
Phe Ile Gly Ile Ser Asp Ala Asn Met Gln Glu Gly Asn Phe Arg Cys	
180 185 190	
Asp Ala Asn Val Ser Ile Arg Pro Lys Gly Asp Glu Lys Leu Tyr Thr	

	195		200		205
Arg	Val	Glu	Ile	Lys	Asn
	210		215		220
Ile	Glu	Tyr	Glu	Ile	Glu
225		230		235	
Leu					

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...444
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATGGGAGTGG	ATTGA	ATG	CAA	GAA	ATT	GAA	ATT	TTT	TGC	GAT	GGC	TCT	TCT	51
		Met	Gln	Glu	Ile	Glu	Ile	Phe	Cys	Asp	Gly	Ser	Ser	
		1				5					10			
TTA	GGC	AAT	CCC	GGG	CCA	GGC	GGT	TAT	GCG	GCG	ATT	TTA	CGC	99
Leu	Gly	Asn	Pro	Gly	Pro	Gly	Gly	Tyr	Ala	Ala	Ile	Leu	Arg	
	15					20						25		
GAT	AAA	GAA	AAA	ACC	ATC	AGT	GGG	GGC	GAA	GAA	TTC	ACC	ACG	147
Asp	Lys	Glu	Lys	Thr	Ile	Ser	Gly	Gly	Glu	Glu	Phe	Thr	Thr	
	30					35					40			
CGC	ATG	GAA	TTA	AGA	GCG	CTC	AAT	GAA	GCG	TTA	AAA	ATT	TTG	195
Arg	Met	Glu	Leu	Arg	Ala	Leu	Asn	Glu	Ala	Leu	Lys	Ile	Leu	
45					50				55				60	
CCA	TGC	CGT	ATC	ACG	CTT	TAT	AGC	GAT	TCG	CAA	TAC	GTG	TGC	243
Pro	Cys	Arg	Ile	Thr	Leu	Tyr	Ser	Asp	Ser	Gln	Tyr	Val	Cys	
			65					70					75	
ATC	AAT	GTG	TGG	CTA	GCT	AAC	TGG	CAA	AAA	AAG	AAT	TTT	TCT	291
Ile	Asn	Val	Trp	Leu	Ala	Asn	Trp	Gln	Lys	Lys	Asn	Phe	Ser	
		80					85					90		
AAA	AAT	GTG	GAT	TTA	TGG	AAA	GAA	TTT	TTA	GAA	GTC	TCT	AAA	339
Lys	Asn	Val	Asp	Leu	Trp	Lys	Glu	Phe	Leu	Glu	Val	Ser	Lys	
	95					100						105		
TCT	ATT	GTG	GCT	GTT	TGG	ATC	AAG	GGG	CAT	AAC	GGG	CAT	GCC	387
Ser	Ile	Val	Ala	Val	Trp	Ile	Lys	Gly	His	Asn	Gly	His	Ala	
	110					115					120			

GAA CGA TGC GAT AGC CTC GCT AAA TTA GAG GCG CAA AAA CGG GTC AAA 435
 Glu Arg Cys Asp Ser Leu Ala Lys Leu Glu Ala Gln Lys Arg Val Lys
 125 130 135 140

ACG ACC ACT TAAAGGGAAA AATGATGAAA AACAAACGCT CTCAAAACAG CCC 487
 Thr Thr Thr

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Gln	Glu	Ile	Glu	Ile	Phe	Cys	Asp	Gly	Ser	Ser	Leu	Gly	Asn	Pro
1				5					10					15	
Gly	Pro	Gly	Gly	Tyr	Ala	Ala	Ile	Leu	Arg	Tyr	Lys	Asp	Lys	Glu	Lys
			20					25					30		
Thr	Ile	Ser	Gly	Gly	Glu	Glu	Phe	Thr	Thr	Asn	Asn	Arg	Met	Glu	Leu
		35					40					45			
Arg	Ala	Leu	Asn	Glu	Ala	Leu	Lys	Ile	Leu	Lys	Arg	Pro	Cys	Arg	Ile
	50					55				60					
Thr	Leu	Tyr	Ser	Asp	Ser	Gln	Tyr	Val	Cys	Gln	Ala	Ile	Asn	Val	Trp
65					70					75				80	
Leu	Ala	Asn	Trp	Gln	Lys	Lys	Asn	Phe	Ser	Lys	Val	Lys	Asn	Val	Asp
			85					90					95		
Leu	Trp	Lys	Glu	Phe	Leu	Glu	Val	Ser	Lys	Gly	His	Ser	Ile	Val	Ala
			100					105					110		
Val	Trp	Ile	Lys	Gly	His	Asn	Gly	His	Ala	Glu	Asn	Glu	Arg	Cys	Asp
		115				120						125			
Ser	Leu	Ala	Lys	Leu	Glu	Ala	Gln	Lys	Arg	Val	Lys	Thr	Thr	Thr	
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 48...1181
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

215	220	225	
CAA AAG CTC CCC ATT GGC TTA GGT CAA GGG CTA TAC GCT AAA TTA GAC			776
Gln Lys Leu Pro Ile Gly Leu Gly Gln Gly Leu Tyr Ala Lys Leu Asp			
230	235	240	
GCT AAA ATC GCT GAA GCG ATG ATG GGG CTT AAT GGG GTG AAA GCG GTT			824
Ala Lys Ile Ala Glu Ala Met Met Gly Leu Asn Gly Val Lys Ala Val			
245	250	255	
GAA ATA GGC AAG GGG GTA GAA AGC TCT TTA TTA AAA GGC TCA GAG TAT			872
Glu Ile Gly Lys Gly Val Glu Ser Ser Leu Leu Lys Gly Ser Glu Tyr			
260	265	270	275
AAT GAT TTA ATG GAT CAA AAG GGG TTT TTG AGC AAT CGT AGC GGA GGG			920
Asn Asp Leu Met Asp Gln Lys Gly Phe Leu Ser Asn Arg Ser Gly Gly			
280	285	290	
GTT TTA GGG GGC ATG AGC AAT GGG GAA GAA ATC ATT GTT AGA GTG CAT			968
Val Leu Gly Gly Met Ser Asn Gly Glu Glu Ile Ile Val Arg Val His			
295	300	305	
TTC AAA CCC ACG CCA AGC ATT TTC CAA CCT CAA CGA ACC ATA GAC ATT			1016
Phe Lys Pro Thr Pro Ser Ile Phe Gln Pro Gln Arg Thr Ile Asp Ile			
310	315	320	
AAT GGC AAT GAG TGC GAA TGC TTG TTA AAG GGC AGG CAT GAT CCT TGC			1064
Asn Gly Asn Glu Cys Glu Cys Leu Leu Lys Gly Arg His Asp Pro Cys			
325	330	335	
ATT GCG ATT AGA GGG AGC GTG GTG TGC GAG AGT TTG TTA GCG TTG GTG			1112
Ile Ala Ile Arg Gly Ser Val Val Cys Glu Ser Leu Leu Ala Leu Val			
340	345	350	355
TTG GCT GAT ATG GTA TTA CTC AAT TTG ACT TCA AAA ATA GAG TAT TTA			1160
Leu Ala Asp Met Val Leu Leu Asn Leu Thr Ser Lys Ile Glu Tyr Leu			
360	365	370	
AAA ACG ATT TAT AAT GAG AAT TAAACGAAAT TGGATACAAT CAGCTTAAAA AGGA			1215
Lys Thr Ile Tyr Asn Glu Asn			
375			
TA			1217

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Arg	Leu	Ser	Ser	Ala	Ser	Lys	Thr	Glu	Gly	Ser	Gln	Met	Asn	Thr
1				5					10					15	

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 20...535
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TCATTGTGCC TGAAGCCAC ATG CGC TAC ATG CTC ATC AAC GAT TAT TAC AAG	52
Met Arg Tyr Met Leu Ile Asn Asp Tyr Tyr Lys	
1 5 10	
GTG TTT TTG GGC GAA AAA GAT AAG GAT TTG TAT GTG AAG CGC TTG GAA	100
Val Phe Leu Gly Glu Lys Asp Lys Asp Leu Tyr Val Lys Arg Leu Glu	
15 20 25	
AAA ATC ACG CCT AAA ATC TAT CTG GCG AGC GTG TTT TTA GAG AAA CAC	148
Lys Ile Thr Pro Lys Ile Tyr Leu Ala Ser Val Phe Leu Glu Lys His	
30 35 40	
ACC CCT TTA AAA AGT CTT TTA GAA AAA ATC CCT AAG GGA AAA AAA GAG	196
Thr Pro Leu Lys Ser Leu Leu Glu Lys Ile Pro Lys Gly Lys Lys Glu	
45 50 55	
ACT ATC ACC TAT CAT AAC CCT TGT CAT GCC AAA AAA ACC CTA AAC GCT	244
Thr Ile Thr Tyr His Asn Pro Cys His Ala Lys Lys Thr Leu Asn Ala	
60 65 70 75	
CAC AAA GAA GTG CGC AAC TTG CTC AAT TTG CAT TAT GAA ATT AAA GAA	292
His Lys Glu Val Arg Asn Leu Leu Asn Leu His Tyr Glu Ile Lys Glu	
80 85 90	
ATG CCG GAC AAT TGT TGC GGT TTT GGG GGG ATT ACG ATG CAA ACA CAA	340
Met Pro Asp Asn Cys Cys Gly Phe Gly Gly Ile Thr Met Gln Thr Gln	
95 100 105	
AAG GCG GGA TTT TCT TTA AAA GTG GGG CTT CTT AGG GCT AAA GAA ATC	388
Lys Ala Gly Phe Ser Leu Lys Val Gly Leu Leu Arg Ala Lys Glu Ile	
110 115 120	
ATA GAC ACC AAA GCT GCA ATT TTG AGC GCT GAA TGC GGG GCA TGC CAT	436
Ile Asp Thr Lys Ala Ala Ile Leu Ser Ala Glu Cys Gly Ala Cys His	
125 130 135	
ATG CAA TTA AAC AAC GCT TTA AAG TCT TTA GAC GAC CCT AAC ACT CCG	484
Met Gln Leu Asn Asn Ala Leu Lys Ser Leu Asp Asp Pro Asn Thr Pro	
140 145 150 155	
CCA TTT TTG CAC CCT TTA GAA CTC ATC GCT AAA GCC TTA AAA AGC GCT	532
Pro Phe Leu His Pro Leu Glu Leu Ile Ala Lys Ala Leu Lys Ser Ala	
160 165 170	
GAA TAAAAAGCCT TTTTAACCCC ATTCTCCAAC ATCTTTTAT ATAATACAGA GCT	588
Glu	

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Arg Tyr Met Leu Ile Asn Asp Tyr Tyr Lys Val Phe Leu Gly Glu
1 5 10 15
Lys Asp Lys Asp Leu Tyr Val Lys Arg Leu Glu Lys Ile Thr Pro Lys
20 25 30
Ile Tyr Leu Ala Ser Val Phe Leu Glu Lys His Thr Pro Leu Lys Ser
35 40 45
Leu Leu Glu Lys Ile Pro Lys Gly Lys Lys Glu Thr Ile Thr Tyr His
50 55 60
Asn Pro Cys His Ala Lys Lys Thr Leu Asn Ala His Lys Glu Val Arg
65 70 75 80
Asn Leu Leu Asn Leu His Tyr Glu Ile Lys Glu Met Pro Asp Asn Cys
85 90 95
Cys Gly Phe Gly Gly Ile Thr Met Gln Thr Gln Lys Ala Gly Phe Ser
100 105 110
Leu Lys Val Gly Leu Leu Arg Ala Lys Glu Ile Ile Asp Thr Lys Ala
115 120 125
Ala Ile Leu Ser Ala Glu Cys Gly Ala Cys His Met Gln Leu Asn Asn
130 135 140
Ala Leu Lys Ser Leu Asp Asp Pro Asn Thr Pro Pro Phe Leu His Pro
145 150 155 160
Leu Glu Leu Ile Ala Lys Ala Leu Lys Ser Ala Glu
165 170

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...317
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGCGTTAAAG CTCTGTATTA TATAAAAAG ATG TTG GAG AAT GGG GTT AAA AAG 53
Met Leu Glu Asn Gly Val Lys Lys
1 5
GCT TTT TAT TCA GCG CTT TTT AAG GCT TTA GCG ATG AGT TCT AAA GGG 101
Ala Phe Tyr Ser Ala Leu Phe Lys Ala Leu Ala Met Ser Ser Lys Gly
10 15 20

[illegible]

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2880 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 16...2814
(D) OTHER INFORMATION:

AAGCCTTAAG AAGCC ATG ACC CAA GCC TGG TTG ATG AAG CCA CTT TTA AAG
Met Thr Gln Ala Trp Leu Met Lys Pro Leu Leu Lys
1 5 10

AAA Lys	AAA Lys	TCA Ser 15	AAA Lys	TCT Ser	TTG Leu	GAA Glu	GCG Ala 20	ATG Met	ATG Met	GCA Ala	ACC Thr	AAT Asn 25	CAC His	AAC Asn	GAT Asp	99
GAA Glu	AAA Lys 30	ACC Thr	CTT Leu	TTT Phe	GAC Asp	GCT Ala 35	ATC Ile	TTA Leu	CTG Leu	CAA Gln	GAT Asp 40	CTA Leu	GCG Ala	GAC Asp	GCT Ala	147
ATG Met 45	TAT Tyr	AAT Asn	GTC Val	ATG Met	CCC Pro 50	ACT Thr	AAA Lys	TTA Leu	GGG Gly	GAC Asp 55	AGG Arg	AAT Asn	TAT Tyr	TGG Trp	GAA Glu 60	195
AAT Asn	TTC Phe	ACT Thr	AAA Lys	AAA Lys 65	ACG Thr	GGC Gly	AAC Asn	ATC Ile	GCA Ala 70	AGG Arg	ACC Thr	TTG Leu	AAC Asn	AAC Asn 75	CGC Arg	243
CTA Leu	AAA Lys	ATT Ile	ATT Ile 80	TTT Phe	GAC Asp	AAA Lys	AAC Asn	CCT Pro 85	GAA Glu	TTT Phe	TTC Phe	CAC His	GGC Gly 90	TTT Phe	TTG Leu	291
GAT Asp	TCC Ser	TTA Leu 95	AGG Arg	GAA Glu	AAT Asn	ATC Ile	CAT His 100	CAA Gln	AAC Asn	ATT Ile	AAA Lys	GAA Glu 105	GAT Asp	GAA Glu	GCC Ala	339
TTA Leu	GAC Asp 110	ATG Met	ATC Ile	ACT Thr	TCT Ser	CAC His 115	ATC Ile	ATC Ile	ACT Thr	AAG Lys	CCC Pro 120	ATT Ile	TTT Phe	GAT Asp	GCA Ala	387
CTT Leu 125	TTT Phe	GGG Gly	GAC Asp	AAC Asn	ATC Ile 130	AAA Lys	AAC Asn	CCT Pro	ATC Ile	GCT Ala 135	AAA Lys	GCC Ala	TTG Leu	GAT Asp	AAA Lys 140	435
ATG Met	GTA Val	GAA Glu	AAA Lys	CTC Leu 145	TCC Ser	ACT Thr	TTA Leu	GGA Gly	TTA Leu 150	GAA Glu	GGA Gly	GAA Glu	ACT Thr	AAA Lys 155	GAT Asp	483
CTG Leu	AAA Lys	AAC Asn	CTC Leu 160	TAT Tyr	GAA Glu	AGC Ser	GTG Val 165	AAA Lys	ACC Thr	GAA Glu	GCC Ala	TTG Leu	CAC His 170	GCC Ala	AAA Lys	531
AGC Ser	CAA Gln	AAA Lys 175	AGC Ser	CAA Gln	CAA Gln	GAA Glu	CTC Leu 180	ATT Ile	AAA Lys	AAC Asn	CTC Leu	TAC Tyr 185	AAC Asn	ACT Thr	TTC Phe	579
TTT Phe	AAA Lys 190	GAA Glu	GCC Ala	TTT Phe	AAA Lys	AAG Lys 195	CAA Gln	AGC Ser	GAA Glu	AAA Lys	CTA Leu 200	GGG Gly	ATC Ile	GTT Val	TAT Tyr	627
ACG Thr 205	CCC Pro	ATA Ile	GAG Glu	GTG Val	GTG Val 210	GAT Asp	TTC Phe	ATT Ile	TTA Leu	AGA Arg 215	GCC Ala	ACT Thr	AAC Asn	GGC Gly	ATT Ile 220	675
TTG Leu	AAA Lys	AAG Lys	CAT His	TTC Phe 225	AAC Asn	ACG Thr	GAT Asp	TTT Phe	AAC Asn 230	GAT Asp	CAA Gln	AGC Ser	ATC Ile	ACG Thr 235	ATT Ile	723
TTT Phe	GAC Asp	CCA Pro	TTC Phe	ACC Thr	GGC Gly	ACC Thr	GGG Gly	AGT Ser	TTT Phe	ATC Ile	GCT Ala	CGT Arg	TTG Leu	CTT Leu	TCT Ser	771

	240							245						250						
AAA Lys	GAA Glu	AAC Asn	GCG Ala	CTC Leu	ATT Ile	AGC Ser	GAT Asp	GAA Glu	GCC Ala	TTA Leu	AAA Lys	GAG Glu	AAG Lys	TTT Phe	CAA Gln	819				
		255						260			265									
AAA Lys	AAT Asn	TTG Leu	TTC Phe	GCT Ala	TTT Phe	GAC Asp	ATC Ile	GTG Val	CTT Leu	TTG Leu	TCT Ser	TAT Tyr	TAT Tyr	ATC Ile	GCT Ala	867				
					275						280									
TTA Leu	ATC Ile	AAT Asn	ATC Ile	ACC Thr	CAA Gln	GCC Ala	GCG Ala	CAA Gln	AAT Asn	AGG Arg	GAT Asp	GGC Gly	TCG Ser	TTA Leu	AAC Asn	915				
285					290						295			300						
AAT Asn	TTC Phe	AAA Lys	AAC Asn	ATC Ile	GCG Ala	CTC Leu	ACG Thr	GAC Asp	AGC Ser	CTG Leu	GAT Asp	TAT Tyr	TTA Leu	GAA Glu	GAA Glu	963				
		305						310						315						
AAA Lys	ACC Thr	AAT Asn	AAA Lys	GGG Gly	GTG Val	CTC Leu	CCT Pro	TTA Leu	TAT Tyr	GAG Glu	GAT Asp	TTG Leu	AAA Lys	GAA Glu	AAC Asn	1011				
		320						325			330									
AAA Lys	GGC Gly	ATC Ile	AAA Lys	GAC Asp	ACT Thr	CTA Leu	GCC Ala	AAC Asn	CAA Gln	AAT Asn	ATT Ile	AGA Arg	GTC Val	ATC Ile	ATC Ile	1059				
		335						340			345									
GGC Gly	AAC Asn	CCG Pro	CCT Pro	TAT Tyr	TCA Ser	GCC Ala	GGC Gly	GCA Ala	AAG Lys	AGC Ser	CAA Gln	AAC Asn	GAT Asp	AAC Asn	AAC Asn	1107				
350					355						360									
CAA Gln	AAC Asn	CTC Leu	TCA Ser	CAC His	CCA Pro	AAG Lys	CTT Leu	GAA Glu	AAA Lys	TTA Leu	GTT Val	TAT Tyr	GAA Glu	AAA Lys	TAC Tyr	1155				
365					370						375			380						
GGA Gly	AAA Lys	AAT Asn	TCC Ser	ACA Thr	TCT Ser	AGA Arg	AGT Ser	GTG Val	GGA Gly	AAA Lys	ACC Thr	ACA Thr	CGA Arg	GAC Asp	ACG Thr	1203				
		385						390						395						
CTC Leu	ATT Ile	CAA Gln	AGC Ser	ATC Ile	CGC Arg	ATG Met	GCG Ala	AGC Ser	GAT Asp	GTT Val	GTT Val	AAA Lys	GAT Asp	AGG Arg	GGG Gly	1251				
		400						405						410						
GTG Val	ATA Ile	GGC Gly	TTT Phe	GTG Val	GTG Val	AAC Asn	GGG Gly	GGT Gly	TTT Phe	ATT Ile	GAC Asp	TCT Ser	AAA Lys	AGC Ser	GCG Ala	1299				
		415						420			425									
GAT Asp	GGG Gly	TTC Phe	AGA Arg	AAA Lys	TGC Cys	GTG Val	GCC Ala	AAA Lys	GAA Glu	TTT Phe	TCG Ser	CAT His	CTT Leu	TAT Tyr	GTA Val	1347				
430					435						440									
TTG Leu	AAT Asn	TTG Leu	AGA Arg	GGC Gly	AAT Asn	CAG Gln	CGC Arg	ACT Thr	TCT Ser	GGG Gly	GAA Glu	GTG Val	TCA Ser	AAA Lys	AAA Lys	1395				
445					450						455			460						
GAG Glu	GGA Gly	GGG Gly	AAA Lys	ATC Ile	TTT Phe	GAT Asp	AGC Ser	GGA Gly	TCG Ser	AGG Arg	GCG Ala	ACG Thr	GTA Val	GCG Ala	ATT Ile	1443				
		465						470						475						

				705				710				715							
GAT	TAT	AGT	TTG	ATC	TCA	CCC	AAT	CAA	GCT	TAC	CCC	TTG	TAT	TAT	TAC	2211			
Asp	Tyr	Ser	Leu	Ile	Ser	Pro	Asn	Gln	Ala	Tyr	Pro	Leu	Tyr	Tyr	Tyr				
720								725				730							
GAT	GAT	TTG	GGG	AAT	CGC	CAT	TAC	GCC	ATC	AGC	GGC	TAT	TGC	TTA	AAC	2259			
Asp	Asp	Leu	Gly	Asn	Arg	His	Tyr	Ala	Ile	Ser	Gly	Tyr	Cys	Leu	Asn				
735								740				745							
CTC	TTC	AGG	AGG	CAT	TAT	GGG	GAT	AAT	CTG	ATC	GCT	GAA	GAA	GAG	ATT	2307			
Leu	Phe	Arg	Arg	His	Tyr	Gly	Asp	Asn	Leu	Ile	Ala	Glu	Glu	Glu	Ile				
750								755				760							
TTT	TAT	TAC	ATT	TAT	GCG	ATT	TTC	CAC	CAT	AAA	GGC	TAT	TTA	GAA	AAA	2355			
Phe	Tyr	Tyr	Ile	Tyr	Ala	Ile	Phe	His	His	Lys	Gly	Tyr	Leu	Glu	Lys				
765				770				775				780							
TAC	AAA	AAT	TCC	CTC	GCC	AAA	GAA	GCG	CCG	CGC	ATC	GCT	TTG	AGC	GAA	2403			
Tyr	Lys	Asn	Ser	Leu	Ala	Lys	Glu	Ala	Pro	Arg	Ile	Ala	Leu	Ser	Glu				
785								790				795							
GAT	TTT	AAA	GAA	CTC	TCT	GTG	CTT	GGC	AAA	GAA	TTG	GCC	GAA	TTG	CAC	2451			
Asp	Phe	Lys	Glu	Leu	Ser	Val	Leu	Gly	Lys	Glu	Leu	Ala	Glu	Leu	His				
800								805				810							
CTG	AAC	TAT	GAG	AGT	GGG	GAA	ATG	CAT	GAT	AAT	ATT	AAA	TAC	ACC	ACA	2499			
Leu	Asn	Tyr	Glu	Ser	Gly	Glu	Met	His	Asp	Asn	Ile	Lys	Tyr	Thr	Thr				
815								820				825							
CTG	ATG	AAC	GCC	GAA	ATA	GAG	GGT	TAT	TAT	GAT	GTG	GAT	AAA	ATG	ACC	2547			
Leu	Met	Asn	Ala	Glu	Ile	Glu	Gly	Tyr	Tyr	Asp	Val	Asp	Lys	Met	Thr				
830				835				840											
AAA	AAA	GGG	GAT	TGC	ATC	ATC	TAT	AAC	CAA	AAC	ATC	GCT	ATC	ACT	AAG	2595			
Lys	Lys	Gly	Asp	Cys	Ile	Ile	Tyr	Asn	Gln	Asn	Ile	Ala	Ile	Thr	Lys				
845				850				855				860							
ATC	CCT	AAA	AAA	GCC	TTT	GAC	TAT	GTC	ATT	AAT	GGC	AAG	AGC	GCG	ATT	2643			
Ile	Pro	Lys	Lys	Ala	Phe	Asp	Tyr	Val	Ile	Asn	Gly	Lys	Ser	Ala	Ile				
865								870				875							
GAC	TGG	GTG	ATC	GAA	CGC	TAT	CAA	AAA	ACT	ATG	GAT	AAA	GAA	AGC	CTG	2691			
Asp	Trp	Val	Ile	Glu	Arg	Tyr	Gln	Lys	Thr	Met	Asp	Lys	Glu	Ser	Leu				
880								885				890							
ATT	GAA	AAC	AAC	CCG	AAC	GAT	TAC	GCC	GGC	GGA	AAA	TAC	GTT	TTT	GAA	2739			
Ile	Glu	Asn	Asn	Pro	Asn	Asp	Tyr	Ala	Gly	Gly	Lys	Tyr	Val	Phe	Glu				
895								900				905							
CTC	CTT	TGT	AGG	GTC	ATC	ACA	CTT	TCG	GTA	AAA	AGC	GTG	GAT	TTG	ATA	2787			
Leu	Leu	Cys	Arg	Val	Ile	Thr	Leu	Ser	Val	Lys	Ser	Val	Asp	Leu	Ile				
910				915				920											
GAA	AAG	ATC	AGC	GAA	AAG	AGG	TTT	GAG	TGATTACATC	GCTTGGGGGT				GTGGAAT					
Glu	Lys	Ile	Ser	Glu	Lys	Arg	Phe	Glu											

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Thr Gln Ala Trp Leu Met Lys Pro Leu Leu Lys Lys Lys Ser Lys
 1 5 10 15
 Ser Leu Glu Ala Met Met Ala Thr Asn His Asn Asp Glu Lys Thr Leu
 20 25 30
 Phe Asp Ala Ile Leu Leu Gln Asp Leu Ala Asp Ala Met Tyr Asn Val
 35 40 45
 Met Pro Thr Lys Leu Gly Asp Arg Asn Tyr Trp Glu Asn Phe Thr Lys
 50 55 60
 Lys Thr Gly Asn Ile Ala Arg Thr Leu Asn Asn Arg Leu Lys Ile Ile
 65 70 75 80
 Phe Asp Lys Asn Pro Glu Phe Phe His Gly Phe Leu Asp Ser Leu Arg
 85 90 95
 Glu Asn Ile His Gln Asn Ile Lys Glu Asp Glu Ala Leu Asp Met Ile
 100 105 110
 Thr Ser His Ile Ile Thr Lys Pro Ile Phe Asp Ala Leu Phe Gly Asp
 115 120 125
 Asn Ile Lys Asn Pro Ile Ala Lys Ala Leu Asp Lys Met Val Glu Lys
 130 135 140
 Leu Ser Thr Leu Gly Leu Glu Gly Glu Thr Lys Asp Leu Lys Asn Leu
 145 150 155 160
 Tyr Glu Ser Val Lys Thr Glu Ala Leu His Ala Lys Ser Gln Lys Ser
 165 170 175
 Gln Gln Glu Leu Ile Lys Asn Leu Tyr Asn Thr Phe Phe Lys Glu Ala
 180 185 190
 Phe Lys Lys Gln Ser Glu Lys Leu Gly Ile Val Tyr Thr Pro Ile Glu
 195 200 205
 Val Val Asp Phe Ile Leu Arg Ala Thr Asn Gly Ile Leu Lys Lys His
 210 215 220
 Phe Asn Thr Asp Phe Asn Asp Gln Ser Ile Thr Ile Phe Asp Pro Phe
 225 230 235 240
 Thr Gly Thr Gly Ser Phe Ile Ala Arg Leu Leu Ser Lys Glu Asn Ala
 245 250 255
 Leu Ile Ser Asp Glu Ala Leu Lys Glu Lys Phe Gln Lys Asn Leu Phe
 260 265 270
 Ala Phe Asp Ile Val Leu Leu Ser Tyr Tyr Ile Ala Leu Ile Asn Ile
 275 280 285
 Thr Gln Ala Ala Gln Asn Arg Asp Gly Ser Leu Asn Asn Phe Lys Asn
 290 295 300
 Ile Ala Leu Thr Asp Ser Leu Asp Tyr Leu Glu Glu Lys Thr Asn Lys
 305 310 315 320
 Gly Val Leu Pro Leu Tyr Glu Asp Leu Lys Glu Asn Lys Gly Ile Lys
 325 330 335
 Asp Thr Leu Ala Asn Gln Asn Ile Arg Val Ile Ile Gly Asn Pro Pro
 340 345 350

Tyr	Ser	Ala	Gly	Ala	Lys	Ser	Gln	Asn	Asp	Asn	Asn	Gln	Asn	Leu	Ser	355	360	365
His	Pro	Lys	Leu	Glu	Lys	Leu	Val	Tyr	Glu	Lys	Tyr	Gly	Lys	Asn	Ser	370	375	380
Thr	Ser	Arg	Ser	Val	Gly	Lys	Thr	Thr	Arg	Asp	Thr	Leu	Ile	Gln	Ser	385	390	395
Ile	Arg	Met	Ala	Ser	Asp	Val	Val	Lys	Asp	Arg	Gly	Val	Ile	Gly	Phe	405	410	415
Val	Val	Asn	Gly	Gly	Phe	Ile	Asp	Ser	Lys	Ser	Ala	Asp	Gly	Phe	Arg	420	425	430
Lys	Cys	Val	Ala	Lys	Glu	Phe	Ser	His	Leu	Tyr	Val	Leu	Asn	Leu	Arg	435	440	445
Gly	Asn	Gln	Arg	Thr	Ser	Gly	Glu	Val	Ser	Lys	Lys	Glu	Gly	Gly	Lys	450	455	460
Ile	Phe	Asp	Ser	Gly	Ser	Arg	Ala	Thr	Val	Ala	Ile	Ile	Phe	Phe	Val	465	470	475
Lys	Asp	Lys	Ser	Thr	Pro	Asp	Asn	Thr	Ile	Phe	Tyr	Tyr	Glu	Val	Glu	485	490	495
Asp	Tyr	Leu	Lys	Arg	Glu	Ala	Lys	Leu	Asn	Trp	Leu	Ala	Asn	Phe	Glu	500	505	510
Asn	Leu	Asp	Phe	Val	Pro	Phe	Glu	Lys	Ile	Thr	Pro	Asn	Asp	Lys	Gly	515	520	525
Asp	Trp	Ile	Asn	Gln	Arg	Asn	Asp	Ala	Phe	Glu	Lys	Leu	Ile	Pro	Leu	530	535	540
Lys	Arg	Asp	Lys	Thr	Leu	Gln	Asn	Asp	Ser	Val	Phe	Asp	Ile	Asn	Ser	545	550	555
Leu	Gly	Val	Val	Ser	Gly	Arg	Asp	Pro	Trp	Val	Tyr	Asn	Phe	Ser	Pro	565	570	575
Asn	Ile	Leu	Thr	Gln	Ser	Val	Gln	Lys	Cys	Ile	Asp	Thr	Tyr	Asn	Ala	580	585	590
Asp	Leu	Lys	Arg	Phe	Asn	Ala	Arg	Phe	Arg	Glu	Ala	Phe	Lys	Gln	Arg	595	600	605
Ala	Gln	Ser	Val	Lys	Ala	Gly	Asp	Leu	Tyr	Lys	Gln	Leu	Asn	Asp	Lys	610	615	620
Glu	Ile	Thr	Thr	Asp	Lys	Thr	Lys	Ile	Ala	Trp	Thr	Asp	Gly	Leu	Lys	625	630	635
Asn	Lys	Leu	Ile	Lys	Asn	Lys	Ser	Ala	Arg	Glu	Ser	Ser	Glu	Glu	Arg	645	650	655
Val	Arg	Leu	Ala	Leu	Tyr	Arg	Pro	Phe	Asn	Lys	Gln	Trp	Leu	Tyr	Trp	660	665	670
Asp	Lys	Asp	Trp	Ile	Asn	Arg	Gln	Arg	Glu	Phe	Ser	Lys	Ile	Phe	Pro	675	680	685
Asp	Lys	Asp	Ala	Gln	Asn	Val	Val	Ile	Asn	Thr	Gly	Val	Gly	Asn	Gly	690	695	700
Lys	Asp	Phe	Ser	Ala	Leu	Val	Ser	Asp	Phe	Ile	Ser	Asp	Tyr	Ser	Leu	705	710	715
Ile	Ser	Pro	Asn	Gln	Ala	Tyr	Pro	Leu	Tyr	Tyr	Tyr	Asp	Asp	Leu	Gly	725	730	735
Asn	Arg	His	Tyr	Ala	Ile	Ser	Gly	Tyr	Cys	Leu	Asn	Leu	Phe	Arg	Arg	740	745	750
His	Tyr	Gly	Asp	Asn	Leu	Ile	Ala	Glu	Glu	Glu	Ile	Phe	Tyr	Tyr	Ile	755	760	765
Tyr	Ala	Ile	Phe	His	His	Lys	Gly	Tyr	Leu	Glu	Lys	Tyr	Lys	Asn	Ser	770	775	780
Leu	Ala	Lys	Glu	Ala	Pro	Arg	Ile	Ala	Leu	Ser	Glu	Asp	Phe	Lys	Glu	785	790	795
Leu	Ser	Val	Leu	Gly	Lys	Glu	Leu	Ala	Glu	Leu	His	Leu	Asn	Tyr	Glu	805	810	815

Ser Gly Glu Met His Asp Asn Ile Lys Tyr Thr Thr Leu Met Asn Ala
820 825 830
Glu Ile Glu Gly Tyr Tyr Asp Val Asp Lys Met Thr Lys Lys Gly Asp
835 840 845
Cys Ile Ile Tyr Asn Gln Asn Ile Ala Ile Thr Lys Ile Pro Lys Lys
850 855 860
Ala Phe Asp Tyr Val Ile Asn Gly Lys Ser Ala Ile Asp Trp Val Ile
865 870 875 880
Glu Arg Tyr Gln Lys Thr Met Asp Lys Glu Ser Leu Ile Glu Asn Asn
885 890 895
Pro Asn Asp Tyr Ala Gly Gly Lys Tyr Val Phe Glu Leu Leu Cys Arg
900 905 910
Val Ile Thr Leu Ser Val Lys Ser Val Asp Leu Ile Glu Lys Ile Ser
915 920 925
Glu Lys Arg Phe Glu
930

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24...1370
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AAGATCAGCG AAAAGAGGTT TGA GTG ATT ACA TCG CTT GGG GGT GTG GAA TAT	53
Val Ile Thr Ser Leu Gly Gly Val Glu Tyr	
1 5 10	
TTT GAA AGG CAA TGT CTT GCT TTC TTA AAA AAT CCA CAA ACT AAT CCA	101
Phe Glu Arg Gln Cys Leu Ala Phe Leu Lys Asn Pro Gln Thr Asn Pro	
15 20 25	
CAA AAT GAG CAA TAC ATT CCA GGA GTG TTT TCG TAT CAA GAA AAC AAA	149
Gln Asn Glu Gln Tyr Ile Pro Gly Val Phe Ser Tyr Gln Glu Asn Lys	
30 35 40	
ATT TCT TTT TCT TTT TTG GTT TTA GGA GAA ATT GAA GAG ATC CAC TCT	197
Ile Ser Phe Ser Phe Leu Val Leu Gly Glu Ile Glu Glu Ile His Ser	
45 50 55	
TTG CAA TAC CAA ACG CTC TAT ATT GTG GAT AAC AAA AAA AGA TAC ACT	245
Leu Gln Tyr Gln Thr Leu Tyr Ile Val Asp Asn Lys Lys Arg Tyr Thr	
60 65 70	
CTT TAC AAG CTT TAT GAT CGC ATT ATT TTG GGT CAT ACT TTA GGG TAT	293
Leu Tyr Lys Leu Tyr Asp Arg Ile Ile Leu Gly His Thr Leu Gly Tyr	
75 80 85 90	

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...1302
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTAAATGAAT TTAAAAGGAA AAAT ATG GCA GTA AGA TTT GGG ATT ATC TTT	51
Met Ala Val Arg Phe Gly Ile Ile Phe	
1 5	
ATA TCT GAC TCT ATT GAT GAT TAT AAA GCC AAA CAA TTA AGA TCA ATT	99
Ile Ser Asp Ser Ile Asp Asp Tyr Lys Ala Lys Gln Leu Arg Ser Ile	
10 15 20 25	
TTA GAA CGC AAG AAA GAG TGT AAT TTT ATA TGG TTT AAT GAA TCA AGT	147
Leu Glu Arg Lys Lys Glu Cys Asn Phe Ile Trp Phe Asn Glu Ser Ser	
30 35 40	
GCT ATA ATT CAC AAT ACT CCT AAA GTT TTT GAA GGA GAG AGT TTT TTT	195
Ala Ile Ile His Asn Thr Pro Lys Val Phe Glu Gly Glu Ser Phe Phe	
45 50 55	
GAT CAT CTT TTC GTT AGT GCA AAA ATT ACT GCT TTT GTG GTA TCC ACA	243
Asp His Leu Phe Val Ser Ala Lys Ile Thr Ala Phe Val Val Ser Thr	
60 65 70	
AAC GAA TCA GAT ACA ATA TTC AAT TTA AAA AAC TAC TTG CTA GTA TTA	291
Asn Glu Ser Asp Thr Ile Phe Asn Leu Lys Asn Tyr Leu Leu Val Leu	
75 80 85	
GCC AAA AAT CTC AAT AAT AGA GAT ATT TGG TAT TGT GAA AAC ACT ATT	339
Ala Lys Asn Leu Asn Asn Arg Asp Ile Trp Tyr Cys Glu Asn Thr Ile	
90 95 100 105	
TGC GAT AAA AAA GGC ACT TAT AAT ATA GAA ATA GAA TTA GTG AGC AAT	387
Cys Asp Lys Lys Gly Thr Tyr Asn Ile Glu Ile Glu Leu Val Ser Asn	
110 115 120	
GCT AAT GAT TTT AGA GGA GTG TTT GGA GAA GTG TTA GGT ATA GTC AAA	435
Ala Asn Asp Phe Arg Gly Val Phe Gly Glu Val Leu Gly Ile Val Lys	
125 130 135	
GAC ACT TTC GGT GAT TTA CTG CAA CTT CTT ACA AAT TTA AAG AAC AAG	483
Asp Thr Phe Gly Asp Leu Leu Gln Leu Leu Thr Asn Leu Lys Asn Lys	
140 145 150	
GAA ATT GAA TTT AAT TTT CAT AAA AAA ATT AAT TAC GGA TTG CCT TTT	531
Glu Ile Glu Phe Asn Phe His Lys Lys Ile Asn Tyr Gly Leu Pro Phe	
155 160 165	
GGG ATT ATC TTT ATC GCT AGC AAC TCT GAC AAC CCT ATT GAT ATT GAC	579
Gly Ile Ile Phe Ile Ala Ser Asn Ser Asp Asn Pro Ile Asp Ile Asp	
170 175 180 185	
AAT AAA ACC AAA AAG TTA AAA TCA TGC TTT CGT GAT GAT GAG AGT AAC	627

TCC TGATGATTTA AAGAATTTAA AGGAACGATT ATTTATAGAT ATT
Ser

1345

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Ala	Val	Arg	Phe	Gly	Ile	Ile	Phe	Ile	Ser	Asp	Ser	Ile	Asp	Asp
1				5				10					15		
Tyr	Lys	Ala	Lys	Gln	Leu	Arg	Ser	Ile	Leu	Glu	Arg	Lys	Lys	Glu	Cys
		20					25					30			
Asn	Phe	Ile	Trp	Phe	Asn	Glu	Ser	Ser	Ala	Ile	Ile	His	Asn	Thr	Pro
	35					40					45				
Lys	Val	Phe	Glu	Gly	Glu	Ser	Phe	Phe	Asp	His	Leu	Phe	Val	Ser	Ala
	50				55					60					
Lys	Ile	Thr	Ala	Phe	Val	Val	Ser	Thr	Asn	Glu	Ser	Asp	Thr	Ile	Phe
	65				70				75					80	
Asn	Leu	Lys	Asn	Tyr	Leu	Leu	Val	Leu	Ala	Lys	Asn	Leu	Asn	Asn	Arg
			85					90					95		
Asp	Ile	Trp	Tyr	Cys	Glu	Asn	Thr	Ile	Cys	Asp	Lys	Lys	Gly	Thr	Tyr
		100					105					110			
Asn	Ile	Glu	Ile	Glu	Leu	Val	Ser	Asn	Ala	Asn	Asp	Phe	Arg	Gly	Val
	115					120					125				
Phe	Gly	Glu	Val	Leu	Gly	Ile	Val	Lys	Asp	Thr	Phe	Gly	Asp	Leu	Leu
	130				135					140					
Gln	Leu	Leu	Thr	Asn	Leu	Lys	Asn	Lys	Glu	Ile	Glu	Phe	Asn	Phe	His
	145				150				155					160	
Lys	Lys	Ile	Asn	Tyr	Gly	Leu	Pro	Phe	Gly	Ile	Ile	Phe	Ile	Ala	Ser
			165					170					175		
Asn	Ser	Asp	Asn	Pro	Ile	Asp	Ile	Asp	Asn	Lys	Thr	Lys	Lys	Leu	Lys
		180					185					190			
Ser	Cys	Phe	Arg	Asp	Asp	Glu	Ser	Asn	Cys	Phe	Ile	Asp	Cys	Pro	Ile
	195					200					205				
Thr	Ile	Glu	Asp	Tyr	Leu	Ile	Leu	Asp	Asn	Leu	Lys	Ser	Cys	Phe	Val
	210				215					220					
Ile	Gln	Asn	Lys	Pro	Asn	Val	Thr	Leu	Phe	Asp	Asn	Asp	Glu	Asn	Asp
	225				230				235					240	
Arg	Pro	Phe	Asn	Leu	Lys	Arg	Tyr	Leu	Leu	Gly	Leu	Lys	Glu	Lys	Leu
			245					250					255		
Gly	Phe	Glu	Pro	Thr	Gly	Ile	Phe	Tyr	Cys	Glu	Asn	Ala	Asn	Thr	His
		260					265					270			
Lys	Ile	Glu	Leu	Ile	Gly	Asn	Asp	Ser	Asp	Phe	Arg	Glu	Val	Leu	Leu
	275					280				285					
Glu	Phe	Ser	Glu	Asn	Ile	Pro	Lys	Ala	Pro	Asn	Glu	Leu	Pro	Gln	Phe
	290				295					300					
Leu	Thr	Asn	Phe	Lys	Asn	Ser	Lys	Ile	Pro	Asn	Gly	Asn	Ile	Ser	Phe
	305			310					315					320	
Ser	Pro	Pro	Lys	Asn	Ser	Pro	Ser	Ile	Ser	Ser	Tyr	Ala	Leu	Ser	Asp

				325					330					335			
Lys	Ile	Lys	Arg	Glu	Val	Arg	Asp	Thr	Phe	Asp	Arg	Tyr	Leu	Trp	His		
			340					345					350				
Gly	Tyr	Ser	Lys	Ile	Pro	Gln	Glu	Lys	Arg	Ile	Ala	Lys	Ile	Lys	Glu		
		355					360					365					
Gln	Val	Lys	Glu	Glu	Ile	Lys	Leu	Asn	Pro	Ser	Phe	Arg	Asn	Tyr	Arg		
	370					375					380						
Val	Asp	Ser	Glu	Gln	Asn	Arg	Lys	Ile	Asn	Glu	Ile	Ala	Glu	Gly	Leu		
385					390				395						400		
Lys	Ser	Gly	Lys	Ile	Ile	Gly	Lys	Lys	Val	Ile	Ala	Asn	Ala	Phe	Asp		
			405					410					415				
Leu	Asn	Ala	Ser	Leu	Leu	Phe	Tyr	Tyr	Ser								
			420					425									

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...705
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TTGCTAATGC GTTCGATCTA A ATG CTA GCT TAT TGT TTT ATT ACT CCT GAT	51
Met Leu Ala Tyr Cys Phe Ile Thr Pro Asp	
1 5 10	
GAT TTA AAG AAT TTA AAG GAA CGA TTA TTT ATA GAT ATT ATC AAT GCT	99
Asp Leu Lys Asn Leu Lys Glu Arg Leu Phe Ile Asp Ile Ile Asn Ala	
15 20 25	
ATC AAC CAA AAA AAG AGA GTC GCG CTC GAT CAT GCT CAA ATA GAT GAC	147
Ile Asn Gln Lys Lys Arg Val Ala Leu Asp His Ala Gln Ile Asp Asp	
30 35 40	
ATC CAG TAT AAT GTG CTT GAT AAT GCG TTT TAT TTT ATC TTT GAT GTT	195
Ile Gln Tyr Asn Val Leu Asp Asn Ala Phe Tyr Phe Ile Phe Asp Val	
45 50 55	
GGT AAC CCT TCT CAA TTA GCT ATT AAA GTG CCT AGA AAA TCT TTA GAA	243
Gly Asn Pro Ser Gln Leu Ala Ile Lys Val Pro Arg Lys Ser Leu Glu	
60 65 70	
AAT GAT GAG TTG CCC AAC ACT AAA AAA AAC ATA TTC AAT GGA TTA ATA	291
Asn Asp Glu Leu Pro Asn Thr Lys Lys Asn Ile Phe Asn Gly Leu Ile	
75 80 85 90	
AGA ACT ATC TAT GGG TGT ATT GAT GAT GAA AAT TCA TTT TTA TTA GAA	339
Arg Thr Ile Tyr Gly Cys Ile Asp Asp Glu Asn Ser Phe Leu Leu Glu	

	95	100	105	
AAC GAT AAA ACC ATC AAG GAT TTA AAT ATT CAG GAT TTA TTG GGG CCA				387
Asn Asp Lys Thr Ile Lys Asp Leu Asn Ile Gln Asp Leu Leu Gly Pro	110	115	120	
TTA AAA ACT CAA GCA TTT CCA TTA TCA TAC ATT ATT ACT GAC GCT ATC				435
Leu Lys Thr Gln Ala Phe Pro Leu Ser Tyr Ile Ile Thr Asp Ala Ile	125	130	135	
AAT CAA AAA GAA GGG GTG GCT CTC GAT TAC GCT CTA ATA AAC GAT ATT				483
Asn Gln Lys Glu Gly Val Ala Leu Asp Tyr Ala Leu Ile Asn Asp Ile	140	145	150	
AAG TAT AAT TTG CTT GAT AAC ACA TTC CAT TTT ATC TTT GAT GTT GGT				531
Lys Tyr Asn Leu Leu Asp Asn Thr Phe His Phe Ile Phe Asp Val Gly	155	160	165	170
AAT CCT TTG TTG AAA GAG TCA AGT CAA TTT ATT ATT GAA GTG CCT AGA				579
Asn Pro Leu Leu Lys Glu Ser Ser Gln Phe Ile Ile Glu Val Pro Arg	175	180	185	
GAG GCG TTG GAT CTA GAG AAT GTT GAT CGG CTT GTT GAA TAT ACG CTG				627
Glu Ala Leu Asp Leu Glu Asn Val Asp Arg Leu Val Glu Tyr Thr Leu	190	195	200	
TCT CCT AAT AAT CAT AGT CAA AGT TCT TTA GTG TAT CAT ATT TCT GAA				675
Ser Pro Asn Asn His Ser Gln Ser Ser Leu Val Tyr His Ile Ser Glu	205	210	215	
GGC TCT TAT ATC ATT CAC TTA ATA GAT GAC TAAACTTAAA TGAAA				720
Gly Ser Tyr Ile Ile His Leu Ile Asp Asp	220	225		

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Leu	Ala	Tyr	Cys	Phe	Ile	Thr	Pro	Asp	Asp	Leu	Lys	Asn	Leu	Lys
1				5				10					15		
Glu	Arg	Leu	Phe	Ile	Asp	Ile	Ile	Asn	Ala	Ile	Asn	Gln	Lys	Lys	Arg
		20						25				30			
Val	Ala	Leu	Asp	His	Ala	Gln	Ile	Asp	Asp	Ile	Gln	Tyr	Asn	Val	Leu
		35				40					45				
Asp	Asn	Ala	Phe	Tyr	Phe	Ile	Phe	Asp	Val	Gly	Asn	Pro	Ser	Gln	Leu
50					55			60							
Ala	Ile	Lys	Val	Pro	Arg	Lys	Ser	Leu	Glu	Asn	Asp	Glu	Leu	Pro	Asn
65				70				75					80		
Thr	Lys	Lys	Asn	Ile	Phe	Asn	Gly	Leu	Ile	Arg	Thr	Ile	Tyr	Gly	Cys

				85					90					95			
Ile	Asp	Asp	Glu	Asn	Ser	Phe	Leu	Leu	Glu	Asn	Asp	Lys	Thr	Ile	Lys		
			100						105					110			
Asp	Leu	Asn	Ile	Gln	Asp	Leu	Leu	Gly	Pro	Leu	Lys	Thr	Gln	Ala	Phe		
		115						120				125					
Pro	Leu	Ser	Tyr	Ile	Ile	Thr	Asp	Ala	Ile	Asn	Gln	Lys	Glu	Gly	Val		
		130				135					140						
Ala	Leu	Asp	Tyr	Ala	Leu	Ile	Asn	Asp	Ile	Lys	Tyr	Asn	Leu	Leu	Asp		
145					150					155					160		
Asn	Thr	Phe	His	Phe	Ile	Phe	Asp	Val	Gly	Asn	Pro	Leu	Leu	Lys	Glu		
			165						170					175			
Ser	Ser	Gln	Phe	Ile	Ile	Glu	Val	Pro	Arg	Glu	Ala	Leu	Asp	Leu	Glu		
		180						185					190				
Asn	Val	Asp	Arg	Leu	Val	Glu	Tyr	Thr	Leu	Ser	Pro	Asn	Asn	His	Ser		
		195					200					205					
Gln	Ser	Ser	Leu	Val	Tyr	His	Ile	Ser	Glu	Gly	Ser	Tyr	Ile	Ile	His		
	210					215					220						
Leu	Ile	Asp	Asp														
225																	

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...561
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TTTGGGCATG CTTGGTGATC TTAA ATG AGT CAA GGT GAT GGG GTG GAA GGA	51
Met Ser Gln Gly Asp Gly Val Glu Gly	
1 5	
AAT AAT ATG GAT ACT ACG AAA GAG AAC TTG AAT GGC TCA AAA GAG CGT	99
Asn Asn Met Asp Thr Thr Lys Glu Asn Leu Asn Gly Ser Lys Glu Arg	
10 15 20 25	
TTG AGC GAT TGG GAA TAT CGA TGG GCA ATG GCT CTA GTC TAT GGA GGA	147
Leu Ser Asp Trp Glu Tyr Arg Trp Ala Met Ala Leu Val Tyr Gly Gly	
30 35 40	
TGT ATC TCC ATA ACC ACT AGG ATT TTT TAT GAC ATA AAT GGT TCA GCT	195
Cys Ile Ser Ile Thr Thr Arg Ile Phe Tyr Asp Ile Asn Gly Ser Ala	
45 50 55	
AGC GAT CCG CTT TTT GAC CCT AAA TAC AGC TAT TAT GTG TGG TTA GTG	243
Ser Asp Pro Leu Phe Asp Pro Lys Tyr Ser Tyr Tyr Val Trp Leu Val	
60 65 70	

Arg	Asp	Phe	Tyr	Val	Met	Leu	Leu	Thr	Met	Pro	Phe	Ile	Ala	Ala	Ile
130						135					140				
His	Glu	Val	Ser	Ala	Tyr	Cys	Gly	His	Pro	Ser	Asn	Leu	Leu	Val	Glu
145					150					155					160
Gly	Leu	Val	Ile	Leu	Gly	Phe	Gln	Gly	Phe	Leu	Lys	Leu	Cys	Ala	Lys
			165						170					175	
Trp	Gly	Trp													

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 72...404
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTGTGGTAT	AAATATTCTT	ATCAAGGTGT	GCCAAACATG	CCTTGAATCT	CAATTTTGA	60
ATCTCAATTT	T ATG AAA	GGA TTT	GTT ATG	AGT GGA	TTA AGA	110
	Met Lys	Gly Phe	Val Met	Ser Gly	Leu Arg	
	1		5		10	
TGT GTA	GTG GTT	TTA TGC	GGT GCA	ATG GCT	AAT GTG	158
Cys Val	Val Val	Leu Cys	Gly Ala	Met Ala	Asn Val	
	15		20		25	
CCT AAA	ATA GAG	GCA AGG	GGT GAA	TTA GGC	AAA TTT	206
Pro Lys	Ile Glu	Ala Arg	Gly Glu	Leu Gly	Lys Phe	
	30		35		40	
GTT GGG	GGT TTT	GTT GGT	GAT AAA	ATG GGC	GGA TTT	254
Val Gly	Gly Phe	Val Gly	Asp Lys	Met Gly	Gly Phe	
	50			55		
ATA GGA	GGA TAT	ATT GGG	TCT GAA	ATA GGC	GAT AGG	302
Ile Gly	Gly Tyr	Ile Gly	Ser Glu	Ile Gly	Asp Arg	
	65			70		
ATC CGT	GGT GTT	GAT AGA	GAG CCA	CAA AAC	AAA GAA	350
Ile Arg	Gly Val	Asp Arg	Glu Pro	Gln Asn	Lys Glu	
	80			85		
AGA GAA	CCT ATC	CGT GAT	CTT TAT	GAT TAC	GGC TAT	398
Arg Glu	Pro Ile	Arg Asp	Leu Tyr	Asp Tyr	Gly Tyr	
	95		100		105	
GCT TGG	TGATCTTAAA	TGAGTCAAGA				424
Ala Trp						

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Met Lys Gly Phe Val Met Ser Gly Leu Arg Thr Phe Ser Cys Val Val
 1           5           10           15
Val Leu Cys Gly Ala Met Ala Asn Val Ala Ile Ala Ser Pro Lys Ile
          20           25           30
Glu Ala Arg Gly Glu Leu Gly Lys Phe Ile Gly Gly Gly Val Gly Gly
          35           40           45
Phe Val Gly Asp Lys Met Gly Gly Phe Val Gly Gly Ala Ile Gly Gly
          50           55           60
Tyr Ile Gly Ser Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly
65           70           75           80
Val Asp Arg Glu Pro Gln Asn Lys Glu Pro Gln Ala Pro Arg Glu Pro
          85           90           95
Ile Arg Asp Leu Tyr Asp Tyr Gly Tyr Ser Phe Gly His Ala Trp
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 132...569
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```

GATTTTAGTG ATGACGAGTT TCACCCGTTT GATCGTGGTG TTTTCTTTTT TAAGGACCGC      60
TTTGGGCACG CAACAAACCC CCCCCCACTC AAATTTTAGT CTCGCTCTCT TTGATATTGA      120
CTTTTTTCAT C ATG GAA CCT AGC CTA AAA AAG GCC TAT GAT ACA GGG ATT      170
          Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp Thr Gly Ile
              1           5           10

AAG CCT TAT ATG GAT AAA AAG ATT TCT TAC ACC GAA GCG TTT GAA AAA      218
Lys Pro Tyr Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala Phe Glu Lys
          15           20           25

```

AGC GCT CTG CCC TTC AAG GAA TTC ATG CTT AAA AAC ACA CGA GAA AAG	266
Ser Ala Leu Pro Phe Lys Glu Phe Met Leu Lys Asn Thr Arg Glu Lys	
30 35 40 45	
GAT CTA GCC CTT TTT TTT AGG ATT AGA AAC CTC CCT AAC CCT AAA ACC	314
Asp Leu Ala Leu Phe Phe Arg Ile Arg Asn Leu Pro Asn Pro Lys Thr	
50 55 60	
CCT GAT GAG GTG AGT TTG AGC GTT TTG ATC CCG GCA TTT ATG ATA AGC	362
Pro Asp Glu Val Ser Leu Ser Val Leu Ile Pro Ala Phe Met Ile Ser	
65 70 75	
GAG TTG AAA ACA GCG TTT CAA ATC GGC TTT TTA CTC TAC TTG CCT TTT	410
Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Leu Leu Tyr Leu Pro Phe	
80 85 90	
TTG GTG ATT GAT ATG GTG ATC AGC TCT ATT TTA ATG GCG ATG GGC ATG	458
Leu Val Ile Asp Met Val Ile Ser Ser Ile Leu Met Ala Met Gly Met	
95 100 105	
ATG ATG CTC CCG CCT GTA ATG ATT TCT CTG CCT TTT AAA ATT TTA GTG	506
Met Met Leu Pro Pro Val Met Ile Ser Leu Pro Phe Lys Ile Leu Val	
110 115 120 125	
TTT ATT CTG GTA GAT GGG TTT AAT TTA TTG ACC GAA AAT TTA GTG GCG	554
Phe Ile Leu Val Asp Gly Phe Asn Leu Leu Thr Glu Asn Leu Val Ala	
130 135 140	
AGT TTT AAA ATG GTT TGATATTAAC AAGCATTCAA GCGATAAAAG CTTGAAGCTA G	610
Ser Phe Lys Met Val	
145	
TTTAAAACTC ATAATTCAAA	630

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp Thr Gly Ile Lys Pro Tyr	
1 5 10 15	
Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala Phe Glu Lys Ser Ala Leu	
20 25 30	
Pro Phe Lys Glu Phe Met Leu Lys Asn Thr Arg Glu Lys Asp Leu Ala	
35 40 45	
Leu Phe Phe Arg Ile Arg Asn Leu Pro Asn Pro Lys Thr Pro Asp Glu	
50 55 60	
Val Ser Leu Ser Val Leu Ile Pro Ala Phe Met Ile Ser Glu Leu Lys	
65 70 75 80	
Thr Ala Phe Gln Ile Gly Phe Leu Leu Tyr Leu Pro Phe Leu Val Ile	
85 90 95	

Asp	Met	Val	Ile	Ser	Ser	Ile	Leu	Met	Ala	Met	Gly	Met	Met	Met	Leu
			100						105				110		
Pro	Pro	Val	Met	Ile	Ser	Leu	Pro	Phe	Lys	Ile	Leu	Val	Phe	Ile	Leu
		115					120					125			
Val	Asp	Gly	Phe	Asn	Leu	Leu	Thr	Glu	Asn	Leu	Val	Ala	Ser	Phe	Lys
	130					135					140				
Met	Val														
145															

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...2313
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AAAAGGTGGT AA ATG AAA AGA ATT TTA GTC TCT TTG GCT GTT TTG AGT CAT	51
Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His	
1 5 10	
AGC GCG CAT GCT GTC AAA ACT CAT AAT TTG GAA AGG GTG GAA GCT TCA	99
Ser Ala His Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser	
15 20 25	
GGG GTG GCT AAC GAT AAG GAA GCG CCT TTA AGC TGG AGG AGC AAG GAA	147
Gly Val Ala Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu	
30 35 40 45	
GTG AGA AAC TAT ATG GGA TCT CGC ACG GTG ATT TCT AAC AAG CAA CTC	195
Val Arg Asn Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu	
50 55 60	
ACT AAA AGC GCC AAT CAG AGC ATT GAA GAA GCT TTG CAA AAT GTG CCA	243
Thr Lys Ser Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro	
65 70 75	
GGC GTG CAT ATT AGA AAC GCT ACG GGT ATT GGA GCT GTG CCT AGC TTT	291
Gly Val His Ile Arg Asn Ala Thr Gly Ile Gly Ala Val Pro Ser Phe	
80 85 90	
TCT GTT AGG GGC TTT GGT GGG GGA AGT TCA GGG CAT TCC AAT ACG GCT	339
Ser Val Arg Gly Phe Gly Gly Gly Ser Ser Gly His Ser Asn Thr Ala	
95 100 105	
ATG GTT TTA GTC AAT GGG ATC CCT ATT TAT GTT GCG CCC TAT GTT GAT	387
Met Val Leu Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Asp	
110 115 120 125	

ATT Ile	AGC Ser	ATT Ile	CCT Pro	ATT Ile 130	TTC Phe	CCT Pro	GTA Val	ACC Thr	TTT Phe 135	CAA Gln	TCT Ser	GTA Val	GAT Asp	AGA Arg 140	ATC Ile	435
AGC Ser	GTA Val	ACC Thr	AAG Lys 145	GGT Gly	GGG Gly	GAG Glu	AGC Ser	GTG Val 150	CGT Arg	TAT Tyr	GGC Gly	CCT Pro	AAT Asn 155	GTT Val	TTT Phe	483
GGC Gly	GGT Gly	GTG Val 160	ATT Ile	AAT Asn	GTG Val	ATC Ile	ACT Thr 165	AAG Lys	GGC Gly	ATT Ile	CCT Pro	ACC Thr 170	AAG Lys	TGG Trp	GAG Glu	531
AGT Ser	CAG Gln 175	GTG Val	AGC Ser	GAG Glu	AGG Arg	GCC Ala 180	ACT Thr	TTT Phe	TGG Trp	GGC Gly	AAA Lys 185	TCT Ser	GAA Glu	AAT Asn	GGG Gly	579
GGC Gly 190	TTT Phe	TTC Phe	AAT Asn	CAA Gln 195	AAT Asn	TCT Ser	AAA Lys	AAC Asn	CTT Leu	GAC Asp 200	AAA Lys	AGC Ser	TTA Leu	GCC Ala	AAT Asn 205	627
AAC Asn	ATG Met	CTT Leu	TTT Phe	GAC Asp 210	ACT Thr	TAC Tyr	TTA Leu	AGA Arg	ACA Thr 215	GGG Gly	GGC Gly	ATG Met	ATG Met	AAT Asn 220	AAG Lys	675
CAT His	TTT Phe	GGA Gly	ATC Ile 225	CAA Gln	GCT Ala	CAA Gln	GCC Ala	AAC Asn 230	TGG Trp	CTT Leu	AAA Lys	GGG Gly	CAA Gln 235	GGG Gly	TTT Phe	723
AGA Arg	TAC Tyr 240	AAC Asn	AGC Ser	CCT Pro	ACG Thr	AAC Asn	ATT Ile 245	CAA Gln	AAC Asn	TAC Tyr	ATG Met 250	CTA Leu	GAT Asp	TCC Ser	TTG Leu	771
TAT Tyr	CAA Gln 255	ATT Ile	AAT Asn	GAT Asp	AGT Ser	AAT Asn 260	AAG Lys	ATC Ile	ACT Thr	GCT Ala	TTT Phe 265	TTC Phe	CAA Gln	TAC Tyr	TAT Tyr	819
AAT Asn 270	TAT Tyr	TTT Phe	ATG Met	GCA Ala	GAC Asp 275	CCC Pro	GGA Gly	TCT Ser	TTA Leu	GGC Gly 280	ATA Ile	GAA Glu	GCG Ala	TAT Tyr	AAT Asn 285	867
CAA Gln	AAT Asn	CGT Arg	TTT Phe 290	CAA Gln	AAC Asn	AAC Asn	CGC Arg	CCT Pro 295	AAT Asn	AAC Asn	AAT Asn	AAA Lys	AGC Ser	GGG Gly 300	AGA Arg	915
GCG Ala	AAG Lys	CGR Xaa 305	TGG Trp	GGA Gly	GCT Ala	GTG Val	TAT Tyr	CAA Gln 310	AAC Asn	TTT Phe	TTT Phe	GGG Gly 315	GAT Asp	ACG Thr	GAC Asp	963
AAA Lys	ATA Ile 320	GGT Gly	GGG Gly	GAT Asp	TTC Phe	ACT Thr	TTT Phe 325	AGT Ser	TAC Tyr	TAT Tyr	GGG Gly 330	CAT His	GAC Asp	ATG Met	TCA Ser	1011
AGG Arg	GAT Asp 335	TTT Phe	CAA Gln	TTT Phe	GAT Asp	TCT Ser 340	AAT Asn	TTT Phe	TTG Leu	AAT Asn	GTC Val 345	AAT Asn	ACC Thr	AAT Asn	CCT Pro	1059
AAA Lys	TTA Leu	GGC Gly	CCT Pro	GTT Val	TAT Tyr	ACC Thr	GAT Asp	CAA Gln	AAT Asn	TAT Tyr	CCA Pro	GGA Gly	TTT Phe	TTT Phe	ATT Ile	1107

350		355		360		365	
TTT GAT CAT TTA AGG CGT TAC ATA ATG AAC GCT TTT GAG CCT AAT TTG	1155						
Phe Asp His Leu Arg Arg Tyr Ile Met Asn Ala Phe Glu Pro Asn Leu							
		370		375		380	
AAC TTA GTT GTC AAT ACC AAT AAA GTT AAG CAA ACT TTT AAT GTG GGC	1203						
Asn Leu Val Val Asn Thr Asn Lys Val Lys Gln Thr Phe Asn Val Gly							
		385		390		395	
ATG CGT TTT ATG ACA ATG GAT ATG TAT TTC AGA TTG GAT CAA AGC ACA	1251						
Met Arg Phe Met Thr Met Asp Met Tyr Phe Arg Leu Asp Gln Ser Thr							
		400		405		410	
TGC GAA AAA ACC GAT ATT TTT AAT GGG GTG TGC CGC ATG CCT CCT TTT	1299						
Cys Glu Lys Thr Asp Ile Phe Asn Gly Val Cys Arg Met Pro Pro Phe							
		415		420		425	
GTT CTT TCT AAA AAA CCC AGC AAC AAT CAA AAC CTG TTT AAC AAC TAT	1347						
Val Leu Ser Lys Lys Pro Ser Asn Asn Gln Asn Leu Phe Asn Asn Tyr							
		430		435		440	445
ACA GCG GTA TGG TTG AGC GAT AAA ATA GAG CTT TTT GAT TCT AAA TTG	1395						
Thr Ala Val Trp Leu Ser Asp Lys Ile Glu Leu Phe Asp Ser Lys Leu							
		450		455		460	
GTG ATA ACT CCA GGG CTT AGA TAC ACT TTT TTG AAC TAT AAC AAC AAA	1443						
Val Ile Thr Pro Gly Leu Arg Tyr Thr Phe Leu Asn Tyr Asn Asn Lys							
		465		470		475	
GAG CCA GAA AAG CAT GAT TTT TCT GTG TGG AAT ATT ACA AAA AAG CGT	1491						
Glu Pro Glu Lys His Asp Phe Ser Val Trp Asn Ile Thr Lys Lys Arg							
		480		485		490	
CAA AAC GAA TGG AGT CCC GCC CTT AAC ATT GGC TAT AAA CCT ATG GAA	1539						
Gln Asn Glu Trp Ser Pro Ala Leu Asn Ile Gly Tyr Lys Pro Met Glu							
		495		500		505	
AAT TGG ATA TGG TAT GCG AAC TAC CGC CGC AGT TTT ATC CCC CCA CAA	1587						
Asn Trp Ile Trp Tyr Ala Asn Tyr Arg Arg Ser Phe Ile Pro Pro Gln							
		510		515		520	525
CAT ACA ATG CTA GGC ATT ACT AGG ACT AAT TAC AAC CAA ATT TTT AAT	1635						
His Thr Met Leu Gly Ile Thr Arg Thr Asn Tyr Asn Gln Ile Phe Asn							
		530		535		540	
GAA ATT GAA GTG GGG CAA CGC TAT AGT TAT AAA AAT CTA TTG AGC TTT	1683						
Glu Ile Glu Val Gly Gln Arg Tyr Ser Tyr Lys Asn Leu Leu Ser Phe							
		545		550		555	
AAC ACG AAT TAT TTT GTG ATT TTT GCC AAG CGT TAC TAT GCG GGA GGC	1731						
Asn Thr Asn Tyr Phe Val Ile Phe Ala Lys Arg Tyr Tyr Ala Gly Gly							
		560		565		570	
TAT AGC CCA CAG CCT ATT AAC GCT AGG AGT CAA GGG GTA GAA TTG GAA	1779						
Tyr Ser Pro Gln Pro Ile Asn Ala Arg Ser Gln Gly Val Glu Leu Glu							
		575		580		585	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met	Lys	Arg	Ile	Leu	Val	Ser	Leu	Ala	Val	Leu	Ser	His	Ser	Ala	His
1			5					10						15	
Ala	Val	Lys	Thr	His	Asn	Leu	Glu	Arg	Val	Glu	Ala	Ser	Gly	Val	Ala
			20					25					30		
Asn	Asp	Lys	Glu	Ala	Pro	Leu	Ser	Trp	Arg	Ser	Lys	Glu	Val	Arg	Asn
		35					40					45			
Tyr	Met	Gly	Ser	Arg	Thr	Val	Ile	Ser	Asn	Lys	Gln	Leu	Thr	Lys	Ser
	50					55					60				
Ala	Asn	Gln	Ser	Ile	Glu	Glu	Ala	Leu	Gln	Asn	Val	Pro	Gly	Val	His
65					70					75					80
Ile	Arg	Asn	Ala	Thr	Gly	Ile	Gly	Ala	Val	Pro	Ser	Phe	Ser	Val	Arg
				85					90					95	
Gly	Phe	Gly	Gly	Gly	Ser	Ser	Gly	His	Ser	Asn	Thr	Ala	Met	Val	Leu
			100					105					110		
Val	Asn	Gly	Ile	Pro	Ile	Tyr	Val	Ala	Pro	Tyr	Val	Asp	Ile	Ser	Ile
	115						120					125			
Pro	Ile	Phe	Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile	Ser	Val	Thr
	130					135					140				
Lys	Gly	Gly	Glu	Ser	Val	Arg	Tyr	Gly	Pro	Asn	Val	Phe	Gly	Gly	Val
145					150					155					160
Ile	Asn	Val	Ile	Thr	Lys	Gly	Ile	Pro	Thr	Lys	Trp	Glu	Ser	Gln	Val
				165					170					175	
Ser	Glu	Arg	Ala	Thr	Phe	Trp	Gly	Lys	Ser	Glu	Asn	Gly	Gly	Phe	Phe
			180					185					190		
Asn	Gln	Asn	Ser	Lys	Asn	Leu	Asp	Lys	Ser	Leu	Ala	Asn	Asn	Met	Leu
			195				200					205			
Phe	Asp	Thr	Tyr	Leu	Arg	Thr	Gly	Gly	Met	Met	Asn	Lys	His	Phe	Gly
	210					215					220				
Ile	Gln	Ala	Gln	Ala	Asn	Trp	Leu	Lys	Gly	Gln	Gly	Phe	Arg	Tyr	Asn
225					230					235					240
Ser	Pro	Thr	Asn	Ile	Gln	Asn	Tyr	Met	Leu	Asp	Ser	Leu	Tyr	Gln	Ile
			245						250					255	
Asn	Asp	Ser	Asn	Lys	Ile	Thr	Ala	Phe	Phe	Gln	Tyr	Tyr	Asn	Tyr	Phe
			260					265					270		
Met	Ala	Asp	Pro	Gly	Ser	Leu	Gly	Ile	Glu	Ala	Tyr	Asn	Gln	Asn	Arg
		275					280					285			
Phe	Gln	Asn	Asn	Arg	Pro	Asn	Asn	Asn	Lys	Ser	Gly	Arg	Ala	Lys	Xaa
	290					295					300				
Trp	Gly	Ala	Val	Tyr	Gln	Asn	Phe	Phe	Gly	Asp	Thr	Asp	Lys	Ile	Gly
305					310					315					320
Gly	Asp	Phe	Thr	Phe	Ser	Tyr	Tyr	Gly	His	Asp	Met	Ser	Arg	Asp	Phe
			325						330					335	
Gln	Phe	Asp	Ser	Asn	Phe	Leu	Asn	Val	Asn	Thr	Asn	Pro	Lys	Leu	Gly
			340					345					350		
Pro	Val	Tyr	Thr	Asp	Gln	Asn	Tyr	Pro	Gly	Phe	Phe	Ile	Phe	Asp	His
	355						360					365			
Leu	Arg	Arg	Tyr	Ile	Met	Asn	Ala	Phe	Glu	Pro	Asn	Leu	Asn	Leu	Val
	370					375					380				
Val	Asn	Thr	Asn	Lys	Val	Lys	Gln	Thr	Phe	Asn	Val	Gly	Met	Arg	Phe
385					390					395					400
Met	Thr	Met	Asp	Met	Tyr	Phe	Arg	Leu	Asp	Gln	Ser	Thr	Cys	Glu	Lys
			405						410					415	
Thr	Asp	Ile	Phe	Asn	Gly	Val	Cys	Arg	Met	Pro	Pro	Phe	Val	Leu	Ser
			420					425					430		
Lys	Lys	Pro	Ser	Asn	Asn	Gln	Asn	Leu	Phe	Asn	Asn	Tyr	Thr	Ala	Val

		435					440					445						
Trp	Leu	Ser	Asp	Lys	Ile	Glu	Leu	Phe	Asp	Ser	Lys	Leu	Val	Ile	Thr			
	450					455					460							
Pro	Gly	Leu	Arg	Tyr	Thr	Phe	Leu	Asn	Tyr	Asn	Asn	Lys	Glu	Pro	Glu			
465					470					475					480			
Lys	His	Asp	Phe	Ser	Val	Trp	Asn	Ile	Thr	Lys	Lys	Arg	Gln	Asn	Glu			
				485					490					495				
Trp	Ser	Pro	Ala	Leu	Asn	Ile	Gly	Tyr	Lys	Pro	Met	Glu	Asn	Trp	Ile			
			500					505					510					
Trp	Tyr	Ala	Asn	Tyr	Arg	Arg	Ser	Phe	Ile	Pro	Pro	Gln	His	Thr	Met			
		515					520					525						
Leu	Gly	Ile	Thr	Arg	Thr	Asn	Tyr	Asn	Gln	Ile	Phe	Asn	Glu	Ile	Glu			
	530					535					540							
Val	Gly	Gln	Arg	Tyr	Ser	Tyr	Lys	Asn	Leu	Leu	Ser	Phe	Asn	Thr	Asn			
545					550					555					560			
Tyr	Phe	Val	Ile	Phe	Ala	Lys	Arg	Tyr	Tyr	Ala	Gly	Gly	Tyr	Ser	Pro			
				565					570					575				
Gln	Pro	Ile	Asn	Ala	Arg	Ser	Gln	Gly	Val	Glu	Leu	Glu	Leu	Tyr	Tyr			
			580					585					590					
Ala	Pro	Ile	Arg	Gly	Leu	Gln	Phe	His	Val	Ala	Tyr	Thr	Tyr	Ile	Asp			
		595					600					605						
Ala	Arg	Ile	Thr	Ser	Asn	Ala	Asp	Asp	Ile	Ala	Tyr	Tyr	Phe	Thr	Gly			
	610					615					620							
Ile	Val	Asn	Lys	Pro	Phe	Asp	Ile	Lys	Gly	Lys	Arg	Leu	Pro	Tyr	Val			
625					630					635					640			
Ser	Pro	Asn	Gln	Phe	Ile	Phe	Asp	Met	Met	Tyr	Thr	Tyr	Lys	His	Thr			
				645					650					655				
Thr	Phe	Gly	Ile	Ser	Ser	Tyr	Phe	Tyr	Ser	Arg	Ala	Tyr	Ser	Ser	Met			
			660					665					670					
Leu	Asn	Gln	Ala	Lys	Ser	Gln	Thr	Val	Cys	Leu	Pro	Leu	Asn	Pro	Glu			
		675					680					685						
Tyr	Thr	Gly	Gly	Leu	Glu	Tyr	Gly	Cys	Asn	Ser	Val	Gly	Leu	Leu	Pro			
	690					695					700							
Leu	Tyr	Phe	Val	Leu	Asn	Val	Gln	Val	Ser	Ser	Val	Leu	Trp	Gln	Ser			
705					710					715					720			
Gly	Arg	His	Lys	Ile	Thr	Gly	Ser	Leu	Gln	Ile	Asn	Asn	Leu	Phe	Asn			
				725						730				735				
Met	Lys	Tyr	Tyr	Phe	Arg	Gly	Ile	Gly	Thr	Ser	Pro	Thr	Gly	Arg	Glu			
			740					745					750					
Pro	Ala	Pro	Gly	Arg	Ser	Ile	Thr	Ala	Tyr	Leu	Asn	Tyr	Glu	Phe				
		755					760					765						

(2) INFORMATION FOR SEO ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 19...837
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGATAGGAAT GTAAAGGA	ATG GAA TTT ATG AAA AAG TTT GTA GCT TTA GGG	51
	Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly	
	1 5 10	
CTT CTA TCC GCA GTT TTA AGC TCT TCG TTG TTA GCC GAA GGT GAT GGT	99	
Leu Leu Ser Ala Val Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly		
	15 20 25	
GTT TAT ATA GGG ACT AAT TAT CAG CTT GGA CAA GCC CGT TTG AAT AGT	147	
Val Tyr Ile Gly Thr Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser		
	30 35 40	
AAT ATT TAT AAT ACA GGG GAT TGC ACA GGG AGT GTT GTA GGT TGC CCC	195	
Asn Ile Tyr Asn Thr Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro		
	45 50 55	
CCA GGT CTT ACC GCT AAT AAG CAT AAT CCA GGA GGC ACC AAT ATC AAT	243	
Pro Gly Leu Thr Ala Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn		
	60 65 70 75	
TGG CAT GCT AAA TAC GCT AAT GGG GCT TTG AAT GGT CTT GGG TTG AAT	291	
Trp His Ala Lys Tyr Ala Asn Gly Ala Leu Asn Gly Leu Gly Leu Asn		
	80 85 90	
GTG GGT TAT AAG AAG TTC TTC CAG TTC AAG TCT TTT GAT ATG ACA AGC	339	
Val Gly Tyr Lys Lys Phe Phe Gln Phe Lys Ser Phe Asp Met Thr Ser		
	95 100 105	
AAG TGG TTT GGT TTT AGA GTG TAT GGG CTT TTT GAT TAT GGG CAT GCC	387	
Lys Trp Phe Gly Phe Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala		
	110 115 120	
ACT TTA GGC AAG CAA GTT TAT GCA CCT AAT AAA ATC CAG TTG GAT ATG	435	
Thr Leu Gly Lys Gln Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met		
	125 130 135	
GTC TCT TGG GGT GTG GGG AGC GAT TTG TTA GCT GAT ATT ATT GAT AAC	483	
Val Ser Trp Gly Val Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Asn		
	140 145 150 155	
GAT AAC GCT TCT TTT GGT ATT TTT GGT GGG GTC GCT ATC GGC GGT AAC	531	
Asp Asn Ala Ser Phe Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn		
	160 165 170	
ACT TGG AAA AGC TCA GCG GCA AAC TAT TGG AAA GAG CAA ATC ATT GAA	579	
Thr Trp Lys Ser Ser Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu		
	175 180 185	
GCT AAG GGT CCT GAT GTT TGT ACC CCT ACT TAT TGT AAC CCT AAC GCT	627	
Ala Lys Gly Pro Asp Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala		
	190 195 200	
CCT TAT AGC ACC AAA ACT TCA ACC GTC GCT TTT CAG GTA TGG TTG AAT	675	
Pro Tyr Ser Thr Lys Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn		
	205 210 215	

Asn	Ile	Tyr	Lys	His	Asn	Gly	Val	Glu	Phe	Gly	Val	Arg	Val	Pro	Leu
225					230					235					240
Leu	Ile	Asn	Lys	Phe	Leu	Ser	Ala	Gly	Pro	Asn	Ala	Thr	Asn	Leu	Tyr
				245					250					255	
Tyr	His	Leu	Lys	Arg	Asp	Tyr	Ser	Leu	Tyr	Leu	Gly	Tyr	Asn	Tyr	Thr
			260					265					270		
Phe															

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...522
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CACGGTCATT TTGCTGTGT TTTTAGTCGC GTATTC ATG CAA CTG CTT ATG GAA	54
Met Gln Leu Leu Met Glu	
1 5	
CGC CTT TCT CTT GTC TTC AGG CAT CTT TTC CAT GCG CTT TTT CAA CTC	102
Arg Leu Ser Leu Val Phe Arg His Leu Phe His Ala Leu Phe Gln Leu	
10 15 20	
TTT TGT GTA ATC CAC AAT ATC CTG CGG AGK ACA ACG CCA GCC ATT TTA	150
Phe Cys Val Ile His Asn Ile Leu Arg Xaa Thr Thr Pro Ala Ile Leu	
25 30 35	
GCC AAA TCT TCA TCG CTT GTT TTG CTG AAA TCT TTG GCG TTC AAA GCC	198
Ala Lys Ser Ser Ser Leu Val Leu Leu Lys Ser Leu Ala Phe Lys Ala	
40 45 50	
ACA AAT AGC AAC GCG CTA ACA GAA AGT ATT TTC AAC GCT TTT TTC ATT	246
Thr Asn Ser Asn Ala Leu Thr Glu Ser Ile Phe Asn Ala Phe Phe Ile	
55 60 65 70	
TTT TAT CCT TTT AAA TTA AAT TTA TCT CAC TTA GGA GAG CAA TGC TCG	294
Phe Tyr Pro Phe Lys Leu Asn Leu Ser His Leu Gly Glu Gln Cys Ser	
75 80 85	
TCT TTT TTC TTA ACA GCC CTA CAC CAA ACT TTT CTC GTA TCG CCG CTG	342
Ser Phe Phe Leu Thr Ala Leu His Gln Thr Phe Leu Val Ser Pro Leu	
90 95 100	
CAA ACG CTC ACA TTA AGT CCT TTT GCC TTG ATT TCT TCA TCG CTC AAA	390
Gln Thr Leu Thr Leu Ser Pro Phe Ala Leu Ile Ser Ser Ser Leu Lys	
105 110 115	

CCT TTG GTT TTT TCT TCT AAT TCT TTA CGC ACT TCT TCA CGC ATT TTT 438
 Pro Leu Val Phe Ser Ser Asn Ser Leu Arg Thr Ser Ser Arg Ile Phe
 120 125 130

 TTG AAA TCC TTC GCT CAT TTT GGA AAG ATT CTT CCT AGC GAT CCG GCT 486
 Leu Lys Ser Phe Ala His Phe Gly Lys Ile Leu Pro Ser Asp Pro Ala
 135 140 145 150

 GAA ATT CGC GCG GAA TTT CTT AGC GTC CTC AGC GTT TAAAGTTTTA AGGCGT 538
 Glu Ile Arg Ala Glu Phe Leu Ser Val Leu Ser Val
 155 160

 TTAGACACTT CCATGCGATA AT 560

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Gln Leu Leu Met Glu Arg Leu Ser Leu Val Phe Arg His Leu Phe
 1 5 10 15
 His Ala Leu Phe Gln Leu Phe Cys Val Ile His Asn Ile Leu Arg Xaa
 20 25 30
 Thr Thr Pro Ala Ile Leu Ala Lys Ser Ser Ser Leu Val Leu Leu Lys
 35 40 45
 Ser Leu Ala Phe Lys Ala Thr Asn Ser Asn Ala Leu Thr Glu Ser Ile
 50 55 60
 Phe Asn Ala Phe Phe Ile Phe Tyr Pro Phe Lys Leu Asn Leu Ser His
 65 70 75 80
 Leu Gly Glu Gln Cys Ser Ser Phe Phe Leu Thr Ala Leu His Gln Thr
 85 90 95
 Phe Leu Val Ser Pro Leu Gln Thr Leu Thr Leu Ser Pro Phe Ala Leu
 100 105 110
 Ile Ser Ser Ser Leu Lys Pro Leu Val Phe Ser Ser Asn Ser Leu Arg
 115 120 125
 Thr Ser Ser Arg Ile Phe Leu Lys Ser Phe Ala His Phe Gly Lys Ile
 130 135 140
 Leu Pro Ser Asp Pro Ala Glu Ile Arg Ala Glu Phe Leu Ser Val Leu
 145 150 155 160
 Ser Val

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 41...1132
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

AAGGCATCCA	CCATTAAACCC	TTTTTAAATT	TATTTTAACG	ATG	TTT	TAC	TAT	ACT	55
				Met	Phe	Tyr	Tyr	Thr	
				1				5	
ATA	AAA	TCT	TTT	AAT	TTC	AAA	AGG	TGG	103
Ile	Lys	Ser	Phe	Asn	Phe	Lys	Arg	Trp	
			10					15	
									20
AAA	TTG	TTG	ATT	CTT	TTA	TTT	TGT	TTG	151
Lys	Leu	Leu	Ile	Leu	Leu	Phe	Cys	Leu	
			25					30	
									35
AAT	TTA	CCC	ACC	ATT	GCT	TTA	CTG	GCG	199
Asn	Leu	Pro	Thr	Ile	Ala	Leu	Leu	Ala	
		40						45	
									50
AGT	GGT	GCG	AGC	GCG	AGT	TTG	GGT	AGT	247
Ser	Gly	Ala	Ser	Ala	Ser	Leu	Gly	Ser	
	55					60			
								65	
ATC	AAA	GAG	CTT	TTG	AAG	GCT	ATC	CCT	295
Ile	Lys	Glu	Leu	Leu	Lys	Ala	Ile	Pro	
70					75				
								80	
									85
ATT	CAA	GGG	GAG	CAG	ATT	TCT	AAC	ATC	343
Ile	Gln	Gly	Glu	Gln	Ile	Ser	Asn	Ile	
				90				95	
									100
GAG	GTA	TGG	TTC	AAG	CTC	GCC	AAA	CGT	391
Glu	Val	Trp	Phe	Lys	Leu	Ala	Lys	Arg	
			105					110	
									115
AGC	CGT	ATT	CAA	GGC	GTG	GTC	ATC	ACG	439
Ser	Arg	Ile	Gln	Gly	Val	Val	Ile	Thr	
		120					125		
									130
GAG	AGC	GCG	TAT	TTT	TTA	AAC	TTA	GTT	487
Glu	Ser	Ala	Tyr	Phe	Leu	Asn	Leu	Val	
	135					140			
								145	
GTG	CTG	GTG	GGA	GCG	ATG	CGT	AAT	GCT	535
Val	Leu	Val	Gly	Ala	Met	Arg	Asn	Ala	
150					155				
								160	
									165
GCT	TTG	AAT	TTA	TAT	AAT	GCT	GTG	AGC	583
Ala	Leu	Asn	Leu	Tyr	Asn	Ala	Val	Ser	
			170					175	
									180
GCG	AAT	AAA	GGC	GTG	TTA	GTG	GTG	ATG	631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met	Phe	Tyr	Tyr	Thr	Ile	Lys	Ser	Phe	Asn	Phe	Lys	Arg	Trp	Ser	Ile
1				5					10					15	
Met	Arg	Ile	Phe	Leu	Lys	Leu	Leu	Ile	Leu	Leu	Phe	Cys	Leu	Lys	Gly
			20					25					30		
Gln	Val	Met	Ala	Gln	Asn	Leu	Pro	Thr	Ile	Ala	Leu	Leu	Ala	Thr	Gly
		35					40					45			
Gly	Thr	Ile	Ala	Gly	Ser	Gly	Ala	Ser	Ala	Ser	Leu	Gly	Ser	Tyr	Lys
	50					55					60				
Ser	Gly	Glu	Leu	Gly	Ile	Lys	Glu	Leu	Leu	Lys	Ala	Ile	Pro	Ser	Leu
65					70					75				80	
Asn	Arg	Leu	Ala	Arg	Ile	Gln	Gly	Glu	Gln	Ile	Ser	Asn	Ile	Gly	Ser
				85					90					95	
Gln	Asp	Met	Asn	Glu	Glu	Val	Trp	Phe	Lys	Leu	Ala	Lys	Arg	Ala	Gln
		100						105					110		
Glu	Leu	Leu	Asp	Asp	Ser	Arg	Ile	Gln	Gly	Val	Val	Ile	Thr	His	Gly
		115					120					125			
Thr	Asp	Thr	Leu	Glu	Glu	Ser	Ala	Tyr	Phe	Leu	Asn	Leu	Val	Leu	Arg
	130					135					140				
Ser	Thr	Lys	Pro	Val	Val	Leu	Val	Gly	Ala	Met	Arg	Asn	Ala	Ala	Ser
145					150					155				160	
Leu	Ser	Ala	Asp	Gly	Ala	Leu	Asn	Leu	Tyr	Asn	Ala	Val	Ser	Val	Ala
			165						170					175	
Leu	Asn	Glu	Lys	Ser	Ala	Asn	Lys	Gly	Val	Leu	Val	Val	Met	Asp	Asp
			180					185					190		
Asn	Ile	Phe	Ser	Ala	Arg	Glu	Val	Ile	Lys	Thr	His	Thr	Thr	His	Thr
	195					200					205				
Ser	Thr	Phe	Lys	Ala	Leu	Asn	Ser	Gly	Ala	Ile	Gly	Ser	Val	Tyr	Tyr
	210					215					220				
Gly	Lys	Thr	Arg	Tyr	Tyr	Met	Gln	Pro	Leu	Arg	Lys	His	Thr	Thr	Glu
225					230					235					240
Ser	Glu	Phe	Ser	Leu	Ser	Gln	Leu	Lys	Thr	Pro	Leu	Pro	Lys	Val	Asp
			245						250					255	
Ile	Ile	Tyr	Thr	His	Ala	Gly	Met	Thr	Pro	Asp	Leu	Phe	Gln	Ala	Ser
		260					265						270		
Leu	Asn	Ser	His	Ala	Lys	Gly	Val	Val	Ile	Ala	Gly	Val	Gly	Asn	Gly
	275						280					285			
Asn	Val	Ser	Ala	Gly	Phe	Leu	Lys	Ala	Met	Gln	Glu	Ala	Ser	Gln	Met
	290					295					300				
Gly	Val	Val	Ile	Val	Arg	Ser	Ser	Arg	Val	Asn	Ser	Gly	Glu	Ile	Thr
305					310					315					320
Ser	Gly	Glu	Ile	Asp	Asp	Lys	Ala	Phe	Ile	Thr	Ser	Asp	Asn	Leu	Asn
			325						330					335	
Pro	Gln	Lys	Ala	Arg	Val	Leu	Leu	Gln	Leu	Ala	Leu	Thr	Lys	Thr	Asn
		340						345					350		
Asn	Lys	Glu	Lys	Ile	Gln	Glu	Met	Phe	Glu	Glu	Tyr				
	355					360									

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 37...612
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

AGTAAACAT CGTTAAATA AATTTAAAA GGGTTA	ATG GTG GAT GCC TTT TTC	54
	Met Val Asp Ala Phe Phe	
	1 5	
CAA ATT GCA GTG TTA CTT TTT TCG CTT TTT TTA GGG GCA AGG CTA GGG		102
Gln Ile Ala Val Leu Leu Phe Ser Leu Phe Leu Gly Ala Arg Leu Gly		
	10 15 20	
GGC TTG GGA GTG GGC TAT GCG GGG GGC TTG GGC GTG CTT ATT TTA TGC		150
Gly Leu Gly Val Gly Tyr Ala Gly Gly Leu Gly Val Leu Ile Leu Cys		
	25 30 35	
TTA TTT TTG GGG CTA AAT CCG GGC AAA ATC CCT TTT GAT GTG ATT TTA		198
Leu Phe Leu Gly Leu Asn Pro Gly Lys Ile Pro Phe Asp Val Ile Leu		
	40 45 50	
ATC ATC ATG GCA GTC ATT AGC GCT ATT AGC GCG ATG CAA AAA GCG GGG		246
Ile Ile Met Ala Val Ile Ser Ala Ile Ser Ala Met Gln Lys Ala Gly		
	55 60 65 70	
GGC TTG GAT TAC TTA GTC AAA ATC GCT GAA AAA ATT TTA AGG AAA CAC		294
Gly Leu Asp Tyr Leu Val Lys Ile Ala Glu Lys Ile Leu Arg Lys His		
	75 80 85	
CCC AAG CAA ATC AAT TAC CTT GCG CCA AGC GTG GCG TAT TGT TTA ACG		342
Pro Lys Gln Ile Asn Tyr Leu Ala Pro Ser Val Ala Tyr Cys Leu Thr		
	90 95 100	
ATA CTA GCC GGC ACC GGG CAT ACG GTT TTT TCC TTG ATC CCG GTG ATT		390
Ile Leu Ala Gly Thr Gly His Thr Val Phe Ser Leu Ile Pro Val Ile		
	105 110 115	
GTG GAA GTG AGC CAG AGC CAA AAC ATC AAG CCT AAA GCG CCT TTA AGC		438
Val Glu Val Ser Gln Ser Gln Asn Ile Lys Pro Lys Ala Pro Leu Ser		
	120 125 130	
TTA GCG GTA GTC TCT AGT CAA GTC GCT ATT ACT GCA AGC CCG GTG AGC		486
Leu Ala Val Val Ser Ser Gln Val Ala Ile Thr Ala Ser Pro Val Ser		
	135 140 145 150	
GCA GCG GTN GGT GTT TAT GAG CGG CAT TTT AGA GCC TTT AGG AGC AAA		534
Ala Ala Xaa Gly Val Tyr Glu Arg His Phe Arg Ala Phe Arg Ser Lys		
	155 160 165	
TTA CTT GAC CCT TTT AAT GGT TTG GAT CCC TAC GAC TTT TTT AGC ATG		582
Leu Leu Asp Pro Phe Asn Gly Leu Asp Pro Tyr Asp Phe Phe Ser Met		
	170 175 180	

Socioeconomic status	
SES	1
SES	2
SES	3
SES	4
SES	5
SES	6
SES	7
SES	8
SES	9
SES	10
SES	11
SES	12
SES	13
SES	14
SES	15
SES	16
SES	17
SES	18
SES	19
SES	20
SES	21
SES	22
SES	23
SES	24
SES	25
SES	26
SES	27
SES	28
SES	29
SES	30
SES	31
SES	32
SES	33
SES	34
SES	35
SES	36
SES	37
SES	38
SES	39
SES	40
SES	41
SES	42
SES	43
SES	44
SES	45
SES	46
SES	47
SES	48
SES	49
SES	50
SES	51
SES	52
SES	53
SES	54
SES	55
SES	56
SES	57
SES	58
SES	59
SES	60
SES	61
SES	62
SES	63
SES	64
SES	65
SES	66
SES	67
SES	68
SES	69
SES	70
SES	71
SES	72
SES	73
SES	74
SES	75
SES	76
SES	77
SES	78
SES	79
SES	80
SES	81
SES	82
SES	83
SES	84
SES	85
SES	86
SES	87
SES	88
SES	89
SES	90
SES	91
SES	92
SES	93
SES	94
SES	95
SES	96
SES	97
SES	98
SES	99
SES	100

-135-

CTA ATG ATA GGG CGA GCG GCC TTA AGA GCC CCA TGG ATA TTT TGG CAA	723
Leu Met Ile Gly Arg Ala Ala Leu Arg Ala Pro Trp Ile Phe Trp Gln	
220 225 230	
ATC AGA AAC AAC ACC ACA AAA TTA CCC GCA GTC GTG AAA AAA GAC CTG	771
Ile Arg Asn Asn Thr Thr Lys Leu Pro Ala Val Val Lys Lys Asp Leu	
235 240 245 250	
GTT TTA GAA CAT TTT GAT AAA ATG GTG GAG TTT TAT GGG GAT ATG GGG	819
Val Leu Glu His Phe Asp Lys Met Val Glu Phe Tyr Gly Asp Met Gly	
255 260 265	
GTA ATC ATG TTT AGG AAA AAT TTG CAT GCT TAC GCT AAG GGC GAA ATG	867
Val Ile Met Phe Arg Lys Asn Leu His Ala Tyr Ala Lys Gly Glu Met	
270 275 280	
CAA GCG AGC GCG TTT CGT AAC TGC GTC AAT ACC CTT ACA GAA ATA AAG	915
Gln Ala Ser Ala Phe Arg Asn Cys Val Asn Thr Leu Thr Glu Ile Lys	
285 290 295	
AGC ATG CGA GAG AGC ATA GAG GAA TTT TTT AAT CAA GAA ATG TTG CAA	963
Ser Met Arg Glu Ser Ile Glu Glu Phe Phe Asn Gln Glu Met Leu Gln	
300 305 310	
AGT GAA GTG CCG TTA TGG GTA GAA TTG AAT CAA AAA AGC GTT TGAAAGCGC	1014
Ser Glu Val Pro Leu Trp Val Glu Leu Asn Gln Lys Ser Val	
315 320 325	
TTGTTTTTTTT AGCCAGCTTG GGGG	1038

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met Asp Phe Lys Asn Lys Lys Trp Leu Phe Leu Ala Pro Leu Ala Gly	
1 5 10 15	
Tyr Thr Asp Leu Pro Phe Arg Ser Val Val Lys Lys Phe Gly Val Asp	
20 25 30	
Val Thr Thr Ser Glu Met Val Ser Ser His Ser Leu Val Tyr Ala Phe	
35 40 45	
Asp Lys Thr Ser Lys Met Leu Glu Lys Ser Pro Leu Glu Asp His Phe	
50 55 60	
Met Ala Gln Ile Ser Gly Ser Lys Glu Ser Val Val Lys Glu Ala Val	
65 70 75 80	
Glu Lys Ile Asn Ala Leu Glu His Val Asn Gly Ile Asp Phe Asn Cys	
85 90 95	
Gly Cys Pro Ala Pro Lys Val Ala Asn His Gly Asn Gly Ser Gly Leu	
100 105 110	
Leu Lys Asp Leu Asn His Leu Val Lys Leu Leu Lys Thr Ile Arg Glu	
115 120 125	

CCA AGC TTG AGC ATG ACA ACG ATT GTT AAT GAG CAT GCC AAA GAA TTG	917
Pro Ser Leu Ser Met Thr Thr Ile Val Asn Glu His Ala Lys Glu Leu	
285 290 295	
AGA AAC CTT TTA AAA GAA AAA TAC CAG GTG CAA TTT GCG GGC GGT CAA	965
Arg Asn Leu Leu Lys Glu Lys Tyr Gln Val Gln Phe Ala Gly Gly Gln	
300 305 310	
GAG CCT TAT AAA GAT GCG CTC ATT CGT ATC AAC CAC ATG GGG ATC ATT	1013
Glu Pro Tyr Lys Asp Ala Leu Ile Arg Ile Asn His Met Gly Ile Ile	
315 320 325 330	
CCT GTT TAT AAA AGC GCT TAC GCT TTA AAC GCC CTA GAG TTA GCC CTA	1061
Pro Val Tyr Lys Ser Ala Tyr Ala Leu Asn Ala Leu Glu Leu Ala Leu	
335 340 345	
AAC GAC TTG GAT TTA AGG GAA TTT GAT GGC GTG GCG AAC GCA ACT TTT	1109
Asn Asp Leu Asp Leu Arg Glu Phe Asp Gly Val Ala Asn Ala Thr Phe	
350 355 360	
TTA AAG CAA TAT TAT GGA ATT TAAGGATCAC AATGCATTAT TCTTATGAAA CCTT	1164
Leu Lys Gln Tyr Tyr Gly Ile	
365	
TTTAAA	1170

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Leu Leu Phe Thr Pro Gly Pro Val Ala Ile Asn Glu Glu Met Arg	
1 5 10 15	
Thr Ser Phe Ser Gln Pro Met Pro His His Arg Thr Lys Asp Phe Glu	
20 25 30	
Lys Ile Phe Gln Ser Val Arg Glu Asn Leu Lys Lys Met Thr Gly Leu	
35 40 45	
Glu Glu Val Leu Leu Leu Ser Ser Ser Gly Thr Gly Ala Met Glu Ala	
50 55 60	
Ser Val Ile Ser Leu Cys Gln Lys Glu Leu Leu Phe Val Asn Ala Gly	
65 70 75 80	
Lys Phe Gly Glu Arg Phe Gly Lys Ile Ala Lys Ala His Ser Ile Lys	
85 90 95	
Ala His Glu Leu Val Tyr Glu Trp Asp Thr Pro Ala Gln Val Asp Glu	
100 105 110	
Ile Leu Ser Val Leu Lys Ala Asn Pro Asn Ile Asp Ala Phe Cys Ile	
115 120 125	
Gln Ala Cys Glu Ser Ser Gly Gly Leu Arg His Pro Val Glu Lys Ile	
130 135 140	
Ala Gln Ala Ile Lys Glu Thr Asn Pro Asn Val Phe Val Ile Val Asp	
145 150 155 160	

GAT AAA GAA GTT AAA GGG GGC TTA GGG GTT GTG GCT GAT GAC GCT TTA 201
 Asp Lys Glu Val Lys Gly Gly Leu Gly Val Val Ala Asp Asp Ala Leu
 40 45 50

GCG GGT GTT TTA GCC GGA TTG AGC GCG TTA TTA GTC ATC CAT ATT TTA 249
 Ala Gly Val Leu Ala Gly Leu Ser Ala Leu Leu Val Ile His Ile Leu
 55 60 65

GGA TTT TTT AAC ATT AAA CTT TAATTTTAAG AAAAT 285
 Gly Phe Phe Asn Ile Lys Leu
 70 75

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Trp Leu Ala Met Ala Ile Ser Gly Leu Ser Leu Ala Gly Val Ile
 1 5 10 15
 Leu Ser Phe Ile Phe Phe Arg Ile Tyr Asp Ile Thr Lys Pro Ser Leu
 20 25 30
 Ile Gly Lys Ile Asp Lys Glu Val Lys Gly Gly Leu Gly Val Val Ala
 35 40 45
 Asp Asp Ala Leu Ala Gly Val Leu Ala Gly Leu Ser Ala Leu Leu Val
 50 55 60
 Ile His Ile Leu Gly Phe Phe Asn Ile Lys Leu
 65 70 75

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...957
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

AAAGATAGGA TTAAATATTT TATTTTTTTTA GATGAAAACC ATCATTTTTA TTTGATTGAA 60
 GAATCCAAC ATG CAT TCA AAA TAC TTC GCT CAA ATC AAA GAA AAA AAA TTA 111
 Met His Ser Lys Tyr Phe Ala Gln Ile Lys Glu Lys Lys Leu
 1 5 10

CCT Pro 15	CCC Pro	CTA Leu	ATC Ile	CTC Leu	ACA Thr 20	CAC His	AAT Asn	GGC Gly	TTG Leu	CTT Leu 25	AAA Lys	AAC Asn	TCA Ser	TTT Phe 30	TTA Leu	159
GGT Gly	GCT Ala	AAG Lys	ATT Ile 35	ATA Ile	GAA Glu	TTG Leu	CCT Pro	TTA Leu	GTG Val 40	ATC Ile	AAT Asn	CTC Leu	GTG Val	CAT His 45	GGG Gly	207
GGC Gly	GAT Asp	GGC Gly	GAA Glu 50	GAT Asp	GGG Gly	AAA Lys	TTA Leu	GCG Ala 55	AGC Ser	TTG Leu	TTA Leu	GAA Glu 60	TTT Phe	TAT Tyr	CGT Arg	255
ATC Ile	GCT Ala	TTT Phe 65	ATA Ile	GGC Gly	CCT Pro	AGG Arg 70	ATT Ile	GAA Glu	GCG Ala	AGC Ser	GTG Val 75	CTG Leu	AGT Ser	TAT Tyr	AAC Asn	303
AAA Lys 80	TAT Tyr	TTA Leu	ACC Thr	AAG Lys	CTT Leu	TAC Tyr 85	GCC Ala	AAA Lys	GAC Asp	TTA Leu	GGG Gly 90	GTA Val	AAG Lys	ACT Thr	TTA Leu	351
GAT Asp 95	CAT His	GTT Val	CTT Leu	TTG Leu	AAT Asn 100	GAA Glu	AAA Lys	AAC Asn	CGC Arg	GCT Ala 105	AAC Asn	GCC Ala	TTG Leu	GAT Asp	TTG Leu 110	399
ATG Met	AAC Asn	TTT Phe	AAT Asn	TTC Phe 115	CCT Pro	TTC Phe	ATA Ile	ATC Ile	AAG Lys 120	CCT Pro	AAT Asn	AAC Asn	GCC Ala	GGA Gly 125	AGC Ser	447
TCT Ser	TTA Leu	GGG Gly	GTG Val 130	AAT Asn	GTT Val	GTG Val	AAA Lys	GAA Glu 135	GAA Glu	AAA Lys	GAA Glu	TTG Leu	GTT Val 140	TAC Tyr	GCT Ala	495
TTA Leu	GAC Asp	GGT Gly 145	GCG Ala	TTT Phe	GAA Glu	TAT Tyr	TCT Ser 150	AAA Lys	GAG Glu	GTC Val	TTG Leu	ATA Ile 155	GAG Glu	CCT Pro	TTC Phe	543
ATT Ile 160	CAG Gln	GGA Gly	GTG Val	AAA Lys	GAA Glu	TAC Tyr 165	AAT Asn	TTG Leu	GCC Ala	GGT Gly 170	TGC Cys	AAG Lys	ATC Ile	AAA Lys	AAG Lys	591
GAT Asp 175	TTT Phe	TGT Cys	TTT Phe	TCC Ser	TAT Tyr 180	GTG Val	GAA Glu	GAG Glu	CCT Pro	AAC Asn 185	AAA Lys	CAG Gln	GAA Glu	TTT Phe	TTA Leu 190	639
GAT Asp	TTC Phe	AAA Lys	CAA Gln	AAA Lys 195	TAT Tyr	TTG Leu	GAT Asp	TTT Phe	TCA Ser 200	CGC Arg	AAT Asn	AAA Lys	GCC Ala	CCT Pro 205	AAA Lys	687
GCG Ala	AAT Asn	CTT Leu	TCT Ser 210	AAC Asn	GCC Ala	CTA Leu	GAA Glu	GAG Glu 215	CAA Gln	TTA Leu	AAA Lys	GAA Glu 220	AAT Asn	TTT Phe	AAA Lys	735
AAA Lys	CTC Leu	TAT Tyr 225	AAC Asn	GAT Asp	TTG Leu	TTT Phe	GAT Asp 230	GGC Gly	GCG Ala	ATC Ile	ATT Ile 235	CGT Arg	TGC Cys	GAT Asp	TTT Phe	783
TTT Phe	GTC Val	ATA Ile	AAA Lys	AAT Asn	GAA Glu	GTG Val	TAT Tyr	CTT Leu	AAT Asn	GAG Glu	ATC Ile	AAC Asn	CCC Pro	ATT Ile	CCT Pro	831

240		245		250	
GGC AGT TTG GCC AAT TAT TTG TTT GAT GAT TTT AAA ACA ACG CTA GAA	879				
Gly Ser Leu Ala Asn Tyr Leu Phe Asp Asp Phe Lys Thr Thr Leu Glu					
255		260		265	270
AAT TTA GCG CAA TCA TTA CCC AAA ACC CCT AAG ATC CAA ATC AAA AAC	927				
Asn Leu Ala Gln Ser Leu Pro Lys Thr Pro Lys Ile Gln Ile Lys Asn					
		275		280	285
TCT TAT TTG TTG CAA ATC CAA AAG AAT AAG TAATGGCCAA ACGCAGTATC GCT	980				
Ser Tyr Leu Leu Gln Ile Gln Lys Asn Lys					
		290		295	
TATTTGGATA GCGTTTTTGA CATTTCCTAC ACTTTTATAG A	1021				

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Met	His	Ser	Lys	Tyr	Phe	Ala	Gln	Ile	Lys	Glu	Lys	Lys	Leu	Pro	Pro
1				5					10					15	
Leu	Ile	Leu	Thr	His	Asn	Gly	Leu	Leu	Lys	Asn	Ser	Phe	Leu	Gly	Ala
			20					25					30		
Lys	Ile	Ile	Glu	Leu	Pro	Leu	Val	Ile	Asn	Leu	Val	His	Gly	Gly	Asp
			35				40					45			
Gly	Glu	Asp	Gly	Lys	Leu	Ala	Ser	Leu	Leu	Glu	Phe	Tyr	Arg	Ile	Ala
			50			55					60				
Phe	Ile	Gly	Pro	Arg	Ile	Glu	Ala	Ser	Val	Leu	Ser	Tyr	Asn	Lys	Tyr
65					70					75					80
Leu	Thr	Lys	Leu	Tyr	Ala	Lys	Asp	Leu	Gly	Val	Lys	Thr	Leu	Asp	His
				85					90					95	
Val	Leu	Leu	Asn	Glu	Lys	Asn	Arg	Ala	Asn	Ala	Leu	Asp	Leu	Met	Asn
			100					105					110		
Phe	Asn	Phe	Pro	Phe	Ile	Ile	Lys	Pro	Asn	Asn	Ala	Gly	Ser	Ser	Leu
			115				120					125			
Gly	Val	Asn	Val	Val	Lys	Glu	Glu	Lys	Glu	Leu	Val	Tyr	Ala	Leu	Asp
			130			135					140				
Gly	Ala	Phe	Glu	Tyr	Ser	Lys	Glu	Val	Leu	Ile	Glu	Pro	Phe	Ile	Gln
145					150					155					160
Gly	Val	Lys	Glu	Tyr	Asn	Leu	Ala	Gly	Cys	Lys	Ile	Lys	Lys	Asp	Phe
				165					170					175	
Cys	Phe	Ser	Tyr	Val	Glu	Glu	Pro	Asn	Lys	Gln	Glu	Phe	Leu	Asp	Phe
			180					185					190		
Lys	Gln	Lys	Tyr	Leu	Asp	Phe	Ser	Arg	Asn	Lys	Ala	Pro	Lys	Ala	Asn
			195				200					205			
Leu	Ser	Asn	Ala	Leu	Glu	Glu	Gln	Leu	Lys	Glu	Asn	Phe	Lys	Lys	Leu
			210			215					220				
Tyr	Asn	Asp	Leu	Phe	Asp	Gly	Ala	Ile	Ile	Arg	Cys	Asp	Phe	Phe	Val
225					230					235					240

Ile	Lys	Asn	Glu	Val	Tyr	Leu	Asn	Glu	Ile	Asn	Pro	Ile	Pro	Gly	Ser	
				245					250						255	
Leu	Ala	Asn	Tyr	Leu	Phe	Asp	Asp	Phe	Lys	Thr	Thr	Leu	Glu	Asn	Leu	
			260					265						270		
Ala	Gln	Ser	Leu	Pro	Lys	Thr	Pro	Lys	Ile	Gln	Ile	Lys	Asn	Ser	Tyr	
		275					280						285			
Leu	Leu	Gln	Ile	Gln	Lys	Asn	Lys									
	290					295										

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 47...628
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CAAAGCCTAT GCGAGAGTCA ATTCCGTTGC ATTTTCATTT AGAGGC ATG GAA GTC	55
Met Glu Val	
1	
CCC ATT GAA GGT TTA GAA GAA TTG GTA GAT GAA ACG AAA AAA TGC TTG	103
Pro Ile Glu Gly Leu Glu Glu Leu Val Asp Glu Thr Lys Lys Cys Leu	
5 10 15	
ATA GAA GCT AAG AAA AAC AAA CAA AAC CAT TTC TTG CTG ATT CAA AAA	151
Ile Glu Ala Lys Lys Asn Lys Gln Asn His Phe Leu Leu Ile Gln Lys	
20 25 30 35	
GCT AAC ATC CAA GCA AGA AAA CAA GCC ATG ATA GAT GAA AGT AAA ACC	199
Ala Asn Ile Gln Ala Arg Lys Gln Ala Met Ile Asp Glu Ser Lys Thr	
40 45 50	
ATT ATC CAT GTT GCA TCA GGA GCG GCT GGA GCG GCC GGG CTT ATC CCC	247
Ile Ile His Val Ala Ser Gly Ala Ala Gly Ala Ala Gly Leu Ile Pro	
55 60 65	
ATA CCC TTT AGC GAT GCA CTC GCT ATC GCG CCC ATT CAA GCA GGA ATG	295
Ile Pro Phe Ser Asp Ala Leu Ala Ile Ala Pro Ile Gln Ala Gly Met	
70 75 80	
ATC TAC AAA ATG AAT GAC GCT TTT GGA ATG GAT TTG GAT AAA TCT GTA	343
Ile Tyr Lys Met Asn Asp Ala Phe Gly Met Asp Leu Asp Lys Ser Val	
85 90 95	
GCC GCA TCA TTA ATC ACC GGA TTG TTA GGC GTA ACC GCT GTC GCG CAA	391
Ala Ala Ser Leu Ile Thr Gly Leu Leu Gly Val Thr Ala Val Ala Gln	
100 105 110 115	

GTG GGG AGA ACG CTT GTT AAT GGT TTC CTT AAA TTC ATT CCT GTT GTG	439
Val Gly Arg Thr Leu Val Asn Gly Phe Leu Lys Phe Ile Pro Val Val	
120 125 130	
GGG AGT GTT GCA GGG GGC ACA ACC GCT GTA ATT ATC ACA GAA GGC ATT	487
Gly Ser Val Ala Gly Gly Thr Thr Ala Val Ile Ile Thr Glu Gly Ile	
135 140 145	
GGG TTT GCG TAT TTG AAA GTG CTA GAA AAG TGC TTT AAT GAT GAG ACG	535
Gly Phe Ala Tyr Leu Lys Val Leu Glu Lys Cys Phe Asn Asp Glu Thr	
150 155 160	
GGC GAA GTC AAT TTG CCT GAT GAA GTT GGC ATG ATA ACT TCT CTC TTT	583
Gly Glu Val Asn Leu Pro Asp Glu Val Gly Met Ile Thr Ser Leu Phe	
165 170 175	
AAG GAG AAT TAT CTC AAC TTG GAT ACA ATC AAG AAA TTA ACA CAA TAAGA	633
Lys Glu Asn Tyr Leu Asn Leu Asp Thr Ile Lys Lys Leu Thr Gln	
180 185 190	
TTAGGGGTTA TGAAAAACGC ATGGCATTAG ACAAAGGAT TTGGATGCAT TTT	686

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met	Glu	Val	Pro	Ile	Glu	Gly	Leu	Glu	Glu	Leu	Val	Asp	Glu	Thr	Lys
1				5				10					15		
Lys	Cys	Leu	Ile	Glu	Ala	Lys	Lys	Asn	Lys	Gln	Asn	His	Phe	Leu	Leu
			20					25					30		
Ile	Gln	Lys	Ala	Asn	Ile	Gln	Ala	Arg	Lys	Gln	Ala	Met	Ile	Asp	Glu
		35				40						45			
Ser	Lys	Thr	Ile	Ile	His	Val	Ala	Ser	Gly	Ala	Ala	Gly	Ala	Ala	Gly
	50					55					60				
Leu	Ile	Pro	Ile	Pro	Phe	Ser	Asp	Ala	Leu	Ala	Ile	Ala	Pro	Ile	Gln
65					70				75						80
Ala	Gly	Met	Ile	Tyr	Lys	Met	Asn	Asp	Ala	Phe	Gly	Met	Asp	Leu	Asp
				85				90					95		
Lys	Ser	Val	Ala	Ala	Ser	Leu	Ile	Thr	Gly	Leu	Leu	Gly	Val	Thr	Ala
			100					105					110		
Val	Ala	Gln	Val	Gly	Arg	Thr	Leu	Val	Asn	Gly	Phe	Leu	Lys	Phe	Ile
		115					120					125			
Pro	Val	Val	Gly	Ser	Val	Ala	Gly	Gly	Thr	Thr	Ala	Val	Ile	Ile	Thr
		130				135					140				
Glu	Gly	Ile	Gly	Phe	Ala	Tyr	Leu	Lys	Val	Leu	Glu	Lys	Cys	Phe	Asn
145					150				155						160
Asp	Glu	Thr	Gly	Glu	Val	Asn	Leu	Pro	Asp	Glu	Val	Gly	Met	Ile	Thr
				165				170					175		
Ser	Leu	Phe	Lys	Glu	Asn	Tyr	Leu	Asn	Leu	Asp	Thr	Ile	Lys	Lys	Leu
			180					185					190		

Thr Gln

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 6...821
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AGAAG ATG GGG AAG TTT ATG AAT ACT CTT AAA AAG CAT TTA GCC TTT ATC	50
Met Gly Lys Phe Met Asn Thr Leu Lys Lys His Leu Ala Phe Ile	
1 5 10 15	
ATT CCC CTA GTA GCG TTA TTG TTT AGC TTG GAG TGC GTG TTA TTT ATC	98
Ile Pro Leu Val Ala Leu Leu Phe Ser Leu Glu Cys Val Leu Phe Ile	
20 25 30	
AAT CAA GCG ATC GAA CAG AAA GAA AAA AAA TTG ATT GAA GAT TAT TCG	146
Asn Gln Ala Ile Glu Gln Lys Glu Lys Lys Leu Ile Glu Asp Tyr Ser	
35 40 45	
GTC GTG TTG GCC AGC ACG CAA AAA TTA AAC TTG GAA TTG TTG CGT CAA	194
Val Val Leu Ala Ser Thr Gln Lys Leu Asn Leu Glu Leu Leu Arg Gln	
50 55 60	
AAT TTT AGC GAA ATC ATA GCG TTA AAA GAA ATT GAT CCT AAT TAT TCT	242
Asn Phe Ser Glu Ile Ile Ala Leu Lys Glu Ile Asp Pro Asn Tyr Ser	
65 70 75	
TTA GAA CCT CTT CAA AAA ACC TTA GGC ATA GAT GGG CTT AAG GAA TTA	290
Leu Glu Pro Leu Gln Lys Thr Leu Gly Ile Asp Gly Leu Lys Glu Leu	
80 85 90 95	
AGA AAA AAT TTG CCC TTT TTT TAT TCT TTA CAA CTT TCC ACA TTC CCC	338
Arg Lys Asn Leu Pro Phe Phe Tyr Ser Leu Gln Leu Ser Thr Phe Pro	
100 105 110	
ACT CAA GAG CGT TTA GAA AAC ATT AAA GAA AAA TTG CTC AAA ATC CCT	386
Thr Gln Glu Arg Leu Glu Asn Ile Lys Glu Lys Leu Leu Lys Ile Pro	
115 120 125	
GGC GTT CAA AAA GTT GAA GTC TTT GCC AAA ACT TAC ATG CAA GTG TAT	434
Gly Val Gln Lys Val Glu Val Phe Ala Lys Thr Tyr Met Gln Val Tyr	
130 135 140	
GAT CTC TTG AGT TTT ATT AAA ACA GCG GTC TAT ATC TTT GCG TTA GTG	482

[illegible]

50	55	60	
CAA AAC CGC CAG ATT GGC TCA GAA AGG ATA GGA GAA TCT AAA GTG TTG			240
Gln Asn Arg Gln Ile Gly Ser Glu Arg Ile Gly Glu Ser Lys Val Leu			
65	70	75	80
GTG TTG CAA GAT CTC TAT AAG GGC ATT CAA GCT TTG AAC TTG CAT ATA			288
Val Leu Gln Asp Leu Tyr Lys Gly Ile Gln Ala Leu Asn Leu His Ile			
	85	90	95
GAT GAA GCG TTT TTA AAT TCA TTT AAT TTT AGA GAT TAT GAT TAC ATT			336
Asp Glu Ala Phe Leu Asn Ser Phe Asn Phe Arg Asp Tyr Asp Tyr Ile			
	100	105	110
TTA GAT TGC ATG GAC GAT TTG CCT ATT AAA ACA AGC TTA GCG ATA AAA			384
Leu Asp Cys Met Asp Asp Leu Pro Ile Lys Thr Ser Leu Ala Ile Lys			
	115	120	125
TGC CAG AAT TTC GCT TAC GGA AAA TTT ATC AGC TCT ATG GGG AGT GCG			432
Cys Gln Asn Phe Ala Tyr Gly Lys Phe Ile Ser Ser Met Gly Ser Ala			
	130	135	140
AAA CGC TTG AAC CCT AAA CAC ATC CAA GTG GGG AGC GTG TGG GAA AGC			480
Lys Arg Leu Asn Pro Lys His Ile Gln Val Gly Ser Val Trp Glu Ser			
	145	150	155
TAT GGC GAT AAA TTC GGG CGT AAA TTT AGG GAT TTT TTA AAA AAA CGC			528
Tyr Gly Asp Lys Phe Gly Arg Lys Phe Arg Asp Phe Leu Lys Lys Arg			
	165	170	175
CGT TTT AAA GGG GAT TTT AAA GTG GTT TTT AGC CCT GAA ATT CCG CAT			576
Arg Phe Lys Gly Asp Phe Lys Val Val Phe Ser Pro Glu Ile Pro His			
	180	185	190
TGC ATA GAG CTT GGG AGT TTT AAT GCG GTT ACG GCG AGT TTT GGT TTG			624
Cys Ile Glu Leu Gly Ser Phe Asn Ala Val Thr Ala Ser Phe Gly Leu			
	195	200	205
CAA ATA GCG AGT GAA GTC GTG CAA GAC ATT ATC AAC GAT AAA AGG AAG T			673
Gln Ile Ala Ser Glu Val Val Gln Asp Ile Ile Asn Asp Lys Arg Lys			
	210	215	220
GAGATGAAAG ATTACGAAGA CGAATTGG			701

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Arg	Leu	Ser	Glu	Pro	Ile	Asp	Arg	Phe	Thr	Arg	Ile	Arg	Trp	Leu	Phe
1				5					10					15	

TTG Leu	GGC Gly	GTG Val	CTG Leu	TTT Phe 50	GTT Val	TCT Ser	TAT Tyr	TTT Phe	TTG Leu 55	ATT Ile	GAG Glu	CCT Pro	TTT Phe	TTA Leu 60	AAT Asn	255
TGG Trp	ATG Met	CAA Gln	TTA Leu 65	CAA Gln	GAT Asp	CCT Pro	TCG Ser	CGC Arg 70	CAA Gln	TTG Leu	ACG Thr	CAA Gln 75	GAT Asp	TAT Tyr	TTA Leu	303
GAA Glu	GTC Val	TTA Leu 80	GTT Val	GTA Val	GCG Ala	CTA Leu	CCG Pro 85	AGT Ser	ATT Ile	TTT Phe	TTA Leu	AAA Lys 90	AAT Asn	ATT Ile	TTA Leu	351
GTT Val	TCA Ser 95	GCG Ala	CTC Leu	GCT Ala	AGT Ser	TTT Phe 100	TCA Ser	GAC Asp	ACC Thr	CTA Leu	ACC Thr 105	CCC Pro	TTT Phe	ATT Ile	GTC Val	399
AAA Lys 110	ATC Ile	ATC Ile	ATG Met	GTC Val 115	ATT Ile	GCA Ala	TGC Cys	ATT Ile	TTT Phe 120	TTG Leu	AAT Asn	CAA Gln	GCC Ala	TTG Leu 125	ATT Ile	447
TTT Phe	GGG Gly	GAT Asp	TTT Phe	GGT Gly 130	TTT Phe	AAA Lys	GAA Glu	ATG Met	GGG Gly 135	ATT Ile	GTA Val	GGC Gly	TCT Ser	GCT Ala 140	TTA Leu	495
GCG Ala	AAT Asn	GTG Val	GTT Val 145	GTC Val	TCT Ser	TAT Tyr	TTG Leu	GAA Glu 150	TTA Leu	CTC Leu	GCA Ala	CTT Leu	GGC Gly 155	GTT Val	TGG Trp	543
ATA Ile	CAA Gln 160	ATC Ile	AAA Lys	AAA Lys	ATC Ile	CCT Pro	TTA Leu 165	AAA Lys	TTC Phe	AAA Lys	ATA Ile	ACC Thr 170	TTT Phe	CAT His	TTT Phe	591
TCT Ser	TTT Phe 175	TTA Leu	AAA Lys	ACC Thr	ATG Met	TTT Phe 180	AGA Arg	GTG Val	GGT Gly	TGG Trp	CCA Pro 185	GCC Ala	GGG Gly	TTT Phe	GAG Glu	639
CGC Arg 190	TTA Leu	TTG Leu	AGT Ser	TTA Leu	TTT Phe 195	TCT Ser	TTA Leu	ATC Ile	CTC Leu	TTA Leu 200	TCC Ser	AAA Lys	TTT Phe	GTA Val	GCG Ala 205	687
AGC Ser	TAT Tyr	GGG Gly	GAT Asp	AAA Lys 210	GTG Val	TTA Leu	GCG Ala	GGC Gly	ATG Met 215	CAA Gln	ATA Ile	GGC Gly	ATT Ile	AGG Arg 220	GTT Val	735
GAA Glu	ACC Thr	TTT Phe	TCG Ser 225	TTC Phe	ATG Met	CCC Pro	GGA Gly	TTT Phe 230	GGG Gly	TTT Phe	ATG Met	ATC Ile 235	GCA Ala	GCG Ala	ATG Met	783
GTT Val	TTA Leu	ACA Thr 240	GGG Gly	CAA Gln	AAT Asn	TTA Leu	GGG Gly 245	GCA Ala	AAC Asn	AAG Lys	CCA Pro	AAG Lys 250	ATC Ile	GCC Ala	ACA Thr	831
GAA Glu	TAC Tyr 255	GCG Ala	CAT His	TTG Leu	ATT Ile	TTA Leu 260	AAA Lys	ATC Ile	TCT Ser	ATG Met	GGT Gly 265	TTA Leu	ATG Met	GGG Gly	GTT Val	879
TTA Leu	GGG Gly	ATT Ile	GTT Val	TTA Leu	GTC Val	TTA Leu	TTC Phe	GCT Ala	AAA Lys	GAA Glu	TTT Phe	GCG Ala	AGC Ser	CTT Leu	TTT Phe	927

270		275		280		285	
TCT CAA GAT GAA GAA GTC TTG GAA GTG GCG CGA TCT TAT TTG ATC GCT							975
Ser Gln Asp Glu Glu Val Leu Glu Val Ala Arg Ser Tyr Leu Ile Ala							
	290			295		300	
GTG GGC CTC TCT CAA GCC CCC TTA ATT GGG TAT TTT GTG CTA GAT GGA							1023
Val Gly Leu Ser Gln Ala Pro Leu Ile Gly Tyr Phe Val Leu Asp Gly							
	305			310		315	
GTT TTT AGA GGG GCT GGC ATT TCT AAA GTC TCA CTG TAT ATT AAC ACC							1071
Val Phe Arg Gly Ala Gly Ile Ser Lys Val Ser Leu Tyr Ile Asn Thr							
	320			325		330	
CTA AGC TTA TGG GGG TTA AGG ATC ATG CCC ATT TAC TTG CTT TTA ATT							1119
Leu Ser Leu Trp Gly Leu Arg Ile Met Pro Ile Tyr Leu Leu Leu Ile							
	335			340		345	
CAT CAT TTT AAG GTG GAA TTT ATT TTT GTA GTG ATC GCA TCA GAA ACT							1167
His His Phe Lys Val Glu Phe Ile Phe Val Val Ile Ala Ser Glu Thr							
	350			355		360	365
TTT TTG CGC TCA TTC ATC TAT TAT AAA GTT TTT TCT AAA GGC ATT TGG							1215
Phe Leu Arg Ser Phe Ile Tyr Tyr Lys Val Phe Ser Lys Gly Ile Trp							
	370			375		380	
AAA AGG TGC GGG AAA AAG GCT TGATTATTGC TTGAGCGTAG CGGT							1260
Lys Arg Cys Gly Lys Lys Ala							
	385						

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met	Leu	Phe	Tyr	Gly	Ile	Asn	Thr	Ile	Leu	Tyr	Thr	Gly	Thr	Asn	Ala
1				5				10						15	
Ile	Leu	Ser	Arg	Leu	Val	Gly	Ala	Arg	Asp	Phe	Thr	Gln	Ile	Asn	His
		20						25					30		
Ala	Phe	Ser	Ser	Ile	Phe	Ile	Gly	Ala	Phe	Met	Ile	Cys	Leu	Gly	Val
		35					40					45			
Leu	Phe	Val	Ser	Tyr	Phe	Leu	Ile	Glu	Pro	Phe	Leu	Asn	Trp	Met	Gln
		50				55					60				
Leu	Gln	Asp	Pro	Ser	Arg	Gln	Leu	Thr	Gln	Asp	Tyr	Leu	Glu	Val	Leu
65					70					75				80	
Val	Val	Ala	Leu	Pro	Ser	Ile	Phe	Leu	Lys	Asn	Ile	Leu	Val	Ser	Ala
			85					90						95	
Leu	Ala	Ser	Phe	Ser	Asp	Thr	Leu	Thr	Pro	Phe	Ile	Val	Lys	Ile	Ile
		100					105					110			
Met	Val	Ile	Ala	Cys	Ile	Phe	Leu	Asn	Gln	Ala	Leu	Ile	Phe	Gly	Asp

GTG	GCC	TTA	GTG	GCC	GCA	GNA	TAC	GGA	GTT	AAA	AAA	AAA	GTT	GAT	GCA	99
Val	Ala	Leu	Val	Ala	Ala	Xaa	Tyr	Gly	Val	Lys	Lys	Lys	Val	Asp	Ala	
			15													
GAC	ATT	CTC	AGT	GAA	GAG	ACC	AAT	GAA	TAT	ATT	AAG	TAT	ATC	AAT	GAA	147
Asp	Ile	Leu	Ser	Glu	Glu	Thr	Asn	Glu	Tyr	Ile	Lys	Tyr	Ile	Asn	Glu	
			30													
GGC	AAT	GAC	TTG	CTA	GAG	GAA	GCA	GAA	GAA	GTT	ATT	AAA	GCT	GTG	GCT	195
Gly	Asn	Asp	Leu	Leu	Glu	Glu	Ala	Glu	Glu	Val	Ile	Lys	Ala	Val	Ala	
			45													
TCT	GAT	TGT	GAG	TTT	GCT	CTT	GCG	AGA	TTT	GAA	GAG	AAA	AGG	TGC	TAT	243
Ser	Asp	Cys	Glu	Phe	Ala	Leu	Ala	Arg	Phe	Glu	Glu	Lys	Arg	Cys	Tyr	
			60													
ATT	AGA	AAT	CAT	GTA	ATT	TCA	GAA	TTT	TTG	CAC	CAT	TTT	AAT	CAA	TTA	291
Ile	Arg	Asn	His	Val	Ile	Ser	Glu	Phe	Leu	His	His	Phe	Asn	Gln	Leu	
			75													
GAA	GGA	TTC	GAG	CTT	ACC	AAC	AAA	AAA	GAT	AGC	ATG	GAA	AAT	ATC	CAA	339
Glu	Gly	Phe	Glu	Leu	Thr	Asn	Lys	Lys	Asp	Ser	Met	Glu	Asn	Ile	Gln	
			95													
CTC	GAT	GTA	TCA	AAT	ACA	CTA	AAA	ATT	ATT	GAT	AAA	AAT	CTC	AAG	ATG	387
Leu	Asp	Val	Ser	Asn	Thr	Leu	Lys	Ile	Ile	Asp	Lys	Asn	Leu	Lys	Met	
			110													
AGC	TCT	TTT	GAC	ACC	CTT	GGT	GCC	GTT	GGA	AAT	GTT	GTG	GGA	GGT	TTT	435
Ser	Ser	Phe	Asp	Thr	Leu	Gly	Ala	Val	Gly	Asn	Val	Val	Gly	Gly	Phe	
			125													
TCT	ATG	GGA	TTT	GGT	TTG	GCT	GCT	GGA	GGT	ATA	GTT	GGA	AGT	GTA	GGG	483
Ser	Met	Gly	Phe	Gly	Leu	Ala	Ala	Gly	Gly	Ile	Val	Gly	Ser	Val	Gly	
			140													
CTT	TTA	GCC	GGA	CCC	ACA	CTC	GCT	ATT	TTT	GGA	GCT	TTG	AGA	GCT	GCT	531
Leu	Leu	Ala	Gly	Pro	Thr	Leu	Ala	Ile	Phe	Gly	Ala	Leu	Arg	Ala	Ala	
			155													
GAA	ATG	GAA	AAA	AAA	TTA	GAA	GAT	GCT	AAG	GCT	TAT	TGC	TCT	CAA	GTT	579
Glu	Met	Glu	Lys	Lys	Leu	Glu	Asp	Ala	Lys	Ala	Tyr	Cys	Ser	Gln	Val	
			175													
GAA	GCA	GCC	GTC	AAA	AAA	GCC	GAT	GCG	ATG	ATT	GAT	AAT	CTT	CAA	GCC	627
Glu	Ala	Ala	Val	Lys	Lys	Ala	Asp	Ala	Met	Ile	Asp	Asn	Leu	Gln	Ala	
			190													
GTT	AGG	AAA	ATG	GCA	GAT	CTT	TTC	ACT	AGG	CAG	ATC	ACA	AAA	TTT	GAC	675
Val	Arg	Lys	Met	Ala	Asp	Leu	Phe	Thr	Arg	Gln	Ile	Thr	Lys	Phe	Asp	
			205													
GCA	CTG	TTT	TTC	TCG	CTT	GCT	CAA	GAG	GCA	ATC	GCC	ACG	ATG	AAA	AAG	723
Ala	Leu	Phe	Phe	Ser	Leu	Ala	Gln	Glu	Ala	Ile	Ala	Thr	Met	Lys	Lys	
			220													
CAC	AAC	TAC	GAT	TTT	TCG	CAT	TAC	AAT	CAA	AAA	GAA	CAA	GAT	CAG	CTA	771
His	Asn	Tyr	Asp	Phe	Ser	His	Tyr	Asn	Gln	Lys	Glu	Gln	Asp	Gln	Leu	

235	240	245	250	
GCT ACT GCT TCT TCA ACC CTT AAA ACT TTG GGT GCT TTT TTG AAA GTG				819
Ala Thr Ala Ser Ser Thr Leu Lys Thr Leu Gly Ala Phe Leu Lys Val	255	260	265	
CCT ATC ATG GAC AAA CAC CAA AAG CTC AAT GAA GCT ACA CAA AGT AAG				867
Pro Ile Met Asp Lys His Gln Lys Leu Asn Glu Ala Thr Gln Ser Lys	270	275	280	
CTA GAG TTT ATG CAA AGG GAG ATG AGT AGC CTA GAA GCT AAG CAT TAT				915
Leu Glu Phe Met Gln Arg Glu Met Ser Ser Leu Glu Ala Lys His Tyr	285	290	295	
GAT TCA GTT AAA ATC AAA TTT GGA TTG GTA CGC AGA TTA TTT GAA TTT				963
Asp Ser Val Lys Ile Lys Phe Gly Leu Val Arg Arg Leu Phe Glu Phe	300	305	310	
TTT AGA TCG CTT TGG GGA AAA AAT GGA AGA ATC CAA AGA GCG AAA ACA				1011
Phe Arg Ser Leu Trp Gly Lys Asn Gly Arg Ile Gln Arg Ala Lys Thr	315	320	325	330
ACT CCT GAT CGC TTC CCT TGC ACC TCT TGC GGG CTT TGC TGC AAG AAT				1059
Thr Pro Asp Arg Phe Pro Cys Thr Ser Cys Gly Leu Cys Cys Lys Asn	335	340	345	
ATC GCC GGG ATT ATT GAG CTT ATT GGG TTT GAT GCT GGC AAT GGG GTG				1107
Ile Ala Gly Ile Ile Glu Leu Ile Gly Phe Asp Ala Gly Asn Gly Val	350	355	360	
TGC AAA TTT TTG GAT TTA GAA ACC AAT CTG TGC AAG ATT TAT GAA TCG				1155
Cys Lys Phe Leu Asp Leu Glu Thr Asn Leu Cys Lys Ile Tyr Glu Ser	365	370	375	
CGC CCG TTA ATT TGC AGG ATT GAT GAA GCG CAC AAA AAG CTT TAT CCC				1203
Arg Pro Leu Ile Cys Arg Ile Asp Glu Ala His Lys Lys Leu Tyr Pro	380	385	390	
CAC ATC CCG CTT AAG GAG TTT TAT GCC AAA AAC GCA GAG GTT TGT AAC				1251
His Ile Pro Leu Lys Glu Phe Tyr Ala Lys Asn Ala Glu Val Cys Asn	395	400	405	410
GCT TTG CAA GAA GCA AAC CAT ATG GAT AAG AGC TTT AGG GTT ATT CTT				1299
Ala Leu Gln Glu Ala Asn His Met Asp Lys Ser Phe Arg Val Ile Leu	415	420	425	
AAG AAA TAATTTAGAA TTTATTGTCC CA				1327
Lys Lys				

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 428 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Pro Leu Pro Phe Ile Ile Ala Ala Gly Val Ala Leu Val Ala Ala
1 5 10 15
Xaa Tyr Gly Val Lys Lys Lys Val Asp Ala Asp Ile Leu Ser Glu Glu
20 25 30
Thr Asn Glu Tyr Ile Lys Tyr Ile Asn Glu Gly Asn Asp Leu Leu Glu
35 40 45
Glu Ala Glu Glu Val Ile Lys Ala Val Ala Ser Asp Cys Glu Phe Ala
50 55 60
Leu Ala Arg Phe Glu Glu Lys Arg Cys Tyr Ile Arg Asn His Val Ile
65 70 75 80
Ser Glu Phe Leu His His Phe Asn Gln Leu Glu Gly Phe Glu Leu Thr
85 90 95
Asn Lys Lys Asp Ser Met Glu Asn Ile Gln Leu Asp Val Ser Asn Thr
100 105 110
Leu Lys Ile Ile Asp Lys Asn Leu Lys Met Ser Ser Phe Asp Thr Leu
115 120 125
Gly Ala Val Gly Asn Val Val Gly Gly Phe Ser Met Gly Phe Gly Leu
130 135 140
Ala Ala Gly Gly Ile Val Gly Ser Val Gly Leu Ala Gly Pro Thr
145 150 155 160
Leu Ala Ile Phe Gly Ala Leu Arg Ala Ala Glu Met Glu Lys Lys Leu
165 170 175
Glu Asp Ala Lys Ala Tyr Cys Ser Gln Val Glu Ala Ala Val Lys Lys
180 185 190
Ala Asp Ala Met Ile Asp Asn Leu Gln Ala Val Arg Lys Met Ala Asp
195 200 205
Leu Phe Thr Arg Gln Ile Thr Lys Phe Asp Ala Leu Phe Phe Ser Leu
210 215 220
Ala Gln Glu Ala Ile Ala Thr Met Lys Lys His Asn Tyr Asp Phe Ser
225 230 235 240
His Tyr Asn Gln Lys Glu Gln Asp Gln Leu Ala Thr Ala Ser Ser Thr
245 250 255
Leu Lys Thr Leu Gly Ala Phe Leu Lys Val Pro Ile Met Asp Lys His
260 265 270
Gln Lys Leu Asn Glu Ala Thr Gln Ser Lys Leu Glu Phe Met Gln Arg
275 280 285
Glu Met Ser Ser Leu Glu Ala Lys His Tyr Asp Ser Val Lys Ile Lys
290 295 300
Phe Gly Leu Val Arg Arg Leu Phe Glu Phe Phe Arg Ser Leu Trp Gly
305 310 315 320
Lys Asn Gly Arg Ile Gln Arg Ala Lys Thr Thr Pro Asp Arg Phe Pro
325 330 335
Cys Thr Ser Cys Gly Leu Cys Cys Lys Asn Ile Ala Gly Ile Ile Glu
340 345 350
Leu Ile Gly Phe Asp Ala Gly Asn Gly Val Cys Lys Phe Leu Asp Leu
355 360 365
Glu Thr Asn Leu Cys Lys Ile Tyr Glu Ser Arg Pro Leu Ile Cys Arg
370 375 380
Ile Asp Glu Ala His Lys Lys Leu Tyr Pro His Ile Pro Leu Lys Glu
385 390 395 400
Phe Tyr Ala Lys Asn Ala Glu Val Cys Asn Ala Leu Gln Glu Ala Asn
405 410 415
His Met Asp Lys Ser Phe Arg Val Ile Leu Lys Lys
420 425

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...851
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TATTAACACC GTTAAAGAGG GGGTAATTC ATG TTA GAA AAC ATG CAA GAT ATT	53
Met Leu Glu Asn Met Gln Asp Ile	
1 5	
TCA TTG CAA AGC TCT CAT GAA GTA GGA GTG GAT ATT ACA GAG AGC AAA	101
Ser Leu Gln Ser Ser His Glu Val Gly Val Asp Ile Thr Glu Ser Lys	
10 15 20	
ATG CTT ACA AAA TTT GCA TCC TCG TTA TTA ATG AAT TTA TAT GAA TAT	149
Met Leu Thr Lys Phe Ala Ser Ser Leu Leu Met Asn Leu Tyr Glu Tyr	
25 30 35 40	
ATT GGA AAT GGC AAG GAT CCC AAA GAA GCG TCC GAT CAT GCC ATG AGG	197
Ile Gly Asn Gly Lys Asp Pro Lys Glu Ala Ser Asp His Ala Met Arg	
45 50 55	
GAT GCA AAG GAT GTG GTG CTT AGT TGT GGT AGA GTA GCC TTT CTT AAA	245
Asp Ala Lys Asp Val Val Leu Ser Cys Gly Arg Val Ala Phe Leu Lys	
60 65 70	
GAC ATA GTT TCA AAT AGT CCA AAC GAA ACA ATC CAA AGT TTT GAT GGA	293
Asp Ile Val Ser Asn Ser Pro Asn Glu Thr Ile Gln Ser Phe Asp Gly	
75 80 85	
GAC TTA GAA GTT GCG ATG CAT TTA GAA AAA ATT GGC ATA GAA TGT TAT	341
Asp Leu Glu Val Ala Met His Leu Glu Lys Ile Gly Ile Glu Cys Tyr	
90 95 100	
AAG ATA TTT ATT GAC TAT GGT TCT CAA AAG ATC GAT GAT AAT GAG CTT	389
Lys Ile Phe Ile Asp Tyr Gly Ser Gln Lys Ile Asp Asp Asn Glu Leu	
105 110 115 120	
TCT TGT CGT TTG TTA CAC ACT GGC ACG AAA ATT TTA GGC ACA AAA GCT	437
Ser Cys Arg Leu Leu His Thr Gly Thr Lys Ile Leu Gly Thr Lys Ala	
125 130 135	
ATG GCA GTT GTT GGT CAA ACA TTC ATC CCC ATT CCT GGA GTT GGA GCG	485
Met Ala Val Val Gly Gln Thr Phe Ile Pro Ile Pro Gly Val Gly Ala	
140 145 150	

ATA ATT GGA AAT TTT GTG GGT GCA TTA CTG AGC AAA ACT CTC TGT GAA	533
Ile Ile Gly Asn Phe Val Gly Ala Leu Leu Ser Lys Thr Leu Cys Glu	
155 160 165	
AAT TTG CGA GAT GTT TTA AAA GAG GCT AAA TTG GCG CGC CAA AGG CGT	581
Asn Leu Arg Asp Val Leu Lys Glu Ala Lys Leu Ala Arg Gln Arg Arg	
170 175 180	
ATA GAG ATT GAA AAA GAA TGC CGT GAA AGT ATT AGG CTG TTA GAG ATC	629
Ile Glu Ile Glu Lys Glu Cys Arg Glu Ser Ile Arg Leu Leu Glu Ile	
185 190 195 200	
TAT CGC AAT CAA TTT AAG GAA GTG TTT GAG CGG TAT TTT CAT GGG AAT	677
Tyr Arg Asn Gln Phe Lys Glu Val Phe Glu Arg Tyr Phe His Gly Asn	
205 210 215	
GTA AAA TTC TTT AAT GAG AAT TTT AAT AAT CTT GAG AGG GCG CTT TAT	725
Val Lys Phe Phe Asn Glu Asn Phe Asn Asn Leu Glu Arg Ala Leu Tyr	
220 225 230	
GCA GGA GAT GCG GAT TTG GCC ATA GGA GTC AAT AAT GAG ATT CAA GAA	773
Ala Gly Asp Ala Asp Leu Ala Ile Gly Val Asn Asn Glu Ile Gln Glu	
235 240 245	
AGA CTA GGT CAA AAA CCC TTG TTT AAT AAT ACC CAA GAA TTT TTG GAA	821
Arg Leu Gly Gln Lys Pro Leu Phe Asn Asn Thr Gln Glu Phe Leu Glu	
250 255 260	
CTC ATG AAT AAT GGT GGA AAA ATA GAA ATT TAAAGGAGAA ATCATGGAAG AAC	874
Leu Met Asn Asn Gly Gly Lys Ile Glu Ile	
265 270	
AAAAGGATAT GGGTCAAAGT	894

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Leu Glu Asn Met Gln Asp Ile Ser Leu Gln Ser Ser His Glu Val	
1 5 10 15	
Gly Val Asp Ile Thr Glu Ser Lys Met Leu Thr Lys Phe Ala Ser Ser	
20 25 30	
Leu Leu Met Asn Leu Tyr Glu Tyr Ile Gly Asn Gly Lys Asp Pro Lys	
35 40 45	
Glu Ala Ser Asp His Ala Met Arg Asp Ala Lys Asp Val Val Leu Ser	
50 55 60	
Cys Gly Arg Val Ala Phe Leu Lys Asp Ile Val Ser Asn Ser Pro Asn	
65 70 75 80	
Glu Thr Ile Gln Ser Phe Asp Gly Asp Leu Glu Val Ala Met His Leu	
85 90 95	

Glu Lys Ile Gly Ile Glu Cys Tyr Lys Ile Phe Ile Asp Tyr Gly Ser
 100 105 110
 Gln Lys Ile Asp Asp Asn Glu Leu Ser Cys Arg Leu Leu His Thr Gly
 115 120 125
 Thr Lys Ile Leu Gly Thr Lys Ala Met Ala Val Val Gly Gln Thr Phe
 130 135 140
 Ile Pro Ile Pro Gly Val Gly Ala Ile Ile Gly Asn Phe Val Gly Ala
 145 150 155 160
 Leu Leu Ser Lys Thr Leu Cys Glu Asn Leu Arg Asp Val Leu Lys Glu
 165 170 175
 Ala Lys Leu Ala Arg Gln Arg Arg Ile Glu Ile Glu Lys Glu Cys Arg
 180 185 190
 Glu Ser Ile Arg Leu Leu Glu Ile Tyr Arg Asn Gln Phe Lys Glu Val
 195 200 205
 Phe Glu Arg Tyr Phe His Gly Asn Val Lys Phe Phe Asn Glu Asn Phe
 210 215 220
 Asn Asn Leu Glu Arg Ala Leu Tyr Ala Gly Asp Ala Asp Leu Ala Ile
 225 230 235 240
 Gly Val Asn Asn Glu Ile Gln Glu Arg Leu Gly Gln Lys Pro Leu Phe
 245 250 255
 Asn Asn Thr Gln Glu Phe Leu Glu Leu Met Asn Asn Gly Gly Lys Ile
 260 265 270
 Glu Ile

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...1281
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTTCATTACG CTTACGCTAC AACCCCTTAAG ATCACCAATG TTGTGCCTTT TGGCTCTAGC	60
AGCGTTAAA ATG GTG TTC AAT CAA GAG GTT AAA AAA TTC AAA GAA GTT TCG	111
Met Val Phe Asn Gln Glu Val Lys Lys Phe Lys Glu Val Ser	
1 5 10	
CTC AAA AAT TTC AAG AGT TAT TTG GAA TTA GAA GCC ATT TTA ACC ATT	159
Leu Lys Asn Phe Lys Ser Tyr Leu Glu Leu Glu Ala Ile Leu Thr Ile	
15 20 25 30	
CCT AAA AAG CAT TAC CAA TTC TCC AAG CAA TCG TTC ATC ACG ATC GCG	207
Pro Lys Lys His Tyr Gln Phe Ser Lys Gln Ser Phe Ile Thr Ile Ala	
35 40 45	
CAA TTC AGC CCT AAG TTA GTG CGA GTG GTT ATC GGC TAT GCT CCT AAG	255
Gln Phe Ser Pro Lys Leu Val Arg Val Val Ile Gly Tyr Ala Pro Lys	

			50				55				60							
ATG Met	ACT Thr	TAT Tyr 65	GAA Glu	GTT Val	AAA Lys	ATC Ile	CTT Leu 70	AAA Lys	GAC Asp	AAG Lys	CTT Leu	TAT Tyr 75	GTT Val	TCT Ser	ATC Ile	303		
GTG Val 80	GAG Glu	AAA Lys	AAG Lys	CCC Pro	TTA Leu	ATT Ile 85	AGG Arg	CAT His	CAA Gln	ATG Met	GCG Ala 90	TTA Leu	AAA Lys	CCA Pro	CCC Pro	351		
AAA Lys 95	CAC His	CAT His	GCA Ala	CTC Leu	AAA Lys 100	CAC His	ACA Thr	ACG Thr	CCA Pro	AAA Lys 105	CCC Pro	GCC Ala	CAT His	AAG Lys	CCC Pro 110	399		
ATT Ile	AAA Lys	AAA Lys	GAG Glu	GCT Ala 115	AAA Lys	AAG Lys	GTT Val	AAA Lys	GAA Glu 120	AAA Lys	ACG Thr	CCA Pro	ACT Thr	AAA Lys 125	CAT His	447		
GCG Ala	CAT His	TCA Ser	AAA Lys 130	CAC His	ACG Thr	CAT His	TCC Ser	CCA Pro 135	TTG Leu	AAC Asn	GAA Glu	AGG Arg	AGC Ser	ACT Thr	AAA Lys	495		
AAA Lys	GAA Glu	ATT Ile 145	CCT Pro	AAA Lys	AAA Lys	GAA Glu	ATT Ile 150	CCT Pro	AAA Lys	AAA Lys	GAA Glu 155	GCG Ala	GAA Glu	AAT Asn	GAG Glu	543		
AGC Ser 160	AAG Lys	AAC Asn	CAA Gln	GTC Val	TTT Phe	ATA Ile 165	GCA Ala	GAA Glu	AAA Lys	AAT Asn	GAT Asp 170	ACT Thr	TTC Phe	ATC Ile	AAA Lys	591		
ACC Thr 175	AAA Lys	CGC Arg	AAA Lys	AAA Lys	CAC His 180	AAA Lys	AAG Lys	ATC Ile	GTT Val	TTA Leu 185	GAC Asp	GCT Ala	GGG Gly	CAT His	GGG Gly 190	639		
GGG Gly	AAA Lys	GAT Asp	TGC Cys 195	GGG Gly	GCG Ala	ATG Met	AGC Ser	GCG Ala	AAT Asn 200	TTG Leu	GTG Val	TGT Cys	GAA Glu	AAA Lys 205	GAC Asp	687		
ATT Ile	GTT Val	TTA Leu 210	GAA Glu	GTG Val	GTG Val	AAG Lys	TTT Phe	TTA Leu 215	CAC His	AAA Lys	GAG Glu	CTT Leu 220	AAA Lys	AAA Lys	AGA Arg	735		
GAT Asp	TAT Tyr 225	AGC Ser	GTT Val	TTA Leu	TTG Leu	ACA Thr	AGG Arg 230	GAT Asp	AAG Lys	GAT Asp	ATT Ile 235	TAT Tyr	ATT Ile	GAT Asp	TTA Leu	783		
GTG Val 240	GCT Ala	CGC Arg	ACG Thr	GAA Glu	TTA Leu	GCC Ala 245	AAT Asn	AAA Lys	AAA Lys	AGC Ser	GCG Ala 250	GAT Asp	TTA Leu	TTC Phe	ATC Ile	831		
TCA Ser 255	GTG Val	CAT His	GCC Ala	AAT Asn	TCC Ser 260	ATC Ile	CCC Pro	AAA Lys	CAT His	TCC Ser 265	ACT Thr	TCT Ser	AAC Asn	GCT Ala	CAT His 270	879		
GGT Gly	ATA Ile	GAG Glu	ACT Thr 275	TAT Tyr	TTT Phe	TTA Leu	TCC Ser	ACC Thr	GCA Ala 280	AGG Arg	AGC Ser	GAA Glu	AGG Arg	GCT Ala 285	AGG Arg	927		

[illegible]

TGAAATTAAA	TATTAACATA	TATTAAGGAA	AGAGCT	ATG Met	GTA Val	TCA Ser	ACA Thr	CTC Leu	AAA Lys		54					
CCG Pro	CTA Leu	AAA Lys	ATC Ile	GGT Gly	AAG Lys	CAC His	ACC Thr	ATA Ile	AAA Lys	TTC Phe	CCT Pro	ATC Ile	TTT Phe	CAA Gln	GGG Gly	102
			10					15					20			
GGA Gly	ATG Met	GGT Gly	GTG Val	GGG Gly	ATT Ile	AGC Ser	TGG Trp	GAT Asp	GAA Glu	CTA Leu	GCT Ala	GGA Gly	AAT Asn	GTT Val	GCC Ala	150
		25					30					35				
AAA Lys	GAA Glu	GGG Gly	GCT Ala	TTA Leu	GGA Gly	GTG Val	ATT Ile	TCA Ser	GCC Ala	GTA Val	GGG Gly	ACT Thr	GGT Gly	TAT Tyr	TAT Tyr	198
	40					45					50					
AAA Lys	AAC Asn	ATG Met	CGT Arg	TTT Phe	GTA Val	GAA Glu	AGG Arg	ATT Ile	GTG Val	GCT Ala	AAA Lys	AAA Lys	CCC Pro	TTT Phe	GAA Glu	246
					60					65					70	
GCC Ala	TTG Leu	AAT Asn	TTT Phe	TAC Tyr	TCC Ser	AAA Lys	AAA Lys	GCG Ala	TTG Leu	AAT Asn	GAG Glu	ATT Ile	TTT Phe	GCA Ala	AAC Asn	294
				75					80					85		
GCT Ala	AGG Arg	AAG Lys	ATT Ile	TGC Cys	GGG Gly	AAC Asn	AAC Asn	CCT Pro	TTA Leu	GGA Gly	GCG Ala	AAT Asn	ATT Ile	TTA Leu	TAC Tyr	342
			90					95					100			
GCT Ala	ATC Ile	AAT Asn	GAC Asp	TAT Tyr	GGC Gly	CGT Arg	GTT Val	TTA Leu	AGG Arg	GAC Asp	TCT Ser	TGT Cys	GAA Glu	GCG Ala	GGA Gly	390
		105					110					115				
GCG Ala	AAT Asn	ATC Ile	ATT Ile	ATT Ile	ACA Thr	GGG Gly	GCT Ala	GGT Gly	TTG Leu	CCC Pro	ACC Thr	AAC Asn	ATG Met	CCT Pro	GAA Glu	438
		120				125					130					
TTC Phe	GCT Ala	AAG Lys	GAT Asp	TTT Phe	AGC Ser	GAT Asp	GTG Val	GCG Ala	CTC Leu	ATC Ile	CCT Pro	ATT Ile	ATT Ile	TCT Ser	TCA Ser	486
	135				140					145					150	
GCG Ala	AAG Lys	GCT Ala	TTA Leu	AAA Lys	ATC Ile	CTT Leu	TGT Cys	AAA Lys	AGA Arg	TGG Trp	AGC Ser	GAT Asp	CGC Arg	TAT Tyr	AAA Lys	534
				155				160						165		
AGA Arg	ATC Ile	CCG Pro	GAC Asp	GCG Ala	TTC Phe	ATT Ile	GTG Val	GAA Glu	GGG Gly	CCT Pro	TTG Leu	AGT Ser	GGG Gly	GGG Gly	CAT His	582
			170					175					180			
CAG Gln	GGC Gly	TTT Phe	AAA Lys	TAC Tyr	GAA Glu	GAT Asp	TGT Cys	TTC Phe	AAA Lys	GAA Glu	GAA Glu	TTC Phe	CGA Arg	TTA Leu	GAA Glu	630
		185					190					195				
AAC Asn	TTA Leu	GTG Val	CCT Pro	AAA Lys	GTC Val	GTG Val	GAA Glu	GCT Ala	TCT Ser	AAA Lys	GAA Glu	TGG Trp	GGG Gly	AAT Asn	ATC Ile	678
	200					205					210					
CCT Pro	ATC Ile	ATC Ile	GCC Ala	GCT Ala	GGG Gly	GGG Gly	ATT Ile	TGG Trp	GAT Asp	AGG Arg	AAG Lys	GAT Asp	ATA Ile	GAC Asp	ACC Thr	726

215	220	225	230	
ATG TTA AGT CTT GGA GCG AGT GGG GTG CAG ATG GCG ACT CGT TTT TTA				774
Met Leu Ser Leu Gly Ala Ser Gly Val Gln Met Ala Thr Arg Phe Leu	235	240	245	
GGC ACG AAA GAA TGC GAC GCT AAA GTG TAT GCC GAT CTT TTG CCC ACG				822
Gly Thr Lys Glu Cys Asp Ala Lys Val Tyr Ala Asp Leu Leu Pro Thr	250	255	260	
CTC AAA AAA GAA GAT ATT TTA CTC ATT AAA TCG CCT GTA GGT TAT CCG				870
Leu Lys Lys Glu Asp Ile Leu Leu Ile Lys Ser Pro Val Gly Tyr Pro	265	270	275	
GCT AGG GCT ATT AAT ACG GGA GTG ATC AAG CGC ATT GAA GAG GGT AAC				918
Ala Arg Ala Ile Asn Thr Gly Val Ile Lys Arg Ile Glu Glu Gly Asn	280	285	290	
GCG CCC AAA ATC GCA TGC GTG AGC AAT TGT GTA GCG CCT TGC AAC AGG				966
Ala Pro Lys Ile Ala Cys Val Ser Asn Cys Val Ala Pro Cys Asn Arg	295	300	305	310
GGT GAA GAG GCT AAA AAG GTG GGC TAT TGT ATC GCT GAT GGT TTG GGG				1014
Gly Glu Glu Ala Lys Lys Val Gly Tyr Cys Ile Ala Asp Gly Leu Gly	315	320	325	
CGC AGT TAT TTA GGG AAC AGA GAA GAG GGG CTT TAT TTT ACC GGG GCT				1062
Arg Ser Tyr Leu Gly Asn Arg Glu Glu Gly Leu Tyr Phe Thr Gly Ala	330	335	340	
AAT GGC TAT AGA GTG GAT AAG ATT ATC AGC GTG CAT GAA TTG ATT AAA				1110
Asn Gly Tyr Arg Val Asp Lys Ile Ile Ser Val His Glu Leu Ile Lys	345	350	355	
GAG CTT ACA GAG GGT TAATTTGTAG TGCTTGTGAG GTTAGGGGTT GTTGCA				1161
Glu Leu Thr Glu Gly	360			

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Val Ser Thr Leu Lys Pro Leu Lys Ile Gly Lys His Thr Ile Lys	
1 5 10 15	
Phe Pro Ile Phe Gln Gly Gly Met Gly Val Gly Ile Ser Trp Asp Glu	
20 25 30	
Leu Ala Gly Asn Val Ala Lys Glu Gly Ala Leu Gly Val Ile Ser Ala	
35 40 45	
Val Gly Thr Gly Tyr Tyr Lys Asn Met Arg Phe Val Glu Arg Ile Val	

TAGACAGGAT AG ATG AAC GAA ATT GAT AAA TCC GTT GAT ATC GGA TTC TTA															51	
Met Asn Glu Ile Asp Lys Ser Val Asp Ile Gly Phe Leu																
1 5 10																
CGG	ATT	CTT	GAT	GTT	ATT	AAA	AAA	GTT	ACG	ACC	CCA	AAG	GGT	GGC	ATT	99
Arg	Ile	Leu	Asp	Val	Ile	Lys	Lys	Val	Thr	Thr	Pro	Lys	Gly	Gly	Ile	
15 20 25																
GAA	ATC	TTA	AGG	ACT	TTA	ATT	GAT	TTT	ACG	CCC	AAA	ATT	GAA	AAC	GCC	147
Glu	Ile	Leu	Arg	Thr	Leu	Ile	Asp	Phe	Thr	Pro	Lys	Ile	Glu	Asn	Ala	
30 35 40 45																
CTG	AAT	TTA	GCG	GCC	AAA	AGC	CAT	AAG	GGG	CAA	TAC	AGA	AAA	AGC	GGC	195
Leu	Asn	Leu	Ala	Ala	Lys	Ser	His	Lys	Gly	Gln	Tyr	Arg	Lys	Ser	Gly	
50 55 60																
GAG	CCT	TAT	ATT	GTC	CAT	CCT	ATT	TGC	GTG	GCA	AGC	TTG	GTA	GCG	TTT	243
Glu	Pro	Tyr	Ile	Val	His	Pro	Ile	Cys	Val	Ala	Ser	Leu	Val	Ala	Phe	
65 70 75																
TGT	GGG	GGC	GAT	GAG	GCG	ATG	GTG	TGT	GCT	GCG	CTT	TTG	CAT	GAT	GTG	291
Cys	Gly	Gly	Asp	Glu	Ala	Met	Val	Cys	Ala	Ala	Leu	Leu	His	Asp	Val	
80 85 90																
GTG	GAA	GAC	ACG	CCT	TGT	AAG	ATT	GAA	ACG	ATT	GAG	CAA	GAA	TTT	GGG	339
Val	Glu	Asp	Thr	Pro	Cys	Lys	Ile	Glu	Thr	Ile	Glu	Gln	Glu	Phe	Gly	
95 100 105																
CAA	GAT	GTG	GCT	AAT	TTA	GTG	GAT	GCG	CTC	ACT	AAA	ATC	ACT	GAA	ATC	387
Gln	Asp	Val	Ala	Asn	Leu	Val	Asp	Ala	Leu	Thr	Lys	Ile	Thr	Glu	Ile	
110 115 120 125																
AGG	AAA	GAA	GAA	TTA	GGC	GTG	AGC	TCT	CAA	GAT	CCC	AGA	ATG	GTG	GTT	435
Arg	Lys	Glu	Glu	Leu	Gly	Val	Ser	Ser	Gln	Asp	Pro	Arg	Met	Val	Val	
130 135 140																
TCA	GCG	CTC	ACT	TTC	AGA	AAG	ATT	TTA	ATT	AGC	GCG	ATA	CAA	GAT	CCA	483
Ser	Ala	Leu	Thr	Phe	Arg	Lys	Ile	Leu	Ile	Ser	Ala	Ile	Gln	Asp	Pro	
145 150 155																
AGA	GCC	TTA	GTG	GTA	AAG	ATT	AGC	GAC	AGG	TTG	CAC	AAC	ATG	CTC	ACC	531
Arg	Ala	Leu	Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	His	Asn	Met	Leu	Thr	
160 165 170																
TTA	GAC	GCC	TTG	CCT	CAT	GAC	AAG	CAA	GTG	CGT	ATT	TCT	AAA	GAG	ACT	579
Leu	Asp	Ala	Leu	Pro	His	Asp	Lys	Gln	Val	Arg	Ile	Ser	Lys	Glu	Thr	
175 180 185																
CTA	GCG	GTG	TAT	GCC	CCT	ATA	GCG	AGC	CGA	TTG	GGC	ATG	TCT	TCA	ATC	627
Leu	Ala	Val	Tyr	Ala	Pro	Ile	Ala	Ser	Arg	Leu	Gly	Met	Ser	Ser	Ile	
190 195 200 205																
AAA	AAT	GAA	TTA	GAA	GAC	AAG	AGC	TTT	TAT	TAT	ATT	TAT	CCA	GAA	GAG	675
Lys	Asn	Glu	Leu	Glu	Asp	Lys	Ser	Phe	Tyr	Tyr	Ile	Tyr	Pro	Glu	Glu	
210 215 220																
TAT	AAA	AAT	ATC	AAG	GAA	TAT	TTG	CAC	AAA	AAC	AAG	CAG	TCT	TTA	CTC	723
Tyr	Lys	Asn	Ile	Lys	Glu	Tyr	Leu	His	Lys	Asn	Lys	Gln	Ser	Leu	Leu	

			225				230				235							
TTA Leu	AAG Lys	CTC Leu 240	AAC Asn	GCT Ala	TTT Phe	GCG Ala	AGC Ser 245	AAG Lys	TTA Leu	GAA Glu	AAA Lys 250	AAA Lys	CTT Leu	TTT Phe	GAT Asp	771		
AGT Ser 255	GGG Gly	TTT Phe	AGC Ser	CAT His	TCG Ser	GAT Asp 260	TTT Phe	AAA Lys	CTC Leu	GTT Val	ACA Thr 265	AGG Arg	GTG Val	AAA Lys	CGC Arg	819		
CCT Pro 270	TAT Tyr	TCT Ser	ATC Ile	TAT Tyr	CTT Leu 275	AAG Lys	ATG Met	CAA Gln	CGA Arg	AAG Lys 280	GGC Gly	GCG Ala	GTT Val	AAT Asn	ATT Ile 285	867		
GAT Asp	GAA Glu	ATT Ile	TTG Leu	GAC Asp 290	TTG Leu	TTA Leu	GCC Ala	ATT Ile	AGG Arg 295	ATT Ile	TTA Leu	TTG Leu	AAA Lys	AAC Asn 300	CCG Pro	915		
ATT Ile	GAT Asp	TGC Cys 305	TAT Tyr	AAA Lys	GTT Val	TTA Leu	GGG Gly 310	ATT Ile	ATC Ile	CAT His	TTG Leu	AAT Asn	TTC Phe 315	AAA Lys	CCC Pro	963		
ATT Ile	GTC Val	TCT Ser 320	CGT Arg	TTT Phe	AAA Lys	GAT Asp	TAC Tyr 325	ATC Ile	GCT Ala	TTG Leu	CCC Pro 330	AAA Lys	GAA Glu	AAT Asn	GGC Gly	1011		
TAT Tyr 335	AAG Lys	ACG Thr	ATA Ile	CAC His	ACG Thr	ACC Thr 340	ATT Ile	TTT Phe	GAT Asp	GAA Glu	TCT Ser 345	TCT Ser	GTT Val	TAT Tyr	GAA Glu	1059		
GTG Val 350	CAG Gln	ATC Ile	CGC Arg	ACC Thr	TTT Phe 355	GAT Asp	ATG Met	CAT His	ATG Met	GGG Gly 360	GCG Ala	GAG Glu	TAT Tyr	GGT Gly	AAT Asn 365	1107		
TCA Ser	GCC Ala	CAC His	TGG Trp 370	AAG Lys	TAT Tyr	AAA Lys	GCC Ala	GGG Gly	GGC Gly 375	GTG Val	GAT Asp	CAT His	GAA Glu	GAT Asp 380	CAT His	1155		
CAT His	GAG Glu	GGC Gly	ATG Met 385	AGA Arg	TGG Trp	TTG Leu	CAA Gln	AAT Asn 390	TTT Phe	AAA Lys	TAC Tyr	CAT His	GAC Asp 395	AGC Ser	GAT Asp	1203		
TTG Leu	AAA Lys 400	AAC Asn	GAC Asp	CCT Pro	AAG Lys	GAA Glu	TTT Phe 405	TAC Tyr	GAA Glu	CTC Leu	GCT Ala 410	AAG Lys	AAC Asn	GAT Asp	TTG Leu	1251		
TAT Tyr 415	CGT Arg	GAA Glu	GAT Asp	ATT Ile	GTC Val	GTT Val 420	TTT Phe	TCG Ser	CCT Pro	CAT His	GGG Gly 425	GAC Asp	ACT Thr	TAC Tyr	ACT Thr	1299		
TTA Leu 430	CCG Pro	GTG Val	GGT Gly	GCG Ala	ATC Ile 435	GCT Ala	TTA Leu	GAT Asp	TTT Phe	GCT Ala 440	TAC Tyr	ATG Met	GTG Val	CAT His	AGC Ser 445	1347		
GAT Asp	TTG Leu	GGC Gly	GAT Asp	AAA Lys 450	GCC Ala	ACG Thr	GAC Asp	GCT Ala	TAT Tyr 455	ATC Ile	AAT Asn	AGT Ser	AAA Lys	AAA Lys 460	GCC Ala	1395		

TTA CTC AAT CAG GAA TTA AGA AGT GGG GAT GTG GTT AAA ATC ATT AAA	1443
Leu Leu Asn Gln Glu Leu Arg Ser Gly Asp Val Val Lys Ile Ile Lys	
465 470 475	
GGC GAT AAA ATA ATA CCT CGT TTC ATT TGG ATG GAT CAG CTT AAA ACT	1491
Gly Asp Lys Ile Ile Pro Arg Phe Ile Trp Met Asp Gln Leu Lys Thr	
480 485 490	
TCT AAG GCT AAA AAC CAT TTG CGC ATC CAA AGA AGA AAC CGC TTG AAA	1539
Ser Lys Ala Lys Asn His Leu Arg Ile Gln Arg Arg Asn Arg Leu Lys	
495 500 505	
GAG GTT GAC ACT AAG AGC ATG ATC AAT ATC TTA GCG ACT TTT TTT GGG	1587
Glu Val Asp Thr Lys Ser Met Ile Asn Ile Leu Ala Thr Phe Phe Gly	
510 515 520 525	
CGC TCT GTT TTT GAA GAC ATG GAT TTA AAG GAT TAT AAA AAC TTT GAA	1635
Arg Ser Val Phe Glu Asp Met Asp Leu Lys Asp Tyr Lys Asn Phe Glu	
530 535 540	
GAA AGA TTA ACA GAT TGC GGG GTG GAG ACC ACC TTA ACA GAA GCG ATG	1683
Glu Arg Leu Thr Asp Cys Gly Val Glu Thr Thr Leu Thr Glu Ala Met	
545 550 555	
AAA AGT TTT GAA AAT TTA GCC AAA CTC ACT GAA GAA ATT GAA AAT AAG	1731
Lys Ser Phe Glu Asn Leu Ala Lys Leu Thr Glu Glu Ile Glu Asn Lys	
560 565 570	
GTG TTT TCT TTA AAA GAA GAT GCG ATT TTA GAA TAC CAA GAG ATG AGT	1779
Val Phe Ser Leu Lys Glu Asp Ala Ile Leu Glu Tyr Gln Glu Met Ser	
575 580 585	
TTA TGG ACT CGA GGT TTA AGG TAT TTG GGC TTT AAA ACC AAT GTC TTG	1827
Leu Trp Thr Arg Gly Leu Arg Tyr Leu Gly Phe Lys Thr Asn Val Leu	
590 595 600 605	
AAT TTT TTA GCC CCC AAT CGG CAG TGG CAG TGT AAG GAA TTA GAA CAT	1875
Asn Phe Leu Ala Pro Asn Arg Gln Trp Gln Cys Lys Glu Leu Glu His	
610 615 620	
TTT AGC GTT TGT TCA AGC AAC GCT TTA GAA ATC AAA CAG GTG TTG TTG	1923
Phe Ser Val Cys Ser Ser Asn Ala Leu Glu Ile Lys Gln Val Leu Leu	
625 630 635	
AAT GAT TGT TGT TAC CCT AAA TAT GGC GAT GAA ATC ATT GCG ATT GTA	1971
Asn Asp Cys Cys Tyr Pro Lys Tyr Gly Asp Glu Ile Ile Ala Ile Val	
640 645 650	
ACG GAT TTA AAA GAT CCA AAA GCG ATT GCG CAC CAT AAA TTT TGC AAA	2019
Thr Asp Leu Lys Asp Pro Lys Ala Ile Ala His His Lys Phe Cys Lys	
655 660 665	
AAA GCG ATG GCG GAA GTA GAT GCT AAA GTG CCT ATG GTT TAT ATA GAA	2067
Lys Ala Met Ala Glu Val Asp Ala Lys Val Pro Met Val Tyr Ile Glu	
670 675 680 685	
TGG CAC AAG CGG GAT CGA ACG ATT TAT AAA ATG ATG TTT TAT TTG GGC	2115
Trp His Lys Arg Asp Arg Thr Ile Tyr Lys Met Met Phe Tyr Leu Gly	

Leu	Pro	His	Asp	Lys	Gln	Val	Arg	Ile	Ser	Lys	Glu	Thr	Leu	Ala	Val
			180					185					190		
Tyr	Ala	Pro	Ile	Ala	Ser	Arg	Leu	Gly	Met	Ser	Ser	Ile	Lys	Asn	Glu
		195					200					205			
Leu	Glu	Asp	Lys	Ser	Phe	Tyr	Tyr	Ile	Tyr	Pro	Glu	Glu	Tyr	Lys	Asn
	210					215					220				
Ile	Lys	Glu	Tyr	Leu	His	Lys	Asn	Lys	Gln	Ser	Leu	Leu	Leu	Lys	Leu
225					230					235					240
Asn	Ala	Phe	Ala	Ser	Lys	Leu	Glu	Lys	Lys	Leu	Phe	Asp	Ser	Gly	Phe
				245					250					255	
Ser	His	Ser	Asp	Phe	Lys	Leu	Val	Thr	Arg	Val	Lys	Arg	Pro	Tyr	Ser
			260					265					270		
Ile	Tyr	Leu	Lys	Met	Gln	Arg	Lys	Gly	Ala	Val	Asn	Ile	Asp	Glu	Ile
		275					280					285			
Leu	Asp	Leu	Leu	Ala	Ile	Arg	Ile	Leu	Leu	Lys	Asn	Pro	Ile	Asp	Cys
	290					295					300				
Tyr	Lys	Val	Leu	Gly	Ile	Ile	His	Leu	Asn	Phe	Lys	Pro	Ile	Val	Ser
305					310					315					320
Arg	Phe	Lys	Asp	Tyr	Ile	Ala	Leu	Pro	Lys	Glu	Asn	Gly	Tyr	Lys	Thr
				325					330					335	
Ile	His	Thr	Thr	Ile	Phe	Asp	Glu	Ser	Ser	Val	Tyr	Glu	Val	Gln	Ile
				340				345					350		
Arg	Thr	Phe	Asp	Met	His	Met	Gly	Ala	Glu	Tyr	Gly	Asn	Ser	Ala	His
							360					365			
Trp	Lys	Tyr	Lys	Ala	Gly	Gly	Val	Asp	His	Glu	Asp	His	His	Glu	Gly
	370					375					380				
Met	Arg	Trp	Leu	Gln	Asn	Phe	Lys	Tyr	His	Asp	Ser	Asp	Leu	Lys	Asn
385					390					395					400
Asp	Pro	Lys	Glu	Phe	Tyr	Glu	Leu	Ala	Lys	Asn	Asp	Leu	Tyr	Arg	Glu
				405					410					415	
Asp	Ile	Val	Val	Phe	Ser	Pro	His	Gly	Asp	Thr	Tyr	Thr	Leu	Pro	Val
			420					425					430		
Gly	Ala	Ile	Ala	Leu	Asp	Phe	Ala	Tyr	Met	Val	His	Ser	Asp	Leu	Gly
			435				440					445			
Asp	Lys	Ala	Thr	Asp	Ala	Tyr	Ile	Asn	Ser	Lys	Lys	Ala	Leu	Leu	Asn
						455					460				
Gln	Glu	Leu	Arg	Ser	Gly	Asp	Val	Val	Lys	Ile	Ile	Lys	Gly	Asp	Lys
465					470					475					480
Ile	Ile	Pro	Arg	Phe	Ile	Trp	Met	Asp	Gln	Leu	Lys	Thr	Ser	Lys	Ala
				485					490					495	
Lys	Asn	His	Leu	Arg	Ile	Gln	Arg	Arg	Asn	Arg	Leu	Lys	Glu	Val	Asp
			500					505					510		
Thr	Lys	Ser	Met	Ile	Asn	Ile	Leu	Ala	Thr	Phe	Phe	Gly	Arg	Ser	Val
			515				520					525			
Phe	Glu	Asp	Met</												

Cys Tyr Pro Lys Tyr Gly Asp Glu Ile Ile Ala Ile Val Thr Asp Leu
 645 650 655
 Lys Asp Pro Lys Ala Ile Ala His His Lys Phe Cys Lys Lys Ala Met
 660 665 670
 Ala Glu Val Asp Ala Lys Val Pro Met Val Tyr Ile Glu Trp His Lys
 675 680 685
 Arg Asp Arg Thr Ile Tyr Lys Met Met Phe Tyr Leu Gly Glu Lys Lys
 690 695 700
 Ser Val Leu Ala Gly Leu Leu Thr Phe Leu Asn Arg Asn Glu Cys Asn
 705 710 715 720
 Ile Val Gly Val Ser Tyr Leu Gly Tyr Lys Asp Lys Tyr Ser Ser His
 725 730 735
 Cys Glu Val Ser Phe Glu Ile Ala Thr Asp Lys Ala Asp Trp Ile Arg
 740 745 750
 Ala Leu Ile Asn Arg Lys Tyr Gln Asp Arg Ile Val Glu Leu Ser Ser
 755 760 765
 Leu Asp Asp Ala Tyr Glu Ser
 770 775

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 10...279
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AAAAGGAGA GTG GCG GTG AAA AAA ATC GTT GTG AGT TGG TGT GTG GCG TTG	51
Val Ala Val Lys Lys Ile Val Val Ser Trp Cys Val Ala Leu	
1 5 10	
GCT TTT TTA AGC GCG GAT TCA GCA CAA GCC AAT AAA GCG ATC AGT AAT	99
Ala Phe Leu Ser Ala Asp Ser Ala Gln Ala Asn Lys Ala Ile Ser Asn	
15 20 25 30	
GCG GAT TTG ATT AAA GAG ATA AGG GAT TTA AAA AAA ATC ATC AGC GCG	147
Ala Asp Leu Ile Lys Glu Ile Arg Asp Leu Lys Lys Ile Ile Ser Ala	
35 40 45	
CAA AAC ACT GAG ATT AAC AAC TTA AGA AAA GTG CAA GAA GTG TTG TCT	195
Gln Asn Thr Glu Ile Asn Asn Leu Arg Lys Val Gln Glu Val Leu Ser	
50 55 60	
GGG CAA TTA GGG GAC ATG CGT AAG GAT ATA TTA AGC ACT AGA GAT TAT	243
Gly Gln Leu Gly Asp Met Arg Lys Asp Ile Leu Ser Thr Arg Asp Tyr	
65 70 75	
TGC ATT AGC TTA AGG CCT TAT ATC TAT AAT TGG CGC TAGGGGATAA TCCAAA	295

Cys Ile Ser Leu Arg Pro Tyr Ile Tyr Asn Trp Arg
 80 85 90

AAATGAAAGC ATGCG

310

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Val	Ala	Val	Lys	Lys	Ile	Val	Val	Ser	Trp	Cys	Val	Ala	Leu	Ala	Phe
1				5				10					15		
Leu	Ser	Ala	Asp	Ser	Ala	Gln	Ala	Asn	Lys	Ala	Ile	Ser	Asn	Ala	Asp
			20					25					30		
Leu	Ile	Lys	Glu	Ile	Arg	Asp	Leu	Lys	Lys	Ile	Ile	Ser	Ala	Gln	Asn
		35					40						45		
Thr	Glu	Ile	Asn	Asn	Leu	Arg	Lys	Val	Gln	Glu	Val	Leu	Ser	Gly	Gln
		50				55					60				
Leu	Gly	Asp	Met	Arg	Lys	Asp	Ile	Leu	Ser	Thr	Arg	Asp	Tyr	Cys	Ile
65					70					75					80
Ser	Leu	Arg	Pro	Tyr	Ile	Tyr	Asn	Trp	Arg						
					85				90						

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1569
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGAAAAAGAA	CTCAAAGAGC	TGCAAAAAAA	ACAAAAACAC	GAGTAACAAC	C	ATG	ATT	57								
						Met	Ile									
						1										
AAC	ACG	ATG	TTT	TGC	GCG	ACC	ATG	CAA	AGG	GGA	GTG	GCG	GAA	ATC	GTG	105
Asn	Thr	Met	Phe	Cys	Ala	Thr	Met	Gln	Arg	Gly	Val	Ala	Glu	Ile	Val	
		5					10					15				
GCT	GTG	GAA	GCG	ACT	TTC	ACA	AGG	GCT	TTG	CCG	GCG	TTT	GTG	ATT	TCA	153
Ala	Val	Glu	Ala	Thr	Phe	Thr	Arg	Ala	Leu	Pro	Ala	Phe	Val	Ile	Ser	

	20				25				30								
GGG Gly 35	TTA Leu	GCT Ala	AAT Asn	AGC Ser	TCT Ser 40	ATC Ile	CAA Gln	GAA Glu	GCC Ala	AAA Lys 45	CAG Gln	CGG Arg	GTT Val	CAA Gln	TCG Ser 50	201	
GCT Ala	TTA Leu	CAA Gln	AAT Asn 55	AAC Asn 55	GAT Asp	TTC Phe	ACT Thr	TTC Phe	CCG Pro 60	CCT Pro	TTA Leu	AAA Lys	ATC Ile	ACC Thr 65	ATC Ile	249	
AAC Asn	CTT Leu	TCC Ser	CCC Pro 70	TCA Ser	GAT Asp	TTG Leu	CCT Pro	AAA Lys 75	TCC Ser	GGG Gly	AGT Ser	CAT His	TTT Phe 80	GAT Asp	TTG Leu	297	
CCT Pro	ATC Ile	GCT Ala 85	CTT Leu	TTA Leu	ATC Ile	GCT Ala 90	TTG Leu	CAA Gln	AAA Lys	CAA Gln	GAG Glu 95	TTG Leu 95	GCT Ala	TTT Phe	AAA Lys	345	
GAG Glu	TGG Trp 100	TTT Phe	GCT Ala	TTT Phe	GGG Gly 105	GAG Glu 105	TTA Leu	GGG Gly	CTT Leu	GAT Asp	GGC Gly 110	AAG Lys	ATC Ile	AAA Lys	CCC Pro	393	
AAT Asn 115	CCT Pro	AAC Asn	ATT Ile	TTC Phe	CCC Pro 120	ATG Met	CTT Leu	TTA Leu	GAC Asp	ATT Ile 125	GCC Ala	ATT Ile	AAA Lys	CAC His	CCC Pro 130	441	
CAT His	GCT Ala	AAG Lys	ATC Ile	ATT Ile 135	GCG Ala	CCT Pro	AAG Lys	GCC Ala	AAT Asn 140	GAA Glu	GAG Glu	CTT Leu	TTT Phe	TCG Ser 145	CTT Leu	489	
ATC Ile	CCT Pro	AAT Asn 150	TTG Leu	CAA Gln	TGC Cys	TTT Phe	TTT Phe	GTG Val 155	GGG Gly	CAT His	TTT Phe	AAA Lys	GAA Glu 160	GCG Ala	TTA Leu	537	
GAA Glu	ATC Ile	TTG Leu 165	CAA Gln	AAC Asn	CCT Pro	GAA Glu	ACC Thr 170	AAA Lys	GCA Ala	GAC Asp	ACC Thr	CAC His 175	ACG Thr	AAA Lys	AAA Lys	585	
CTA Leu	CCC Pro 180	TTT Phe	AAA Lys	ACG Thr	ATA Ile	GAA Glu 185	TTG Leu	AAC Asn	GAT Asp	AAA Lys	GAG Glu 190	TAT Tyr	TAT Tyr	TTT Phe	TCA Ser	633	
GAC Asp 195	GCC Ala	TAT Tyr	GCC Ala	TTA Leu	GAT Asp 200	TTT Phe	AAA Lys	GAA Glu	GTT Val	AAG Lys 205	GGG Gly	CAA Gln	GCT Ala	GTC Val	GCT Ala 210	681	
AAA Lys	GAG Glu	GCC Ala	GCT Ala 215	TTG Leu	ATC Ile	GCT Ala	AGC Ser	GCT Ala	GGG Gly 220	TTT Phe	CAT His	AAC Asn	TTG Leu	ATT Ile 225	TTA Leu	729	
GAG Glu	GGA Gly	AGT Ser	CCA Pro 230	GGG Gly	TGT Cys	GGG Gly	AAA Lys	AGC Ser 235	ATG Met	ATC Ile	ATT Ile	AAT Asn	CGC Arg 240	ATG Met	CGT Arg	777	
TAT Tyr	ATC Ile	TTG Leu 245	CCT Pro	CCA Pro	TTA Leu	AGC Ser 250	CTG Leu	AAT Asn	GAA Glu	ATC Ile	CTA Leu	GAA Glu 255	GCG Ala	ACA Thr	AAA Lys	825	

485

490

495

GCG CTG AGT TTT AGA AAG ATT TCT TAAAAGGATT TTTATAAGGG AGAAAAAATG 1599
 Ala Leu Ser Phe Arg Lys Ile Ser
 500 505

CAAGAATACC ACATTCATAA TTTGGATTGC CC 1631

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Ile Asn Thr Met Phe Cys Ala Thr Met Gln Arg Gly Val Ala Glu
 1 5 10 15
 Ile Val Ala Val Glu Ala Thr Phe Thr Arg Ala Leu Pro Ala Phe Val
 20 25 30
 Ile Ser Gly Leu Ala Asn Ser Ser Ile Gln Glu Ala Lys Gln Arg Val
 35 40 45
 Gln Ser Ala Leu Gln Asn Asn Asp Phe Thr Phe Pro Pro Leu Lys Ile
 50 55 60
 Thr Ile Asn Leu Ser Pro Ser Asp Leu Pro Lys Ser Gly Ser His Phe
 65 70 75 80
 Asp Leu Pro Ile Ala Leu Leu Ile Ala Leu Gln Lys Gln Glu Leu Ala
 85 90 95
 Phe Lys Glu Trp Phe Ala Phe Gly Glu Leu Gly Leu Asp Gly Lys Ile
 100 105 110
 Lys Pro Asn Pro Asn Ile Phe Pro Met Leu Leu Asp Ile Ala Ile Lys
 115 120 125
 His Pro His Ala Lys Ile Ile Ala Pro Lys Ala Asn Glu Glu Leu Phe
 130 135 140
 Ser Leu Ile Pro Asn Leu Gln Cys Phe Phe Val Gly His Phe Lys Glu
 145 150 155 160
 Ala Leu Glu Ile Leu Gln Asn Pro Glu Thr Lys Ala Asp Thr His Thr
 165 170 175
 Lys Lys Leu Pro Phe Lys Thr Ile Glu Leu Asn Asp Lys Glu Tyr Tyr
 180 185 190
 Phe Ser Asp Ala Tyr Ala Leu Asp Phe Lys Glu Val Lys Gly Gln Ala
 195 200 205
 Val Ala Lys Glu Ala Ala Leu Ile Ala Ser Ala Gly Phe His Asn Leu
 210 215 220
 Ile Leu Glu Gly Ser Pro Gly Cys Gly Lys Ser Met Ile Ile Asn Arg
 225 230 235 240
 Met Arg Tyr Ile Leu Pro Pro Leu Ser Leu Asn Glu Ile Leu Glu Ala
 245 250 255
 Thr Lys Leu Arg Ile Leu Ser Glu Gln Asp Ser Ala Tyr Tyr Pro Leu
 260 265 270
 Arg Ser Phe Arg Asn Pro His Gln Ser Ala Ser Lys Ser Ser Ile Leu
 275 280 285
 Gly Ser Ser Ser Leu Arg Glu Pro Lys Pro Gly Glu Ile Ala Leu Ala
 290 295 300

Ser	Glu	Gly	Ile	Gly	Leu	Ala	Ala	Ile	Gln	Val	Gly	Leu	Pro	Leu	Arg		
			45				50						55				
ATG	CTC	ATC	ATC	AAC	CTC	CCG	CAA	GAA	GAC	GGC	GTG	CAA	CAC	AAA	GAA	244	
Met	Leu	Ile	Ile	Asn	Leu	Pro	Gln	Glu	Asp	Gly	Val	Gln	His	Lys	Glu		
			60				65						70				
GAC	TGC	TTG	GAA	ATC	ATT	AAC	CCT	AAG	TTT	ATA	GAA	ACT	GGG	GGA	TCA		
Asp	Cys	Leu	Glu	Ile	Ile	Asn	Pro	Lys	Phe	Ile	Glu	Thr	Gly	Gly	Ser	292	
			75				80						85				
ATG	ATG	TAT	AGA	GAA	GGG	TGC	TTG	TCT	GTG	CCG	GGA	TTT	TAC	GAA	GAA		
Met	Met	Tyr	Arg	Glu	Gly	Cys	Leu	Ser	Val	Pro	Gly	Phe	Tyr	Glu	Glu	340	
			90				95						100				105
GTG	GAG	CGT	TTT	GAA	AAG	GTT	AAG	ATA	GAG	TAT	CAA	AAC	CGC	TTC	GCT		
Val	Glu	Arg	Phe	Glu	Lys	Val	Lys	Ile	Glu	Tyr	Gln	Asn	Arg	Phe	Ala	388	
			110				115						120				
GAA	GTG	AAA	GTT	TTA	GAA	GCG	AGC	GAG	CTT	TTA	GCG	GTA	GCC	ATT	CAG		
Glu	Val	Lys	Val	Leu	Glu	Ala	Ser	Glu	Leu	Leu	Ala	Val	Ala	Ile	Gln	436	
			125				130						135				
CAT	GAG	ATC	GAT	CAC	CTC	AAT	GGC	GTG	TTA	TTC	GTG	GAT	AAA	TTA	TCC		
His	Glu	Ile	Asp	His	Leu	Asn	Gly	Val	Leu	Phe	Val	Asp	Lys	Leu	Ser	484	
			140				145						150				
ATT	TTG	AAG	CGT	AAG	AAA	TTT	GAA	AAA	GAA	CTC	AAA	GAG	CTG	CAA	AAA		
Ile	Leu	Lys	Arg	Lys	Lys	Phe	Glu	Lys	Glu	Leu	Lys	Glu	Leu	Gln	Lys	532	
			155				160						165				
AAA	CAA	AAA	CAC	GAG	TAACAACCAT		GATTAACACG		ATGTTTTGCG		CGACCATGCA		A			588	
Lys	Gln	Lys	His	Glu													
			170														
AGGGGAGTGG			CGGAAAT														605

(2) INFORMATION FOR SEO ID NO:118:

(ii) MOLECULE TYPE: protein

Met	Ala	Leu	Leu	Glu	Ile	Ile	His	Tyr	Pro	Ser	Lys	Ile	Leu	Arg	Thr
1				5					10					15	
Ile	Ser	Lys	Glu	Val	Val	Ser	Phe	Asp	Ser	Lys	Leu	His	Gln	Gln	Leu
			20					25					30		
Asp	Asp	Met	His	Glu	Thr	Met	Ile	Ala	Ser	Glu	Gly	Ile	Gly	Leu	Ala
		35					40					45			
Ala	Ile	Gln	Val	Gly	Leu	Pro	Leu	Arg	Met	Leu	Ile	Ile	Asn	Leu	Pro
	50					55					60				
Gln	Glu	Asp	Gly	Val	Gln	His	Lys	Glu	Asp	Cys	Leu	Glu	Ile	Ile	Asn

65					70					75					80
Pro	Lys	Phe	Ile	Glu	Thr	Gly	Gly	Ser	Met	Met	Tyr	Arg	Glu	Gly	Cys
				85					90					95	
Leu	Ser	Val	Pro	Gly	Phe	Tyr	Glu	Glu	Val	Glu	Arg	Phe	Glu	Lys	Val
			100					105					110		
Lys	Ile	Glu	Tyr	Gln	Asn	Arg	Phe	Ala	Glu	Val	Lys	Val	Leu	Glu	Ala
		115					120					125			
Ser	Glu	Leu	Leu	Ala	Val	Ala	Ile	Gln	His	Glu	Ile	Asp	His	Leu	Asn
		130				135					140				
Gly	Val	Leu	Phe	Val	Asp	Lys	Leu	Ser	Ile	Leu	Lys	Arg	Lys	Lys	Phe
145					150					155					160
Glu	Lys	Glu	Leu	Lys	Glu	Leu	Gln	Lys	Lys	Gln	Lys	His	Glu		
			165					170							

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...495
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CCCCAAACAA TAGGATAAAA A ATG CCG CTC ACT CAT TTG AAT GAA GAA AAT	51
Met Pro Leu Thr His Leu Asn Glu Glu Asn	
1 5 10	
CAG CCT AAA ATG GTG GAT ATA GGG GAT AAA GAA ACC ACT GAA AGA ATC	99
Gln Pro Lys Met Val Asp Ile Gly Asp Lys Glu Thr Thr Glu Arg Ile	
15 20 25	
GCT TTA GCA AGC GGT CGT ATC AGC ATG AAT AAA GAG GCT TAT GAC GCT	147
Ala Leu Ala Ser Gly Arg Ile Ser Met Asn Lys Glu Ala Tyr Asp Ala	
30 35 40	
ATT ATC AAT CAT TGC GTC AAA AAG GGT CCG GTG TTA CAG ACT GCT ATT	195
Ile Ile Asn His Cys Val Lys Lys Gly Pro Val Leu Gln Thr Ala Ile	
45 50 55	
ATT GCT GGA ATT ATG GGG GCT AAA AAG ACA AGC GAG CTC ATT CCC ATG	243
Ile Ala Gly Ile Met Gly Ala Lys Lys Thr Ser Glu Leu Ile Pro Met	
60 65 70	
TGC CAT CCA ATC ATG CTC AAT GGG GTG GAT ATT GAT ATT TTA GAA GAA	291
Cys His Pro Ile Met Leu Asn Gly Val Asp Ile Asp Ile Leu Glu Glu	
75 80 85 90	
AAA GAG ACT TGT AGT TTT AAA CTC TAT GCG AGA GTC AAA ACT CAA GCT	339
Lys Glu Thr Cys Ser Phe Lys Leu Tyr Ala Arg Val Lys Thr Gln Ala	

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Met Pro Leu Thr His Leu Asn Glu Glu Asn Gln Pro Lys Met Val Asp
1 5 10 15
Ile Gly Asp Lys Glu Thr Thr Glu Arg Ile Ala Leu Ala Ser Gly Arg
20 25 30
Ile Ser Met Asn Lys Glu Ala Tyr Asp Ala Ile Ile Asn His Cys Val
35 40 45
Lys Lys Gly Pro Val Leu Gln Thr Ala Ile Ile Ala Gly Ile Met Gly
50 55 60
Ala Lys Lys Thr Ser Glu Leu Ile Pro Met Cys His Pro Ile Met Leu
65 70 75 80
Asn Gly Val Asp Ile Asp Ile Leu Glu Glu Lys Glu Thr Cys Ser Phe
85 90 95
Lys Leu Tyr Ala Arg Val Lys Thr Gln Ala Lys Thr Gly Val Glu Met
100 105 110
Glu Ala Leu Met Ser Val Ser Ile Gly Leu Leu Thr Ile Tyr Asp Met
115 120 125
Val Lys Ala Ile Asp Lys Ser Met Thr Ile Ser Gly Val Met Leu Glu
130 135 140
His Lys Ser Gly Gly Lys Ser Gly Asp Tyr Asn Ala Lys Lys
145 150 155

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...552
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CTTTTAGCTT AAAAAGGAGT TCAA ATG CAA ACG ATT CAT ATA GGC GTT TTG 51
Met Gln Thr Ile His Ile Gly Val Leu
1 5
AGC GCG AGC GAT AGA GCG TCA AAA GGG ATT TAT GAA GAT TTA AGC GGT 99
Ser Ala Ser Asp Arg Ala Ser Lys Gly Ile Tyr Glu Asp Leu Ser Gly
10 15 20 25

AAG GCG ATA CAA GAA GTG TTG AGC GAA TAC TTG CTC AAT CCT TTA GAA	147
Lys Ala Ile Gln Glu Val Leu Ser Glu Tyr Leu Leu Asn Pro Leu Glu	
30 35 40	
TTT TAT TAC GAA ATT GTC GCT GAT GAA AGG GAT TTA ATT GAA AAA TCA	195
Phe Tyr Tyr Glu Ile Val Ala Asp Glu Arg Asp Leu Ile Glu Lys Ser	
45 50 55	
CTG ATT AAA ATG TGC GAT GAA TAC CAA TGC GAT CTA GTC GTT ACT ACA	243
Leu Ile Lys Met Cys Asp Glu Tyr Gln Cys Asp Leu Val Val Thr Thr	
60 65 70	
GGA GGC ACA GGC CCT GCT TTA AGA GAT ATA ACC CCA GAA GCC ACA GAA	291
Gly Gly Thr Gly Pro Ala Leu Arg Asp Ile Thr Pro Glu Ala Thr Glu	
75 80 85	
AAA GTG TGC CAA AAA ATG CTT CCT GGT TTT GGA GAG CTT ATG CGA ATG	339
Lys Val Cys Gln Lys Met Leu Pro Gly Phe Gly Glu Leu Met Arg Met	
90 95 100 105	
ACT AGT TTA AAA TAT GTG CCT ACA GCG ATC CTG TCG CGC CAG AGC GCT	387
Thr Ser Leu Lys Tyr Val Pro Thr Ala Ile Leu Ser Arg Gln Ser Ala	
110 115 120	
GGT ATT AGG AAT AAG AGT TTG ATT ATT AAT CTC CCT GGT AAG CCA AAA	435
Gly Ile Arg Asn Lys Ser Leu Ile Ile Asn Leu Pro Gly Lys Pro Lys	
125 130 135	
AGT ATT AGA GAA TGC TTA GAG GCG GTT TTT CCA GCG ATT CCT TAT TGC	483
Ser Ile Arg Glu Cys Leu Glu Ala Val Phe Pro Ala Ile Pro Tyr Cys	
140 145 150	
GTG GAT TTG ATT TTA GGG AAT TAT ATG CAA GTG AAT GAA AAA AAC ATT	531
Val Asp Leu Ile Leu Gly Asn Tyr Met Gln Val Asn Glu Lys Asn Ile	
155 160 165	
CAA GCG TTT CGC CCC AAA CAA TAGGATAAAA AATGCCGCTC ACTCATTGTA ATGA	586
Gln Ala Phe Arg Pro Lys Gln	
170 175	
AGAAAATCAG CCTAAAATG	605

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Met Gln Thr Ile His Ile Gly Val Leu Ser Ala Ser Asp Arg Ala Ser	
1 5 10 15	
Lys Gly Ile Tyr Glu Asp Leu Ser Gly Lys Ala Ile Gln Glu Val Leu	
20 25 30	

Gly	Ala	Val	Met	Gly	Leu	Met	Leu	Ala	Leu	Gln	Lys	Leu	Asp	Asn	Pro
		115					120					125			
Ala	Glu	Met	Ala	Ala	Gly	Ile	Ala	Gly	Ala	Phe	Thr	Ala	Thr	Val	Thr
	130					135					140				
Gly	Ile	Met	Cys	Ser	Tyr	Ala	Ile	Phe	Gly	Pro	Phe	Gly	His	Lys	Leu
145					150					155					160
Lys	Ala	Lys	Ser	Lys	Asp	Ile	Ile	Lys	Glu	Lys	Thr	Val	Leu	Leu	Glu
				165					170						175
Gly	Ile	Leu	Gly	Ile	Ala	Asn	Gly	Glu	Asn	Pro	Arg	Asp	Leu	Glu	Asn
			180					185					190		
Lys	Leu	Leu	Asn	Tyr	Ile	Ala	Pro	Gly	Glu	Pro	Lys	Lys	Ser	Gln	Phe
		195					200					205			
Glu	Gly														
	210														

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...783
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

TGAGGGCTAA	AG	ATG	GCT	AAG	AAA	AAC	AMA	CCC	ACC	GAA	TGC	CCC	GCC	GGT	51	
	Met	Ala	Lys	Lys	Asn	Xaa	Pro	Thr	Glu	Cys	Pro	Ala	Gly			
	1				5						10					
GAA	AAA	TGG	GCG	GTT	CCT	TAT	GCG	GAC	TTT	TTG	TCG	TTG	TTG	CTC	GCG	99
Glu	Lys	Trp	Ala	Val	Pro	Tyr	Ala	Asp	Phe	Leu	Ser	Leu	Leu	Leu	Ala	
	15				20					25						
CTT	TTT	ATC	GCT	CTT	TAT	GCC	ATT	TCA	GCG	GTC	AAC	AAA	TCC	AAA	GTG	147
Leu	Phe	Ile	Ala	Leu	Tyr	Ala	Ile	Ser	Ala	Val	Asn	Lys	Ser	Lys	Val	
	30				35				40					45		
GAA	GCC	TTA	AAA	ACC	GAA	TTT	ATT	AAG	ATT	TTT	AAT	TAC	GCT	CCC	AAG	195
Glu	Ala	Leu	Lys	Thr	Glu	Phe	Ile	Lys	Ile	Phe	Asn	Tyr	Ala	Pro	Lys	
				50				55					60			
CCA	GAG	GCG	ATG	CAG	CCG	GTT	GTA	GTG	ATC	CCG	CCT	GAT	TCA	GGG	AAA	243
Pro	Glu	Ala	Met	Gln	Pro	Val	Val	Val	Ile	Pro	Pro	Asp	Ser	Gly	Lys	
			65				70						75			
GAA	GAA	GAA	CAA	ATG	GCG	AGC	GAA	AGC	TCC	AAA	CCG	GCT	TCG	CAA	AAT	291
Glu	Glu	Glu	Gln	Met	Ala	Ser	Glu	Ser	Ser	Lys	Pro	Ala	Ser	Gln	Asn	
		80					85				90					
ACC	GAA	ACA	AAA	GCC	ACT	ATC	GCT	CGC	AAA	GGC	GAA	GGC	AGT	GTT	TTA	339

Ala	Val	Pro	Tyr	Ala	Asp	Phe	Leu	Ser	Leu	Leu	Leu	Ala	Leu	Phe	Ile
			20					25					30		
Ala	Leu	Tyr	Ala	Ile	Ser	Ala	Val	Asn	Lys	Ser	Lys	Val	Glu	Ala	Leu
		35					40					45			
Lys	Thr	Glu	Phe	Ile	Lys	Ile	Phe	Asn	Tyr	Ala	Pro	Lys	Pro	Glu	Ala
	50					55					60				
Met	Gln	Pro	Val	Val	Val	Ile	Pro	Pro	Asp	Ser	Gly	Lys	Glu	Glu	Glu
65					70					75				80	
Gln	Met	Ala	Ser	Glu	Ser	Ser	Lys	Pro	Ala	Ser	Gln	Asn	Thr	Glu	Thr
			85						90					95	
Lys	Ala	Thr	Ile	Ala	Arg	Lys	Gly	Glu	Gly	Ser	Val	Leu	Glu	Gln	Ile
			100					105					110		
Asp	Gln	Gly	Ser	Ile	Leu	Lys	Leu	Pro	Ser	Asn	Leu	Leu	Phe	Glu	Asn
		115					120					125			
Ala	Thr	Ser	Asp	Ala	Ile	Asn	Gln	Asp	Met	Met	Leu	Tyr	Ile	Glu	Arg
	130					135					140				
Ile	Ala	Lys	Ile	Ile	Gln	Lys	Leu	Pro	Lys	Arg	Val	His	Ile	Asn	Val
145					150					155					160
Arg	Gly	Phe	Thr	Asp	Asp	Thr	Pro	Leu	Val	Lys	Thr	Arg	Phe	Lys	Ser
			165						170					175	
His	Tyr	Glu	Leu	Ala	Ala	Asn	Arg	Ala	Tyr	Arg	Val	Met	Lys	Val	Leu
			180					185					190		
Ile	Gln	Tyr	Gly	Val	Asn	Pro	Asn	Gln	Leu	Ser	Phe	Ser	Ser	Tyr	Gly
		195					200					205			
Ser	Thr	Asn	Pro	Ile	Ala	Pro	Asn	Asp	Ser	Leu	Glu	Asn	Arg	Met	Lys
	210					215					220				
Asn	Asn	Arg	Val	Glu	Ile	Phe	Phe	Ser	Thr	Asp	Ala	Asn	Asp	Leu	Ser
225					230					235				240	
Lys	Ile	His	Ser	Ile	Leu	Asp	Asn	Glu	Phe	Asn	Pro	His	Lys	Gln	Gln
				245					250					255	
Glu															

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...474
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

TGTTAAGATC	AGTTT	ATG	GAA	CAA	AAT	ATT	TTC	TCC	TTA	CTC	ATT	CAA	AAA		51
		Met	Glu	Gln	Asn	Ile	Phe	Ser	Leu	Leu	Ile	Gln	Lys		
		1				5						10			
AAG TCT TAT AAA AAG CTT GAA ACC CTT TTG AAA CTC AAA AAG CTT AAG															99
Lys Ser Tyr Lys Lys Leu Glu Thr Leu Leu Lys Leu Lys Lys Leu Lys															
	15					20						25			

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Lys	Cys	Tyr	Phe	Phe	Ile	Thr	Phe	Ser	Tyr	Ser	Tyr	Gly	Tyr	Val	Val
1				5				10						15	
Ile	Phe	Leu	Pro	Glu	Asn	Phe	Ile	Leu	Arg	Asn	Ile	Tyr	Val	Gly	Asn
			20					25					30		
Leu	Val	Tyr	Ser	Ala	Thr	Ser	Glu	Gln	Val	Lys	Glu	Leu	Phe	Ser	Gln
			35				40					45			
Phe	Gly	Lys	Val	Phe	Asn	Val	Lys	Leu	Ile	Tyr	Asp	Arg	Glu	Thr	Lys
			50			55					60				
Lys	Pro	Lys	Gly	Phe	Gly	Phe	Val	Glu	Met	Gln	Glu	Glu	Ser	Val	Ser
65					70					75					80
Glu	Ala	Ile	Ala	Lys	Leu	Asp	Asn	Thr	Asp	Phe	Met	Gly	Arg	Thr	Ile
				85				90						95	
Arg	Val	Thr	Glu	Ala	Asn	Pro	Lys	Lys	Ser						
			100					105							

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...1473
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TTAGATTTAA	AATTAGATTA	AGGATAGAAA	ATG AGA ATT TTA CAA AGG GCT TTG	54
			Met Arg Ile Leu Gln Arg Ala Leu	
			1	5
ACT TTT GAA GAT GTG TTG ATG GTG CCT AGA AAG TCT AGC GTT TTA CCT	102			
Thr Phe Glu Asp Val Leu Met Val Pro Arg Lys Ser Ser Val Leu Pro				
10	15	20		
AAA GAT GTG AGC TTA AAG TCT CGC TTA ACT AAA AAC ATT CGT TTG AAT	150			
Lys Asp Val Ser Leu Lys Ser Arg Leu Thr Lys Asn Ile Arg Leu Asn				
25	30	35	40	
ATC CCC TTT ATC AGT GCG GCT ATG GAT ACG GTT ACA GAG CAT AAA ACC	198			

Gly	Val	Ala	Ser	Glu	Lys	Leu	Val	Pro	Glu	Gly	Ile	Glu	Gly	Arg	Val
				405					410					415	
Pro	Tyr	Arg	Gly	Lys	Val	Ser	Asp	Met	Ile	Phe	Gln	Leu	Val	Gly	Gly
			420					425				430			
Val	Arg	Ser	Ser	Met	Gly	Tyr	Gln	Gly	Ala	Lys	Asn	Ile	Leu	Glu	Leu
		435					440					445			
Tyr	Gln	Asn	Ala	Glu	Phe	Val	Glu	Ile	Thr	Ser	Ala	Gly	Leu	Lys	Glu
	450					455					460				
Ser	His	Val	His	Gly	Val	Asp	Ile	Thr	Lys	Glu	Ala	Pro	Asn	Tyr	Tyr
465					470					475					480
Gly															

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...876
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

TAATGAAAAA	TAGTTCATGA	ACGCTTTTGC	ATTAAGGCTC	AAAAAAAGCG	CCGTTTAA	ATG	60
						Met	
						1	
GAT TTT TGT AAA ATA AAA GAA ATT TTA AGG AGG CTT GTG GTG TTG AAA	108						
Asp Phe Cys Lys Ile Lys Glu Ile Leu Arg Arg Leu Val Val Leu Lys							
5 10 15							
GAA TTA CGC CAA AAA CGC CCT TTA GTG CAT AAT ATC ACC AAT TAT GTG	156						
Glu Leu Arg Gln Lys Arg Pro Leu Val His Asn Ile Thr Asn Tyr Val							
20 25 30							
GCG GCG CAA TTT GTG GCT AAT GGT TTG TTA GCT TTA GGG GCA TCG CCT	204						
Ala Ala Gln Phe Val Ala Asn Gly Leu Leu Ala Leu Gly Ala Ser Pro							
35 40 45							
TTA ATG AGC GAT GCG ATT GAT GAA ATG CGA GAT TTA GCG AAA ATT TCT	252						
Leu Met Ser Asp Ala Ile Asp Glu Met Arg Asp Leu Ala Lys Ile Ser							
50 55 60 65							
GAC GCG CTC GCT ATC AAT ATT GGC ACC CTT AAT GAT CGC GCT ATT TTA	300						
Asp Ala Leu Ala Ile Asn Ile Gly Thr Leu Asn Asp Arg Ala Ile Leu							
70 75 80							
TGC GCT AAA GAG GCT ATC AAG CAT TAC AAG GCT TTG AAC AAA CCC ATT	348						
Cys Ala Lys Glu Ala Ile Lys His Tyr Lys Ala Leu Asn Lys Pro Ile							
85 90 95							

GTG Val	TTA Leu	GAT Asp 100	CCT Pro	GTG Val	GGG Gly	TGT Cys	TCA Ser 105	GCG Ala	AGC Ser	GCT Ala	TTG Leu	CGT Arg 110	CAT His	GAC Asp	ACC Thr	396
AGT Ser	TTA Leu 115	GAG Glu	CTT Leu	TTG Leu	AAA Lys 120	AGT Ser	GGT Gly	GGG Gly	ATT Ile	AGC Ser	GCG Ala 125	CTT Leu	AGG Arg	GGT Gly	AAT Asn	444
GCT Ala 130	GCA Ala	GAA Glu	TTA Leu	GGC Gly	TCT Ser 135	TTA Leu	GTG Val	GGG Gly	ATT Ile	TCT Ser 140	TGC Cys	GAA Glu	AGT Ser	AAG Lys	GGG Gly 145	492
CTA Leu	GAC Asp	TCT Ser	AAT Asn 150	GAT Asp	GCC Ala	GCC Ala	ACG Thr	CCT Pro 155	GTA Val	GAA Glu	ATA Ile	ATC Ile	AAA Lys	TTA Leu 160	GCG Ala	540
GCT Ala	CAA Gln	AAA Lys 165	TAT Tyr	TCT Ser	GTG Val	ATA Ile	GCG Ala 170	GTA Val	ATG Met	ACG Thr	GGT Gly	AAA Lys 175	ACA Thr	GAT Asp	TAC Tyr	588
GTG Val	AGC Ser 180	GAT Asp	GGG Gly	AAA Lys	AAG Lys	GTT Val	TTG Leu 185	AGT Ser	ATT Ile	ACT Thr	GGG Gly 190	GGG Gly	AGC Ser	GAG Glu	TAT Tyr	636
TTA Leu 195	GCG Ala	CTC Leu	ATT Ile	ACT Thr	GGG Gly	GCT Ala 200	GGG Gly	TGT Cys	TTG Leu	CAT His 205	GCC Ala 210	GCA Ala	GCA Ala	TGC Cys	GCG Ala	684
AGC Ser 210	TTT Phe	TTA Leu	AGT Ser	TTG Leu	AAA Lys 215	AAA Lys	GAC Asp	CCC Pro	TTA Leu 220	GAT Asp	TCT Ser	ATG Met	GCG Ala	CAA Gln	CTT Leu 225	732
TGC Cys	GCG Ala	CTC Leu	TAT Tyr 230	AAA Lys	CAA Gln	GCC Ala	GCT Ala	TTT Phe 235	AAC Asn	GCG Ala	CAA Gln	AAA Lys	AAG Lys	GTG Val 240	TTG Leu	780
GAA Glu	AAT Asn	AAC Asn	GGC Gly 245	TCT Ser	AAT Asn	GGT Gly	TCG Ser 250	TTC Phe	TTG Leu	TTT Phe	TAT Tyr	TTT Phe 255	TTA Leu	GAT Asp	GCT Ala	828
CTA Leu	AGC Ser 260	TTG Leu	CCC Pro	ATA Ile	GAG Glu	TTA Leu 265	GAA Glu	AAC Asn	AGC Ser	CTT Leu	ATT Ile 270	AAG Lys	GAA Glu	GAG Glu	TGG Trp	877
GAAAATTTAC CCGCAAGTTT TAAGCATTGC TGGCAGCGAT AG																919

- (2) INFORMATION FOR SEQ ID NO:136:

Met	Asp	Phe	Cys	Lys	Ile	Lys	Glu	Ile	Leu	Arg	Arg	Leu	Val	Val	Leu
1				5					10					15	
Lys	Glu	Leu	Arg	Gln	Lys	Arg	Pro	Leu	Val	His	Asn	Ile	Thr	Asn	Tyr
			20					25				30			
Val	Ala	Ala	Gln	Phe	Val	Ala	Asn	Gly	Leu	Leu	Ala	Leu	Gly	Ala	Ser
		35					40					45			
Pro	Leu	Met	Ser	Asp	Ala	Ile	Asp	Glu	Met	Arg	Asp	Leu	Ala	Lys	Ile
		50				55					60				
Ser	Asp	Ala	Leu	Ala	Ile	Asn	Ile	Gly	Thr	Leu	Asn	Asp	Arg	Ala	Ile
65					70					75					80
Leu	Cys	Ala	Lys	Glu	Ala	Ile	Lys	His	Tyr	Lys	Ala	Leu	Asn	Lys	Pro
			85						90					95	
Ile	Val	Leu	Asp	Pro	Val	Gly	Cys	Ser	Ala	Ser	Ala	Leu	Arg	His	Asp
			100					105					110		
Thr	Ser	Leu	Glu	Leu	Leu	Lys	Ser	Gly	Gly	Ile	Ser	Ala	Leu	Arg	Gly
		115				120						125			
Asn	Ala	Ala	Glu	Leu	Gly	Ser	Leu	Val	Gly	Ile	Ser	Cys	Glu	Ser	Lys
		130				135						140			
Gly	Leu	Asp	Ser	Asn	Asp	Ala	Ala	Thr	Pro	Val	Glu	Ile	Ile	Lys	Leu
145					150					155					160
Ala	Ala	Gln	Lys	Tyr	Ser	Val	Ile	Ala	Val	Met	Thr	Gly	Lys	Thr	Asp
			165						170					175	
Tyr	Val	Ser	Asp	Gly	Lys	Lys	Val	Leu	Ser	Ile	Thr	Gly	Gly	Ser	Glu
			180					185					190		
Tyr	Leu	Ala	Leu	Ile	Thr	Gly	Ala	Gly	Cys	Leu	His	Ala	Ala	Ala	Cys
		195					200					205			
Ala	Ser	Phe	Leu	Ser	Leu	Lys	Lys	Asp	Pro	Leu	Asp	Ser	Met	Ala	Gln
		210				215					220				
Leu	Cys	Ala	Leu	Tyr	Lys	Gln	Ala	Ala	Phe	Asn	Ala	Gln	Lys	Lys	Val
225					230					235					240
Leu	Glu	Asn	Asn	Gly	Ser	Asn	Gly	Ser	Phe	Leu	Phe	Tyr	Phe	Leu	Asp
			245						250					255	
Ala	Leu	Ser	Leu	Pro	Ile	Glu	Leu	Glu	Asn	Ser	Leu	Ile	Lys	Glu	Glu
			260					265					270		
Trp															

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 78...971
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ATCCAAATAA	TTGGGCGATT	AAAGAGGGAA	TTTATTCAAT	CAAACCAAAT	AAAAAAATAG	60
TATTTCCAAG	ATTTTATA	ATG TTT TGC	TTT GAA AAT	TTG AAT ATT	CAA AAT	110
		Met Phe Cys	Phe Glu Asn	Leu Asn Ile	Gln Asn	

																1							5							10							
GMT	ATA	AAA	AGT	AAA	AGT	TTT	GGA	GGA	ATA	GTT	AAA	AGT	ATA	TCA	ATG	158																					
Xaa	Ile	Lys	Ser	Lys	Ser	Phe	Gly	Gly	Ile	Val	Lys	Ser	Ile	Ser	Met																						
			15				20					25																									
AAC	GAT	TTA	CAA	CAA	ATA	ACC	ATC	CCC	ATC	CCA	CCC	CTA	GAG	ATC	CAA	206																					
Asn	Asp	Leu	Gln	Gln	Ile	Thr	Ile	Pro	Ile	Pro	Pro	Leu	Glu	Ile	Gln																						
			30				35					40																									
CAA	GAG	ATC	GTT	AAG	ATT	TTG	GAC	GCT	TTC	ACA	GAA	TTA	AAC	ACA	GAA	254																					
Gln	Glu	Ile	Val	Lys	Ile	Leu	Asp	Ala	Phe	Thr	Glu	Leu	Asn	Thr	Glu																						
			45				50					55																									
TTA	AAC	ACA	GAA	TTA	AAA	GCG	CGC	AAA	AAG	CAA	TAT	GAG	TAT	TAC	CAA	302																					
Leu	Asn	Thr	Glu	Leu	Lys	Ala	Arg	Lys	Lys	Gln	Tyr	Glu	Tyr	Tyr	Gln																						
			60				65					70		75																							
AAC	ATG	CTT	TTA	GAC	TTT	AAC	GAT	ATT	AAT	CAA	AAC	CAC	AAA	GAC	GCC	350																					
Asn	Met	Leu	Leu	Asp	Phe	Asn	Asp	Ile	Asn	Gln	Asn	His	Lys	Asp	Ala																						
			80						85			90																									
AAA	ATA	AAA	ACC	TAC	CCT	AAA	CGC	TTG	AAA	ACC	TTA	CTC	CAC	ACT	TTA	398																					
Lys	Ile	Lys	Thr	Tyr	Pro	Lys	Arg	Leu	Lys	Thr	Leu	Leu	His	Thr	Leu																						
			95						100			105																									
GCG	CCT	AAG	GGG	GTG	GAG	TTT	AGG	AAA	TTG	GGG	GAG	GTG	TGT	GAA	AGC	446																					
Ala	Pro	Lys	Gly	Val	Glu	Phe	Arg	Lys	Leu	Gly	Glu	Val	Cys	Glu	Ser																						
			110						115			120																									
ACA	AAT	AAA	AAA	ACA	CTC	AAA	ATA	AGC	GAA	GTA	AGT	GAA	GTA	AAA	AAT	494																					
Thr	Asn	Lys	Lys	Thr	Leu	Lys	Ile	Ser	Glu	Val	Ser	Glu	Val	Lys	Asn																						
			125			130			135																												
AAG	GGA	ATG	TAT	CCA	GTG	ATA	AAT	TCA	GGG	AGG	GAT	TTG	TAT	GGT	TAT	542																					
Lys	Gly	Met	Tyr	Pro	Val	Ile	Asn	Ser	Gly	Arg	Asp	Leu	Tyr	Gly	Tyr																						
			140			145			150			155																									
TAC	CAT	GAT	TTT	AAC	AAT	GAT	GGA	GAA	AAT	ATA	ACT	ATT	GCA	TCT	AGG	590																					
Tyr	His	Asp	Phe	Asn	Asn	Asp	Gly	Glu	Asn	Ile	Thr	Ile	Ala	Ser	Arg																						
			160						165			170																									
GGA	GAA	TAT	GCA	GGA	TTT	ATA	AAC	TAT	TTC	AAT	GAA	AAA	TTT	TTT	GCA	638																					
Gly	Glu	Tyr	Ala	Gly	Phe	Ile	Asn	Tyr	Phe	Asn	Glu	Lys	Phe	Phe	Ala																						
			175						180			185																									
GGG	GGT	CTA	TGT	TAT	CCC	TAT	AAA	GTT	AAA	GAC	ACT	AAC	GAG	CTT	TTA	686																					
Gly	Gly	Leu	Cys	Tyr	Pro	Tyr	Lys	Val	Lys	Asp	Thr	Asn	Glu	Leu	Leu																						
			190						195			200																									
ACA	AAA	TTT	TTA	TAC	TTT	TAT	CTC	AAA	ACT	AAT	GAA	ATC	CAA	ATT	ATG	734																					
Thr	Lys	Phe	Leu	Tyr	Phe	Tyr	Leu	Lys	Thr	Asn	Glu	Ile	Gln	Ile	Met																						
			205			210			215																												
GAG	AAC	CTT	GTT	TTT	CGT	GGC	AGT	ATC	CCC	GCA	CTC	AAT	AAA	GCA	GAT	782																					
Glu	Asn	Leu	Val	Phe	Arg	Gly	Ser	Ile	Pro	Ala	Leu	Asn	Lys	Ala	Asp																						
			220			225			230			235																									

Arg Gly Ser Ile Pro Ala Leu Asn Lys Ala Asp Ile Glu Thr Leu Thr
 225 230 235 240
 Ile Pro Ile Pro Pro Leu Glu Ile Gln Gln Glu Ile Val Lys Ile Leu
 245 250 255
 Asp Gln Phe Ser Ala Leu Thr Thr Asp Leu Leu Ala Gly Ile Pro Ala
 260 265 270
 Glu Ile Lys Ala Arg Lys Lys Gln Tyr Glu Tyr Tyr Arg Glu Lys Leu
 275 280 285
 Leu Thr Phe Lys Pro Leu Gln Asn Lys Glu
 290 295

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 42...1253
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GATTAGGGGA GTTAGAAACC ATTTGCGTGG AAGAAGATCC C ATG TAT GAA TGC GAA	56
Met Tyr Glu Cys Glu	
1 5	
GTG GCG ATT GAA AAA ATC CTA GAA GAT TTA GGC ATT CCT AGC TCT AAA	104
Val Ala Ile Glu Lys Ile Leu Glu Asp Leu Gly Ile Pro Ser Ser Lys	
10 15 20	
CAC AAC GAT TTG ATG AAA ACC CTG CCA AGC AGC GAT AAA TTT AAA ATC	152
His Asn Asp Leu Met Lys Thr Leu Pro Ser Ser Asp Lys Phe Lys Ile	
25 30 35	
CTT CTC GCT CAA GTC TTG TTC CCT AAA CCG GAT ATT TTG CTT TTA GAT	200
Leu Leu Ala Gln Val Leu Phe Pro Lys Pro Asp Ile Leu Leu Leu Asp	
40 45 50	
GAG CCG ACC AAC AAC CTG GAT TTA AAC GCC ATT GAA TGG CTA GAA AAC	248
Glu Pro Thr Asn Asn Leu Asp Leu Asn Ala Ile Glu Trp Leu Glu Asn	
55 60 65	
AAC CTC AAA CGC CAT GAA GGC ACG ATG GTC GTC ATT AGC CAT GAC AGG	296
Asn Leu Lys Arg His Glu Gly Thr Met Val Val Ile Ser His Asp Arg	
70 75 80 85	
CAT TTT TTA AAT GCG GTA TGC ACG CAT ATT TTG GAT TTG GAT TTC CAC	344
His Phe Leu Asn Ala Val Cys Thr His Ile Leu Asp Leu Asp Phe His	
90 95 100	
AGC GTG CGC GAA TTT AGC GGG AAT TAT GAC GAT TGG TAT ATC GCT TCC	392

Ser	Val	Arg	Glu 105	Phe	Ser	Gly	Asn	Tyr 110	Asp	Asp	Trp	Tyr	Ile 115	Ala	Ser	
ACT Thr	CTG Leu	ATC Ile 120	GCT Ala	AAA Lys	CAG Gln	CAA Gln	GAG Glu 125	GCC Ala	GAA Glu	CGC Arg	AAT Asn	AAA Lys 130	AAA Lys	CTC Leu	AAA Lys	440
GAA Glu	AAA Lys 135	GAA Glu	GAG Glu	CTA Leu	GAA Glu	AAA Lys 140	TTC Phe	ATC Ile	GCG Ala	CGC Arg	TTT Phe 145	ARN Xaa	NNN Xaa	NAC Xaa	GCT Ala	488
TCT Ser 150	AAA Lys	GCC Ala	AAG Lys	CAA Gln 155	GCC Ala	ACC Thr	AGC Ser	CGC Arg	CAA Gln 160	AAA Lys	CAA Gln	CTG Leu	GAT Asp	AAA Lys	TTA Leu 165	536
GAC Asp	ATT Ile	CAA Gln	AGT Ser 170	TTA Leu	GCG Ala	GTA Val	TCT Ser	AGC Ser	AGG Arg 175	AGG Arg	GAT Asp	CCT Pro	AGC Ser 180	ATT Ile	ATT Ile	584
TTT Phe	AAA Lys	CCC Pro 185	AAA Lys	CGC Arg	ACC Thr	ATT Ile	GGT Gly 190	AAT Asn	GAA Glu	GCC Ala	TTA Leu	GAG Glu 195	TGC Cys	GAA Glu	AAC Asn	632
ATC Ile	TCT Ser 200	AAA Lys	AGT Ser	TAT Tyr	GAC Asp	GAC Asp	CAA Gln 205	ATC Ile	GTT Val	TTA Leu	AAT Asn	CAA Gln 210	GTG Val	AGC Ser	TTG Leu	680
AAA Lys 215	GTG Val	ATG Met	CCT Pro	AAA Lys	GAC Asp	AAG Lys 220	ATC Ile	GCC Ala	CTC Leu	ATA Ile	GGG Gly 225	CCA Pro	AAC Asn	GGC Gly	GTG Val	728
GGT Gly 230	AAA Lys	TCC Ser	ACG Thr	CTT Leu	TGT Cys 235	AAA Lys	ATT Ile	CTA Leu	GTA Val	GAA Glu 240	GAA Glu	TTA Leu	AAG Lys	CCG Pro	GAT Asp 245	776
AAG Lys	GGC Gly	GTG Val	GTG Val	AAA Lys 250	TGG Trp	GGG Gly	GCG Ala	ACG Thr	GTT Val 255	TCA Ser	AAA Lys	GGC Gly	TAT Tyr	TTC Phe 260	CCT Pro	824
CAA Gln	AAC Asn	GTG Val 265	AGC Ser	GAA Glu	GAA Glu	ATT Ile	AGC Ser	GGG Gly 270	GAA Glu	GAG Glu	ACC Thr	TTG Leu	TAT Tyr 275	CAA Gln	TGG Trp	872
CTC Leu	TTT Phe 280	AAC Asn	TTC Phe	AAT Asn	AAA Lys	AAG Lys	ATT Ile 285	GAA Glu	AGC Ser	GCT Ala	GAG Glu	GTT Val 290	AGG Arg	AAC Asn	GCT Ala	920
TTA Leu	GGG Gly 295	AGG Arg	ATG Met	CTG Leu	TTT Phe	AAT Asn 300	GGC Gly	GAA Glu	GAG Glu	CAA Gln	GAA Glu 305	AAA Lys	TGC Cys	GTG Val	AAC Asn	968
GCT Ala 310	TTA Leu	AGT Ser	GGG Gly	GGC Gly	GAA Glu 315	AAA Lys	CAC His	CGA Arg	ATG Met	GTT Val 320	TTA Leu	TCC Ser	AAG Lys	CTC Leu	ATG Met 325	1016
CTA Leu	GAG Glu	GGG Gly	GGG Gly	AAT Asn 330	TTT Phe	TTA Leu	GTC Val	TTA Leu 335	GAT Asp	GAG Glu	CCA Pro	ACC Thr	AAC Asn	CAT His 340	TTG Leu	1064

GAT TTA GAA GCG ATT ATC GCT TTA GGC GAA GCG CTC TTT AAA TTT GAT	1112
Asp Leu Glu Ala Ile Ile Ala Leu Gly Glu Ala Leu Phe Lys Phe Asp	
345 350 355	
GGG GCG CTG ATT TGC GTA AGC CAT GAC AGA GAG CTC ATT GAT GCG TAT	1160
Gly Ala Leu Ile Cys Val Ser His Asp Arg Glu Leu Ile Asp Ala Tyr	
360 365 370	
GCT AAT AGG ATC ATT GAA TTA GTC CCA AGC CCT AAA GGC GCT TCA ATC	1208
Ala Asn Arg Ile Ile Glu Leu Val Pro Ser Pro Lys Gly Ala Ser Ile	
375 380 385	
ATT GAT TTT AAA GGC AGT TAT GAA GAG TAT TTG GCG AGC AAA AAA TGAAA	1258
Ile Asp Phe Lys Gly Ser Tyr Glu Glu Tyr Leu Ala Ser Lys Lys	
390 395 400	
CCGCAAGACA TTGAAATCGT TCAAAGCGTT TTAGAGATTA CAGGACC	1305

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met	Tyr	Glu	Cys	Glu	Val	Ala	Ile	Glu	Lys	Ile	Leu	Glu	Asp	Leu	Gly
1				5					10					15	
Ile	Pro	Ser	Ser	Lys	His	Asn	Asp	Leu	Met	Lys	Thr	Leu	Pro	Ser	Ser
			20					25					30		
Asp	Lys	Phe	Lys	Ile	Leu	Leu	Ala	Gln	Val	Leu	Phe	Pro	Lys	Pro	Asp
		35					40					45			
Ile	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	Asn	Leu	Asp	Leu	Asn	Ala	Ile
						55					60				
Glu	Trp	Leu	Glu	Asn	Asn	Leu	Lys	Arg	His	Glu	Gly	Thr	Met	Val	Val
65					70					75				80	
Ile	Ser	His	Asp	Arg	His	Phe	Leu	Asn	Ala	Val	Cys	Thr	His	Ile	Leu
				85					90					95	
Asp	Leu	Asp	Phe	His	Ser	Val	Arg	Glu	Phe	Ser	Gly	Asn	Tyr	Asp	Asp
			100					105					110		
Trp	Tyr	Ile	Ala	Ser	Thr	Leu	Ile	Ala	Lys	Gln	Gln	Glu	Ala	Glu	Arg
		115					120					125			
Asn	Lys	Lys	Leu	Lys	Glu	Lys	Glu	Glu	Leu	Glu	Lys	Phe	Ile	Ala	Arg
		130				135					140				
Phe	Xaa	Xaa	Xaa	Ala	Ser	Lys	Ala	Lys	Gln	Ala	Thr	Ser	Arg	Gln	Lys
145					150					155				160	
Gln	Leu	Asp	Lys	Leu	Asp	Ile	Gln	Ser	Leu	Ala	Val	Ser	Ser	Arg	Arg
				165					170					175	
Asp	Pro	Ser	Ile	Ile	Phe	Lys	Pro	Lys	Arg	Thr	Ile	Gly	Asn	Glu	Ala
			180					185					190		
Leu	Glu	Cys	Glu	Asn	Ile	Ser	Lys	Ser	Tyr	Asp	Asp	Gln	Ile	Val	Leu
		195					200					205			
Asn	Gln	Val	Ser	Leu	Lys	Val	Met	Pro	Lys	Asp	Lys	Ile	Ala	Leu	Ile
		210				215					220				

Gly	Pro	Asn	Gly	Val	Gly	Lys	Ser	Thr	Leu	Cys	Lys	Ile	Leu	Val	Glu
225					230					235					240
Glu	Leu	Lys	Pro	Asp	Lys	Gly	Val	Val	Lys	Trp	Gly	Ala	Thr	Val	Ser
			245						250					255	
Lys	Gly	Tyr	Phe	Pro	Gln	Asn	Val	Ser	Glu	Glu	Ile	Ser	Gly	Glu	Glu
			260					265					270		
Thr	Leu	Tyr	Gln	Trp	Leu	Phe	Asn	Phe	Asn	Lys	Lys	Ile	Glu	Ser	Ala
		275					280					285			
Glu	Val	Arg	Asn	Ala	Leu	Gly	Arg	Met	Leu	Phe	Asn	Gly	Glu	Glu	Gln
	290					295					300				
Glu	Lys	Cys	Val	Asn	Ala	Leu	Ser	Gly	Gly	Glu	Lys	His	Arg	Met	Val
305					310					315					320
Leu	Ser	Lys	Leu	Met	Leu	Glu	Gly	Gly	Asn	Phe	Leu	Val	Leu	Asp	Glu
			325						330					335	
Pro	Thr	Asn	His	Leu	Asp	Leu	Glu	Ala	Ile	Ile	Ala	Leu	Gly	Glu	Ala
			340					345					350		
Leu	Phe	Lys	Phe	Asp	Gly	Ala	Leu	Ile	Cys	Val	Ser	His	Asp	Arg	Glu
		355					360					365			
Leu	Ile	Asp	Ala	Tyr	Ala	Asn	Arg	Ile	Ile	Glu	Leu	Val	Pro	Ser	Pro
	370					375					380				
Lys	Gly	Ala	Ser	Ile	Ile	Asp	Phe	Lys	Gly	Ser	Tyr	Glu	Glu	Tyr	Leu
385					390					395					400
Ala	Ser	Lys	Lys												

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...756
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AAAAGCAGGG	ATACTAGA	ATG	CAA	ATG	ATG	CAC	AAT	TTG	AGT	TTT	TTG	GGC				
		Met	Gln	Met	Met	His	Asn	Leu	Ser	Phe	Leu	Gly	51			
		1				5					10					
ATG	TTT	TTA	GCC	GCT	TTG	AGC	ATG	TCT	TTA	GGG	CAT	TGT	GTG	GGC	ATG	99
Met	Phe	Leu	Ala	Ala	Leu	Ser	Met	Ser	Leu	Gly	His	Cys	Val	Gly	Met	
			15					20				25				
TGT	GGG	GGG	ATT	GTG	AGC	GCG	TTC	AGT	CAA	ATA	AGA	TTT	TCT	AAA	GTT	147
Cys	Gly	Gly	Ile	Val	Ser	Ala	Phe	Ser	Gln	Ile	Arg	Phe	Ser	Lys	Val	
		30					35					40				
ACA	AGC	TTT	TCT	TAC	CAG	CTC	ACT	TGC	CAT	GCC	CTT	TAT	AAT	GTA	GGG	195
Thr	Ser	Phe	Ser	Tyr	Gln	Leu	Thr	Cys	His	Ala	Leu	Tyr	Asn	Val	Gly	
	45					50					55					

AGG ATC AGC ACT TAC ATG CTT TTA GGG GCT ATA GCG GCA AGT TTG GGG	243
Arg Ile Ser Thr Tyr Met Leu Leu Gly Ala Ile Ala Ala Ser Leu Gly	
60 65 70 75	
CAT AGT CTT AGC GTG AGC ATG GGT TTT AGG GGT GTT TTA TTC ATT AGC	291
His Ser Leu Ser Val Ser Met Gly Phe Arg Gly Val Leu Phe Ile Ser	
80 85 90	
ATG GGG ATT ATT TTG ATC TGT TTA GCG TTG CTA GGG GCA AGA ATG GAA	339
Met Gly Ile Ile Leu Ile Cys Leu Ala Leu Leu Gly Ala Arg Met Glu	
95 100 105	
AAA TTA AGC TTT CAA ATC CCT TTT ATT TCT TTT TTG ATG AAA AAA ACC	387
Lys Leu Ser Phe Gln Ile Pro Phe Ile Ser Phe Leu Met Lys Lys Thr	
110 115 120	
TTG CAA TCT CAA AAC ATT CTA GGG CTG TAT TTC TTA GGC GTG TTG AAC	435
Leu Gln Ser Gln Asn Ile Leu Gly Leu Tyr Phe Leu Gly Val Leu Asn	
125 130 135	
GGG TTT TTA CCT TGC ATG ATG GTG TAT TCG TTT TTA GCG AGC GTG ATT	483
Gly Phe Leu Pro Cys Met Met Val Tyr Ser Phe Leu Ala Ser Val Ile	
140 145 150 155	
CTC AGT CAT AGC GCG TTT ATG GGA GCG ATG CTA GGC CTT TCT TTT GGG	531
Leu Ser His Ser Ala Phe Met Gly Ala Met Leu Gly Leu Ser Phe Gly	
160 165 170	
CTT GGC ACC AGC ATG CCG TTG TTT TTA ATG GGG ATT TTT TTA AGC AAA	579
Leu Gly Thr Ser Met Pro Leu Phe Leu Met Gly Ile Phe Leu Ser Lys	
175 180 185	
ATT TCC GTT TCT TAC AGG AAA TTT TTC AAT CTT TTG TCT AAA ATT TTA	627
Ile Ser Val Ser Tyr Arg Lys Phe Phe Asn Leu Leu Ser Lys Ile Leu	
190 195 200	
ATG GGG GTT TTT GGG CTT TAT ATC CTT TAT ATG GGG ATC ATG CTC ATT	675
Met Gly Val Phe Gly Leu Tyr Ile Leu Tyr Met Gly Ile Met Leu Ile	
205 210 215	
AAC CAC AAA ATG CCT CAT GCC ATG CAT CAT CAA AAC AAC ACC ACT CAG	723
Asn His Lys Met Pro His Ala Met His His Gln Asn Asn Thr Thr Gln	
220 225 230 235	
CAT GAT CAT AAA GGA GTG CAT TCG CAT GAA CAC TAACAAAGCC CTTTTTTTGG	776
His Asp His Lys Gly Val His Ser His Glu His	
240 245	
ACAGAGACGG CATTATCAAT ATTGA	801

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Gln Met Met His Asn Leu Ser Phe Leu Gly Met Phe Leu Ala Ala
1 5 10 15
Leu Ser Met Ser Leu Gly His Cys Val Gly Met Cys Gly Gly Ile Val
20 25 30
Ser Ala Phe Ser Gln Ile Arg Phe Ser Lys Val Thr Ser Phe Ser Tyr
35 40 45
Gln Leu Thr Cys His Ala Leu Tyr Asn Val Gly Arg Ile Ser Thr Tyr
50 55 60
Met Leu Leu Gly Ala Ile Ala Ala Ser Leu Gly His Ser Leu Ser Val
65 70 75 80
Ser Met Gly Phe Arg Gly Val Leu Phe Ile Ser Met Gly Ile Ile Leu
85 90 95
Ile Cys Leu Ala Leu Leu Gly Ala Arg Met Glu Lys Leu Ser Phe Gln
100 105 110
Ile Pro Phe Ile Ser Phe Leu Met Lys Lys Thr Leu Gln Ser Gln Asn
115 120 125
Ile Leu Gly Leu Tyr Phe Leu Gly Val Leu Asn Gly Phe Leu Pro Cys
130 135 140
Met Met Val Tyr Ser Phe Leu Ala Ser Val Ile Leu Ser His Ser Ala
145 150 155 160
Phe Met Gly Ala Met Leu Gly Leu Ser Phe Gly Leu Gly Thr Ser Met
165 170 175
Pro Leu Phe Leu Met Gly Ile Phe Leu Ser Lys Ile Ser Val Ser Tyr
180 185 190
Arg Lys Phe Phe Asn Leu Leu Ser Lys Ile Leu Met Gly Val Phe Gly
195 200 205
Leu Tyr Ile Leu Tyr Met Gly Ile Met Leu Ile Asn His Lys Met Pro
210 215 220
His Ala Met His His Gln Asn Asn Thr Thr Gln His Asp His Lys Gly
225 230 235 240
Val His Ser His Glu His
245

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...693
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AAC TGC CTN TCN TCG CTC AAC ACG ATT GTA TTA AAC CAT AAT AAA TTG
Asn Cys Xaa Xaa Ser Leu Asn Thr Ile Val Leu Asn His Asn Lys Leu
1 5 10 15

48

[illegible]

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Asn	Cys	Xaa	Xaa	Ser	Leu	Asn	Thr	Ile	Val	Leu	Asn	His	Asn	Lys	Leu
1				5					10					15	
Tyr	Ser	Leu	Glu	Lys	Arg	Gly	Tyr	Val	Ile	Glu	Val	Asp	Leu	Asn	Asp
			20					25					30		
Phe	Asp	Ser	Tyr	Asn	Val	Tyr	Lys	Thr	Pro	Thr	Ile	Gly	Ser	Phe	Lys
		35					40					45			
Phe	Phe	Ser	Ser	Asn	Arg	Leu	Asp	Lys	Gly	Val	Phe	Tyr	Asp	Lys	Asn
	50					55				60					
Arg	Val	Tyr	Tyr	Asp	Arg	Tyr	Tyr	Leu	Asp	Tyr	Asn	Asp	Phe	Lys	Pro
65					70				75						80
Lys	Leu	Tyr	Pro	Val	Glu	Lys	Ser	Ala	Ser	Lys	Lys	Ser	Gln	Lys	
				85				90					95		
Gly	Glu	Lys	Gly	Asn	Ala	Pro	Ile	Tyr	Leu	Gln	Glu	Arg	His	Lys	Ala
			100					105					110		
Lys	Glu	Asn	Lys	Gln	Pro	Leu	Glu	Glu	Asn	Lys	Val	Lys	Pro	Arg	Asn
		115					120					125			
Ser	Gly	Phe	Glu	Glu	Glu	Glu	Val	Lys	Thr	Arg	Arg	Pro	Glu	Pro	Ile
	130						135					140			
Arg	Asp	Gln	Asn	Asn	Ala	Thr	Gln	Gln	Gly	Glu	Thr	Lys	Asn	Asn	Glu
145					150					155					160
Ser	Lys	Asn	Ala	Pro	Val	Leu	Lys	Glu	Asn	Ala	Ala	Lys	Lys	Glu	Val
				165					170					175	
Pro	Lys	Pro	Asn	Ser	Lys	Glu	Glu	Lys	Arg	Arg	Leu	Lys	Glu	Glu	Lys
			180					185					190		
Lys	Lys	Ala	Lys	Ala	Glu	Gln	Arg	Ala	Arg	Glu	Phe	Glu	Gln	Arg	Ala
		195					200					205			
Arg	Glu	His	Gln	Glu	Arg	Asp	Glu	Lys	Glu	Leu	Glu	Glu	Arg	Arg	Lys
	210					215					220				
Ala	Leu	Glu	Met	Asn	Lys	Lys									
225					230										

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1005
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

AGAAAGAAAC CATTCAAGGA ACGCATTGAT TTG ATG AAT AAA CCA TTT TTA ATC	54
Met Asn Lys Pro Phe Leu Ile	
1 5	
TTA CTC ATA GCC CTA ATT GTC TTT AGC GGC TGT AAC ATG AGA AAA TAT	102
Leu Leu Ile Ala Leu Ile Val Phe Ser Gly Cys Asn Met Arg Lys Tyr	
10 15 20	
TTC AAA CCC GCT AAA CAC CAA ATT AAA GGC GAA GCG TAT TTC CCT AAC	150
Phe Lys Pro Ala Lys His Gln Ile Lys Gly Glu Ala Tyr Phe Pro Asn	
25 30 35	
CAT TTG CAA GAA AGT ATC GTT TCG TCT AAT CGT TAT GGA GCC ATT TTG	198
His Leu Gln Glu Ser Ile Val Ser Ser Asn Arg Tyr Gly Ala Ile Leu	
40 45 50 55	
AAA AAT GGA GCG GTT ATA GGC GAT AAA GGT TTA ACG CAG CTA AGA ATC	246
Lys Asn Gly Ala Val Ile Gly Asp Lys Gly Leu Thr Gln Leu Arg Ile	
60 65 70	
GGT AAG AAC TTC AAT TAC GAA AGC AGT TTT TTA AAT GAG AGT CAA GGG	294
Gly Lys Asn Phe Asn Tyr Glu Ser Ser Phe Leu Asn Glu Ser Gln Gly	
75 80 85	
TTT TTT ATT CTT GCG CAA GAT TGT TTG AAC AAG ATT GAT AAA AAA ACA	342
Phe Phe Ile Leu Ala Gln Asp Cys Leu Asn Lys Ile Asp Lys Lys Thr	
90 95 100	
AAC AAA AGC AAG GTG GCT AAG ACT GAA GAA ACG GAA TTG AAA TTA AAG	390
Asn Lys Ser Lys Val Ala Lys Thr Glu Glu Thr Glu Leu Lys Leu Lys	
105 110 115	
GGC GTT GAA GCG GAA GTC CAA GAT AAA GTC TGT CAT CAA GTG GAA TTG	438
Gly Val Glu Ala Glu Val Gln Asp Lys Val Cys His Gln Val Glu Leu	
120 125 130 135	
ATT AGC AAT AAC CCT AAC GCC AGC CAA CAA TCT ATC GTT ATT CCT TTG	486
Ile Ser Asn Asn Pro Asn Ala Ser Gln Gln Ser Ile Val Ile Pro Leu	
140 145 150	
GAG ACT TTT GCC TTG AGC GCA AGC GTT AAA GGG AAT CTT TTA GCG GTG	534
Glu Thr Phe Ala Leu Ser Ala Ser Val Lys Gly Asn Leu Leu Ala Val	
155 160 165	
GTG TTA GCG GAC AAT TCA GCG AAC TTA TAC GAC ATC ACT TCT CAA AAA	582
Val Leu Ala Asp Asn Ser Ala Asn Leu Tyr Asp Ile Thr Ser Gln Lys	
170 175 180	
TTG CTT TTT AGT GAG AAA GGT TCC CCA AGC ACC ACG ATC AAT TCT TTA	630
Leu Leu Phe Ser Glu Lys Gly Ser Pro Ser Thr Thr Ile Asn Ser Leu	
185 190 195	
ATG GCG ATG CCT ATT TTT ATG GAT ACG GTC GTG GTG TTC CCC ATG CTA	678
Met Ala Met Pro Ile Phe Met Asp Thr Val Val Val Phe Pro Met Leu	
200 205 210 215	

Val	Ser	Ala	Phe	Glu	Thr	Phe	Arg	Glu	Glu	Ser	Leu	Val	Cys	Lys	Asp	
45					50					55					60	
GCT	ATT	TTA	GAC	ATT	GTA	GAT	GAA	AAG	GTT	GAA	TTA	GAA	TGC	AAG	GAT	243
Ala	Ile	Leu	Asp	Ile	Val	Asp	Glu	Lys	Val	Glu	Leu	Glu	Cys	Lys	Asp	
			65						70					75		
TGT	TCG	CAT	GTT	TTT	AAG	CCT	AAC	GCG	CTA	GAT	TAT	GGG	GTG	TGT	GAG	291
Cys	Ser	His	Val	Phe	Lys	Pro	Asn	Ala	Leu	Asp	Tyr	Gly	Val	Cys	Glu	
			80					85					90			
AAA	TGC	CAC	AGC	AAG	AAT	GTT	ATT	ATC	ACT	CAA	GGC	AAT	GAA	ATG	CGT	339
Lys	Cys	His	Ser	Lys	Asn	Val	Ile	Ile	Thr	Gln	Gly	Asn	Glu	Met	Arg	
			95					100					105			
TTG	TTG	TCT	TTA	GAA	ATG	TTA	GCG	GAA	TAACCGATGC	AAGAAGAATT	GAACGCT					393
Leu	Leu	Ser	Leu	Glu	Met	Leu	Ala	Glu								
			110					115								
TACCAGCAAG	AAATTGA															410

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met	His	Glu	Tyr	Ser	Val	Val	Ser	Ser	Leu	Ile	Ala	Leu	Cys	Glu	Glu	
1				5					10					15		
His	Ala	Lys	Lys	Asn	Gln	Ala	His	Lys	Ile	Glu	Arg	Val	Val	Val	Gly	
			20					25					30			
Ile	Gly	Glu	Arg	Ser	Ala	Met	Asp	Lys	Ser	Leu	Phe	Val	Ser	Ala	Phe	
		35					40					45				
Glu	Thr	Phe	Arg	Glu	Glu	Ser	Leu	Val	Cys	Lys	Asp	Ala	Ile	Leu	Asp	
	50					55					60					
Ile	Val	Asp	Glu	Lys	Val	Glu	Leu	Glu	Cys	Lys	Asp	Cys	Ser	His	Val	
65					70					75					80	
Phe	Lys	Pro	Asn	Ala	Leu	Asp	Tyr	Gly	Val	Cys	Glu	Lys	Cys	His	Ser	
			85					90						95		
Lys	Asn	Val	Ile	Ile	Thr	Gln	Gly	Asn	Glu	Met	Arg	Leu	Leu	Ser	Leu	
			100					105					110			
Glu	Met	Leu	Ala	Glu												
				115												

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 38...769
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TTGCAAAAAC TCTCATTA AAA ACAAGGAGC AAAAAAG ATG AAA AAG GCG GGC TTT	55
Met Lys Lys Ala Gly Phe	
1 5	
CTT TTT TTA GCG GTA ATG GCT ATC GTT GTT ATG AGT TTA AAC GCT AAA	103
Leu Phe Leu Ala Val Met Ala Ile Val Val Met Ser Leu Asn Ala Lys	
10 15 20	
GAT CCG AAT GTG TTG CGT AAG ATT GTT TTT GAG AAA TGT CTG CCT AAT	151
Asp Pro Asn Val Leu Arg Lys Ile Val Phe Glu Lys Cys Leu Pro Asn	
25 30 35	
TAT GAG AAA AAT CAG AAT CCT TCG CCA TGC ATA GAA GTC AAA CCC GAT	199
Tyr Glu Lys Asn Gln Asn Pro Ser Pro Cys Ile Glu Val Lys Pro Asp	
40 45 50	
GCC GGC TAT GTG GTT TTA AAA GAT ATT AAC GGC CCG TTG CAA TAT TTG	247
Ala Gly Tyr Val Val Leu Lys Asp Ile Asn Gly Pro Leu Gln Tyr Leu	
55 60 65 70	
TTG ATG CCA ACA ACT CAC ATT AGC GGT ATT GAA AGC CCT TTG TTA CTT	295
Leu Met Pro Thr Thr His Ile Ser Gly Ile Glu Ser Pro Leu Leu Leu	
75 80 85	
GAT CCT TCT ACG CCT AAC TTT TTT TAT TTA TCC TGG CAA GCG CGT GAT	343
Asp Pro Ser Thr Pro Asn Phe Phe Tyr Leu Ser Trp Gln Ala Arg Asp	
90 95 100	
TTT ATG AGT AAA AAA TAC GGC CAA CCC ATT CCT GAT TAT GCG ATT TCT	391
Phe Met Ser Lys Lys Tyr Gly Gln Pro Ile Pro Asp Tyr Ala Ile Ser	
105 110 115	
TTG ACG ATT AAC TCT AGC AAA GGG CGA TCG CAA AAC CAT TTT CAT ATC	439
Leu Thr Ile Asn Ser Ser Lys Gly Arg Ser Gln Asn His Phe His Ile	
120 125 130	
CAT ATC TCT TGC ATT AGT CTT GAA GCA CGC AAA CAG CTG GAT AAT AAC	487
His Ile Ser Cys Ile Ser Leu Glu Ala Arg Lys Gln Leu Asp Asn Asn	
135 140 145 150	
CTA AAA AAA ATC AAC AGC CGT TGG TCG CCA TTA CCG GGC GGT TTG AAT	535
Leu Lys Lys Ile Asn Ser Arg Trp Ser Pro Leu Pro Gly Gly Leu Asn	
155 160 165	
GGG CAT AAA TAC TTG GCG CGT CGG GTA ACA GAG AGC GAG TTA GTG CAA	583
Gly His Lys Tyr Leu Ala Arg Arg Val Thr Glu Ser Glu Leu Val Gln	
170 175 180	

AAA AGC CCG TTT GTC ATG CTT AAT AAA GAA GTG CCT AAT GCG TAC AAA	631
Lys Ser Pro Phe Val Met Leu Asn Lys Glu Val Pro Asn Ala Tyr Lys	
185 190 195	
CGC ATG GGG GAC TAT GGC TTA GCG GTG GTG CAA CAA AGC GAT AAC TCC	679
Arg Met Gly Asp Tyr Gly Leu Ala Val Val Gln Gln Ser Asp Asn Ser	
200 205 210	
TTT GTC TTA TTA GCG ACA CAA TTT AAC CCA TTG ACT TTA AAT CGC GCT	727
Phe Val Leu Leu Ala Thr Gln Phe Asn Pro Leu Thr Leu Asn Arg Ala	
215 220 225 230	
TCA GCC GAA GAG ATT CAA GAT CAT GAA TGC GCG ATT TTG CAC TAAAGCGAG	778
Ser Ala Glu Glu Ile Gln Asp His Glu Cys Ala Ile Leu His	
235 240	
TTAGATTCTT AAGCTTGAGC GATAACCTTT AAAAAGCGTT ATGGGGTGGT GTTGCAAAAC	838
CC	840

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met	Lys	Lys	Ala	Gly	Phe	Leu	Phe	Leu	Ala	Val	Met	Ala	Ile	Val	Val
1				5				10					15		
Met	Ser	Leu	Asn	Ala	Lys	Asp	Pro	Asn	Val	Leu	Arg	Lys	Ile	Val	Phe
			20					25					30		
Glu	Lys	Cys	Leu	Pro	Asn	Tyr	Glu	Lys	Asn	Gln	Asn	Pro	Ser	Pro	Cys
		35					40					45			
Ile	Glu	Val	Lys	Pro	Asp	Ala	Gly	Tyr	Val	Val	Leu	Lys	Asp	Ile	Asn
	50					55					60				
Gly	Pro	Leu	Gln	Tyr	Leu	Leu	Met	Pro	Thr	Thr	His	Ile	Ser	Gly	Ile
65					70					75					80
Glu	Ser	Pro	Leu	Leu	Leu	Asp	Pro	Ser	Thr	Pro	Asn	Phe	Phe	Tyr	Leu
			85						90					95	
Ser	Trp	Gln	Ala	Arg	Asp	Phe	Met	Ser	Lys	Lys	Tyr	Gly	Gln	Pro	Ile
			100					105					110		
Pro	Asp	Tyr	Ala	Ile	Ser	Leu	Thr	Ile	Asn	Ser	Ser	Lys	Gly	Arg	Ser
		115					120					125			
Gln	Asn	His	Phe	His	Ile	His	Ile	Ser	Cys	Ile	Ser	Leu	Glu	Ala	Arg
	130					135					140				
Lys	Gln	Leu	Asp	Asn	Asn	Leu	Lys	Lys	Ile	Asn	Ser	Arg	Trp	Ser	Pro
145					150				155						160
Leu	Pro	Gly	Gly	Leu	Asn	Gly	His	Lys	Tyr	Leu	Ala	Arg	Arg	Val	Thr
			165						170					175	
Glu	Ser	Glu	Leu	Val	Gln	Lys	Ser	Pro	Phe	Val	Met	Leu	Asn	Lys	Glu
			180					185					190		
Val	Pro	Asn	Ala	Tyr	Lys	Arg	Met	Gly	Asp	Tyr	Gly	Leu	Ala	Val	Val
		195					200					205			
Gln	Gln	Ser	Asp	Asn	Ser	Phe	Val	Leu	Leu	Ala	Thr	Gln	Phe	Asn	Pro

210	215	220
Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His Glu Cys		
225	230	235
Ala Ile Leu His		240

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...441
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

ATATTGAAAG ATAATCAAAA A ATG AAG ACA AGC GCT AAA GTA TTA TTG ACT	51
Met Lys Thr Ser Ala Lys Val Leu Leu Thr	
1 5 10	
TTA TTG ATT GTA ATA TCA TTA GGT AAG GGA TTA AAT AGT CTC ATA TCA	99
Leu Leu Ile Val Ile Ser Leu Gly Lys Gly Leu Asn Ser Leu Ile Ser	
15 20 25	
GCT TGG CGT GGC AAA GAT GAT GCG ATC CCC ATT GAA ACA AGA CTC CAT	147
Ala Trp Arg Gly Lys Asp Asp Ala Ile Pro Ile Glu Thr Arg Leu His	
30 35 40	
AAA AAC AAA CTG ACA ATC ATT TCT AAA ACA GAC AGC ATA GAA ATC CAA	195
Lys Asn Lys Leu Thr Ile Ile Ser Lys Thr Asp Ser Ile Glu Ile Gln	
45 50 55	
GAC ATT CAG TTT AAT AGA GAG AAT TGT TCT CAC ACT TAT ACT AGT AAG	243
Asp Ile Gln Phe Asn Arg Glu Asn Cys Ser His Thr Tyr Thr Ser Lys	
60 65 70	
GAT TTG GAA AAA ATT CAA AAA GAT TTA GAA GAG CTT GAA GAA GGA GTG	291
Asp Leu Glu Lys Ile Gln Lys Asp Leu Glu Glu Leu Glu Glu Gly Val	
75 80 85 90	
CCT GAA TTG TTC GAG GAG CTT GAG CGT GAT GAA GAG TCC ATC GCT AAA	339
Pro Glu Leu Phe Glu Glu Leu Glu Arg Asp Glu Glu Ser Ile Ala Lys	
95 100 105	
AAT AAA AAA ACG ATC CAA GAG TAT CAA AAT AAA ATT GCT AAT TTT CAA	387
Asn Lys Lys Thr Ile Gln Glu Tyr Gln Asn Lys Ile Ala Asn Phe Gln	
110 115 120	
AAA TAC TAT AAA GAT ATA AAA GAT ATT GAC GAT TAT TCG GCG TTA ATG	435
Lys Tyr Tyr Lys Asp Ile Lys Asp Ile Asp Asp Tyr Ser Ala Leu Met	

5

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

Leu	Lys	Lys	Ile	Phe	Leu	Thr	Asn	Ser	Leu	Gly	Ile	Leu	Cys	Ser
			5					10					15	
Leu	Phe	Gly	Phe	Leu	Arg	Asp	Leu	Met	Met	Ala	Asn	Ile	Leu	Gly
		20					25					30		
Leu	Val	Tyr	Ser	Asp	Ile	Phe	Val	Ala	Phe	Lys	Leu	Pro	Asn	
		35				40				45				

Leu Phe Arg Arg Ile Phe Ala Glu Gly Ser Phe Ser Gln Ser Phe Leu
 50 55 60
 Pro Ser Phe Ile Arg Ser Ser Ile Lys Gly Ser Phe Ala Ser Leu Val
 65 70 75 80
 Gly Leu Ile Phe Cys Ile Val Leu Phe Met Trp Cys Leu Leu Val Ala
 85 90 95
 Leu Asn Pro Leu Trp Leu Ala Lys Leu Leu Ala Tyr Gly Phe Asp Glu
 100 105 110
 Glu Thr Leu Lys Leu Cys Ala Pro Ile Val Ala Ile Asn Phe Trp Xaa
 115 120 125
 Leu Leu Leu Val Phe Ile Thr Thr Phe Leu Gly Ala Leu Leu Gln Xaa
 130 135 140
 Gln Thr Gln Leu Phe Cys Gln Arg Leu
 145 150

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...1016
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TTCTTTGTTC AGATTAAATCG TTCTTAAAAG GAAGCGTG ATG CTT AAA ACC TAT CAT	56
Met Leu Lys Thr Tyr His	
1 5	
ATC GCC TTA GCT TGC GTG ATT TTA GCG GTG GTG GTG CTG TTG TTT GGA	104
Ile Ala Leu Ala Cys Val Ile Leu Ala Val Val Val Leu Leu Phe Gly	
10 15 20	
GGG GAG TCC TTG AGC TTG GAA GAA TGG CAA GAA GTG TGC CTT AAT GTG	152
Gly Glu Ser Leu Ser Leu Glu Glu Trp Gln Glu Val Cys Leu Asn Val	
25 30 35	
AAA AAC CAC TTT TTG CAC AAT GAA GAA CTG AGC TCT TTA AGT ATT ATT	200
Lys Asn His Phe Leu His Asn Glu Glu Leu Ser Ser Leu Ser Ile Ile	
40 45 50	
ATT TTA GAA ATA CGA CTA CCA CGA GTG ATT TTA GCG CTC CTG GTG GGA	248
Ile Leu Glu Ile Arg Leu Pro Arg Val Ile Leu Ala Leu Leu Val Gly	
55 60 65 70	
GCG AGT TTG TCT GGG AGT GGG GTG GTG ATG CAA ACG ATT TTT AGA AAC	296
Ala Ser Leu Ser Gly Ser Gly Val Val Met Gln Thr Ile Phe Arg Asn	
75 80 85	
CCC TTA GTG GAT CCC TTT TTA CTA GGG ATT TCT AGC GGG GCG ATG CTA	344

Pro	Leu	Val	Asp	Pro	Phe	Leu	Leu	Gly	Ile	Ser	Ser	Gly	Ala	Met	Leu	
			90					95				100				
GGC	GTG	GCG	ATG	GCG	ATA	GCG	GTA	GTG	GAG	TCT	AAC	ATT	GCG	ATT	TTG	392
Gly	Val	Ala	Met	Ala	Ile	Ala	Val	Val	Glu	Ser	Asn	Ile	Ala	Ile	Leu	
			105				110				115					
GCG	TTT	TTT	GGG	GCG	ATT	TTA	GCT	AGC	CTT	GCT	GTT	TTG	GCG	ATG	AAT	440
Ala	Phe	Phe	Gly	Ala	Ile	Leu	Ala	Ser	Leu	Ala	Val	Leu	Ala	Met	Asn	
			120				125				130					
AGG	GTT	TTG	GGT	AAT	TCC	GTC	CTT	TCG	TTG	GTG	CTT	TCA	GGG	GTG	GTG	488
Arg	Val	Leu	Gly	Asn	Ser	Val	Leu	Ser	Leu	Val	Leu	Ser	Gly	Val	Val	
			135				140				145				150	
TTG	AGC	GCG	TTT	TTA	AGC	GCC	TTA	GCC	GGA	GCG	ATA	AAA	TTC	TTT	GTG	536
Leu	Ser	Ala	Phe	Leu	Ser	Ala	Leu	Ala	Gly	Ala	Ile	Lys	Phe	Phe	Val	
			155				160				165					
ATC	CCC	CAA	AAA	GCG	CAA	GCG	ATT	GTC	GTG	TGG	CTT	TTA	GGG	AGC	TTG	584
Ile	Pro	Gln	Lys	Ala	Gln	Ala	Ile	Val	Val	Trp	Leu	Leu	Gly	Ser	Leu	
			170				175				180					
TCG	TTG	AGC	AGT	TAT	AAG	GAT	TGC	TTG	ATC	GCT	TTC	ATA	GGG	CTA	TCT	632
Ser	Leu	Ser	Ser	Tyr	Lys	Asp	Cys	Leu	Ile	Ala	Phe	Ile	Gly	Leu	Ser	
			185				190				195					
TTA	GGC	TTT	ATC	CCG	CTT	TTT	TTG	TTA	AGG	TGG	CGC	ATC	AAT	TTA	TTG	680
Leu	Gly	Phe	Ile	Pro	Leu	Phe	Leu	Leu	Arg	Trp	Arg	Ile	Asn	Leu	Leu	
			200				205				210					
AGC	TTG	AGC	GAT	GCG	CAA	AGT	TTG	AGC	TTG	GGG	ATT	AAC	CCG	GTG	CTG	728
Ser	Leu	Ser	Asp	Ala	Gln	Ser	Leu	Ser	Leu	Gly	Ile	Asn	Pro	Val	Leu	
			215				220				225				230	
TTG	CGA	TCG	CTT	TGT	TTG	GTG	TGC	GTG	AGC	GTT	GCG	AGC	GCT	TTA	GCG	776
Leu	Arg	Ser	Leu	Cys	Leu	Val	Cys	Val	Ser	Val	Ala	Ser	Ala	Leu	Ala	
			235				240				245					
GTG	AGC	GTG	TCC	GGC	ACG	ATT	GGC	TGG	ATT	GGG	TTA	GTC	ATT	CCG	CAT	824
Val	Ser	Val	Ser	Gly	Thr	Ile	Gly	Trp	Ile	Gly	Leu	Val	Ile	Pro	His	
			250				255				260					
GTG	GCT	AGG	TTG	TTT	TTT	GGG	GCG	AAT	TTG	CAA	AAA	CTG	CTT	TTA	AGT	872
Val	Ala	Arg	Leu	Phe	Phe	Gly	Ala	Asn	Leu	Gln	Lys	Leu	Leu	Leu	Ser	
			265				270				275					
TCT	TTG	TTA	ATG	GGA	GCG	TTT	TTC	TTG	CTT	CTA	GCG	GAT	GTG	GTG	GCT	920
Ser	Leu	Leu	Met	Gly	Ala	Phe	Phe	Leu	Leu	Leu	Ala	Asp	Val	Val	Ala	
			280				285				290					
AAA	ACC	ATT	ACC	CCC	TAT	GAT	TTA	CCG	GTA	GGC	ATT	GCG	ACA	AGC	GTT	968
Lys	Thr	Ile	Thr	Pro	Tyr	Asp	Leu	Pro	Val	Gly	Ile	Ala	Thr	Ser	Val	
			295				300				305				310	
TTA	GGA	GCG	CCT	TTC	TTC	TTG	TGG	CTT	TTG	TTT	AGA	ACT	AGG	GGG	GTG	T
Leu	Gly	Ala	Pro	Phe	Phe	Leu	Trp</									

GATGGTTTTA GAAGTTAAAA ACCTGTCCTT TAAATATTCT CAAAAACTCA TTTTGGATAA
ATT

1077
1080

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Met	Leu	Lys	Thr	Tyr	His	Ile	Ala	Leu	Ala	Cys	Val	Ile	Leu	Ala	Val
1				5					10					15	
Val	Val	Leu	Leu	Phe	Gly	Gly	Glu	Ser	Leu	Ser	Leu	Glu	Glu	Trp	Gln
			20					25					30		
Glu	Val	Cys	Leu	Asn	Val	Lys	Asn	His	Phe	Leu	His	Asn	Glu	Glu	Leu
		35				40						45			
Ser	Ser	Leu	Ser	Ile	Ile	Ile	Leu	Glu	Ile	Arg	Leu	Pro	Arg	Val	Ile
	50					55					60				
Leu	Ala	Leu	Leu	Val	Gly	Ala	Ser	Leu	Ser	Gly	Ser	Gly	Val	Val	Met
65					70					75					80
Gln	Thr	Ile	Phe	Arg	Asn	Pro	Leu	Val	Asp	Pro	Phe	Leu	Leu	Gly	Ile
				85					90					95	
Ser	Ser	Gly	Ala	Met	Leu	Gly	Val	Ala	Met	Ala	Ile	Ala	Val	Val	Glu
			100					105					110		
Ser	Asn	Ile	Ala	Ile	Leu	Ala	Phe	Phe	Gly	Ala	Ile	Leu	Ala	Ser	Leu
		115					120					125			
Ala	Val	Leu	Ala	Met	Asn	Arg	Val	Leu	Gly	Asn	Ser	Val	Leu	Ser	Leu
		130				135					140				
Val	Leu	Ser	Gly	Val	Val	Leu	Ser	Ala	Phe	Leu	Ser	Ala	Leu	Ala	Gly
145					150					155					160
Ala	Ile	Lys	Phe	Phe	Val	Ile	Pro	Gln	Lys	Ala	Gln	Ala	Ile	Val	Val
				165					170					175	
Trp	Leu	Leu	Gly	Ser	Leu	Ser	Leu	Ser	Ser	Tyr	Lys	Asp	Cys	Leu	Ile
			180					185					190		
Ala	Phe	Ile	Gly	Leu	Ser	Leu	Gly	Phe	Ile	Pro	Leu	Phe	Leu	Leu	Arg
		195					200					205			
Trp	Arg	Ile	Asn	Leu	Leu	Ser	Leu	Ser	Asp	Ala	Gln	Ser	Leu	Ser	Leu
	210					215					220				
Gly	Ile	Asn	Pro	Val	Leu	Leu	Arg	Ser	Leu	Cys	Leu	Val	Cys	Val	Ser
225					230					235					240
Val	Ala	Ser	Ala	Leu	Ala	Val	Ser	Val	Ser	Gly	Thr	Ile	Gly	Trp	Ile
				245						250				255	
Gly	Leu	Val	Ile	Pro	His	Val	Ala	Arg	Leu	Phe	Phe	Gly	Ala	Asn	Leu
			260					265					270		
Gln	Lys	Leu	Leu	Leu	Ser	Ser	Leu	Leu	Met	Gly	Ala	Phe	Phe	Leu	Leu
		275					280					285			
Leu	Ala	Asp	Val	Val	Ala	Lys	Thr	Ile	Thr	Pro	Tyr	Asp	Leu	Pro	Val
		290				295					300				
Gly	Ile	Ala	Thr	Ser	Val	Leu	Gly	Ala	Pro	Phe	Phe	Leu	Trp	Leu	Leu
305					310					315					320
Phe	Arg	Thr	Arg	Gly	Val										
				325											

Variable	Mean	SD	Min	Max
Age	34.5	10.2	22	55
Gender	0.45	0.50	0	1
Marital Status	0.60	0.49	0	1
Education	12.5	1.5	9	16
Income	3500	1500	1000	8000
Health	0.75	0.43	0	1
Smoking	0.30	0.46	0	1
Alcohol	0.20	0.40	0	1
Exercise	0.10	0.30	0	1
Stress	0.50	0.50	0	1
Sleep	0.60	0.49	0	1
Appetite	0.70	0.46	0	1
Mood	0.65	0.48	0	1
Energy	0.70	0.46	0	1
Concentration	0.60	0.49	0	1
Memory	0.65	0.48	0	1
Emotion	0.60	0.49	0	1
Behavior	0.60	0.49	0	1
Thought	0.60	0.49	0	1
Feeling	0.60	0.49	0	1
Perception	0.60	0.49	0	1
Attention	0.60	0.49	0	1
Intuition	0.60	0.49	0	1
Imagination	0.60	0.49	0	1
Reasoning	0.60	0.49	0	1
Logic	0.60	0.49	0	1
Analysis	0.60	0.49	0	1
Synthesis	0.60	0.49	0	1
Evaluation	0.60	0.49	0	1
Comparison	0.60	0.49	0	1
Classification	0.60	0.49	0	1
Organization	0.60	0.49	0	1
Planning	0.60	0.49	0	1
Problem Solving	0.60	0.49	0	1
Decision Making	0.60	0.49	0	1
Communication	0.60	0.49	0	1
Interpersonal Skills	0.60	0.49	0	1
Teamwork	0.60	0.49	0	1
Leadership	0.60	0.49	0	1
Management	0.60	0.49	0	1
Coordination	0.60	0.49	0	1
Organization	0.60	0.49	0	1
Planning	0.60	0.49	0	1
Problem Solving	0.60	0.49	0	1
Decision Making	0.60	0.49	0	1
Communication	0.60	0.49	0	1
Interpersonal Skills	0.60	0.49	0	1
Teamwork	0.60	0.49	0	1
Leadership	0.60	0.49	0	1
Management	0.60	0.49	0	1
Coordination	0.60	0.49	0	1
Organization	0.60	0.49	0	1
Planning	0.60	0.49	0	1
Problem Solving	0.60	0.49	0	1
Decision Making	0.60	0.49	0	1
Communication	0.60	0.49	0	1
Interpersonal Skills	0.60	0.49	0	1
Teamwork	0.60	0.49	0	1
Leadership	0.60	0.49	0	1
Management	0.60	0.49	0	1
Coordination	0.60	0.49	0	1
Organization	0.60	0.49	0	1
Planning	0.60	0.49	0	1
Problem Solving	0.60	0.49	0	1
Decision Making	0.60	0.49	0	1
Communication	0.60	0.49	0	1
Interpersonal Skills	0.60	0.49	0	1
Teamwork	0.60	0.49	0	1
Leadership	0.60	0.49	0	1
Management	0.60	0.49	0	1
Coordination	0.60	0.49	0	1
Organization	0.60	0.49	0	1
Planning	0.60	0.49	0	1
Problem Solving	0.60	0.49	0	1
Decision Making	0.60	0.49	0	1
Communication	0.60	0.49	0	1
Interpersonal Skills	0.60	0.49	0	1
Teamwork	0.60	0.49	0	1
Leadership	0.60	0.49	0	1
Management	0.60	0.49	0	1
Coordination	0.60	0.49	0	1
Organization	0.60	0.49	0	1
Planning	0.60	0.49	0	1

(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION:

[illegible]

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Met Leu Asp Ser Thr Thr Ala Ile Ala Ile Ala Thr Pro Ser Ile Ala
1 5 10 15
Pro Leu Glu Ile Pro Ser Lys Lys Gly Ser Thr Lys Gly Phe Leu Lys
20 25 30
Ile Val Cys Ile Thr Thr Pro Leu Pro Asp Lys Leu Ala Pro Thr Arg
35 40 45
Ser Ala Lys Ile Thr Arg Gly Ser Arg Ile Ser Lys Ile Ile Ile Leu
50 55 60
Lys Glu Leu Ser Ser Ser Leu Cys Lys Lys Trp Phe Phe Thr Leu Arg
65 70 75 80
His Thr Ser Cys His Ser Ser Lys Leu Lys Asp Ser Pro Pro Asn Asn
85 90 95
Ser Thr Thr Thr Ala Lys Ile Thr Gln Ala Lys Ala Ile
100 105

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...662
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

AGGAAAAATG GCTGGGGTGC AAGGATTCGA ACCTCGGA ATG CCA GGA CCA AAA CCT 56
Met Pro Gly Pro Lys Pro
1 5
GGT GCC TTA CCG CTT GGC GAC ACC CCA AAA ACT AAA GAA AGC ATT ATA 104
Gly Ala Leu Pro Leu Gly Asp Thr Pro Lys Thr Lys Glu Ser Ile Ile
10 15 20
CAA AAG CTT TTT AAA AAA GTC AAG CTA AAA CGC TAT AAT TTT ATC ATG 152
Gln Lys Leu Phe Lys Lys Val Lys Leu Lys Arg Tyr Asn Phe Ile Met
25 30 35
GAA AAT GGA TTT GAC CCC ATC ATT TAT AAA CGC TAT TTG AAA AAG AAA 200
Glu Asn Gly Phe Asp Pro Ile Ile Tyr Lys Arg Tyr Leu Lys Lys Lys
40 45 50
GAA ACC TTT TTG CTG TTT AAA AAA ATC GCT CAA GCG TCT GCG TTT AAA 248
Glu Thr Phe Leu Leu Phe Lys Lys Ile Ala Gln Ala Ser Ala Phe Lys
55 60 65 70

AAT TTA AAA CTC CAA CTC AAA CGA AGA GAA ATA ATC AAC CGC TAT GTT	296
Asn Leu Lys Leu Gln Leu Lys Arg Arg Glu Ile Ile Asn Arg Tyr Val	
75 80 85	
TCT CAA GCT TTG GGG GAT TTA AAA AAA GGG TTT AGA TAC GCT AAA GTA	344
Ser Gln Ala Leu Gly Asp Leu Lys Lys Gly Phe Arg Tyr Ala Lys Val	
90 95 100	
GAA CAC CAA ATC CTA AAA ATC TAT TTC ACG CAC CCT AGC TAT TTG AAA	392
Glu His Gln Ile Leu Lys Ile Tyr Phe Thr His Pro Ser Tyr Leu Lys	
105 110 115	
GCC TTT AAA ATA GAA GAA GCC TAT TAC ACC AAC CAC CTG AAA GCC CAT	440
Ala Phe Lys Ile Glu Glu Ala Tyr Tyr Thr Asn His Leu Lys Ala His	
120 125 130	
TTA AAA GAA ACG CAA AAA ACC CTA AAA GCC CTA GAT TAC CCC TTT GAT	488
Leu Lys Glu Thr Gln Lys Thr Leu Lys Ala Leu Asp Tyr Pro Phe Asp	
135 140 145 150	
TTT AAG ACT ATC CAA GCG AGC GTG AAA AAA AGG GCT TAT CAA AAA CCA	536
Phe Lys Thr Ile Gln Ala Ser Val Lys Lys Arg Ala Tyr Gln Lys Pro	
155 160 165	
GTT GTT AAA AAA GAA AAA CCC CCT AAA AGC GTG AAT GTC AAT TGC GAA	584
Val Val Lys Lys Glu Lys Pro Pro Lys Ser Val Asn Val Asn Cys Glu	
170 175 180	
GGT TTG AGC GAT TTC ACT AAA AAG CAA TTT TTA AAG CTC AAA CGC GCT	632
Gly Leu Ser Asp Phe Thr Lys Lys Gln Phe Leu Lys Leu Lys Arg Ala	
185 190 195	
TGT AAC GAT AAT ACG CTG CGC ACG CCC CCT TGAGAGCTGA CCATGCAACT GCC	685
Cys Asn Asp Asn Thr Leu Arg Thr Pro Pro	
200 205	
GATCGGGTTT TCGGGGTGC AAGTTT	711

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Met Pro Gly Pro Lys Pro Gly Ala Leu Pro Leu Gly Asp Thr Pro Lys	
1 5 10 15	
Thr Lys Glu Ser Ile Ile Gln Lys Leu Phe Lys Lys Val Lys Leu Lys	
20 25 30	
Arg Tyr Asn Phe Ile Met Glu Asn Gly Phe Asp Pro Ile Ile Tyr Lys	
35 40 45	
Arg Tyr Leu Lys Lys Lys Glu Thr Phe Leu Leu Phe Lys Lys Ile Ala	
50 55 60	

GAT CCC CAA TTA GAA ATT GAT GGC CCC TTA CAA TTT GAC GCT TCC ATT 351
 Asp Pro Gln Leu Glu Ile Asp Gly Pro Leu Gln Phe Asp Ala Ser Ile
 75 80 85

GAT AAA AGC GTA GCC AAG AAA AAA TGC CTA ACA GCC AAG TGG CTG GGC 399
 Asp Lys Ser Val Ala Lys Lys Lys Cys Leu Thr Ala Lys Trp Leu Gly
 90 95 100 105

AAG CTA GCG TTT TTA TTT TCC CGG ATT TAAACGCTGG GAACATCGCT TATAAAG 453
 Lys Leu Ala Phe Leu Phe Ser Arg Ile
 110

CGGTGCAACG GAGCGCTAAA GCCGTGGCGA TAG 486

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Met	Cys	Leu	Asp	Thr	Gln	Val	Leu	Val	Phe	Gly	Asp	Cys	Ala	Ile	Ile	
1				5					10					15		
Pro	Asn	Pro	Ser	Pro	Lys	Glu	Leu	Ala	Glu	Ile	Ala	Thr	Thr	Ser	Ala	
			20					25					30			
Gln	Thr	Ala	Lys	Gln	Phe	Asn	Ile	Ala	Pro	Lys	Val	Ala	Leu	Leu	Ser	
		35					40					45				
Tyr	Ala	Thr	Gly	Asp	Ser	Ala	Gln	Gly	Glu	Met	Ile	Asp	Lys	Ile	Asn	
		50				55					60					
Glu	Ala	Leu	Thr	Ile	Ala	Gln	Lys	Leu	Asp	Pro	Gln	Leu	Glu	Ile	Asp	
					70				75					80		
Gly	Pro	Leu	Gln	Phe	Asp	Ala	Ser	Ile	Asp	Lys	Ser	Val	Ala	Lys	Lys	
				85				90					95			
Lys	Cys	Leu	Thr	Ala	Lys	Trp	Leu	Gly	Lys	Leu	Ala	Phe	Leu	Phe	Ser	
			100				105						110			
Arg	Ile															

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 38...1111
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

AGGGCAGGTT TTCACCCCTA AAAAGATAGT GGATTTC ATG CTC ACT CTC AAA CAC	55
Met Leu Thr Leu Lys His	
1 5	
AAT CAT GGG AGT GTT TTA GAA CCG AGT GCT GGC GAT GGG AGT TTT TTA	103
Asn His Gly Ser Val Leu Glu Pro Ser Ala Gly Asp Gly Ser Phe Leu	
10 15 20	
AAG CGC TTA AAA AAG GCC GTA AGG ATT GAA ATC GAT CCT AAA ATC TGC	151
Lys Arg Leu Lys Lys Ala Val Arg Ile Glu Ile Asp Pro Lys Ile Cys	
25 30 35	
CCT AAA AAT GCC CTT TGC ATG GAC TTT TTT GAC TAC CCT TTA GAA AAT	199
Pro Lys Asn Ala Leu Cys Met Asp Phe Phe Asp Tyr Pro Leu Glu Asn	
40 45 50	
CAA TTT GAC ACC ATT ATT GGT AAC CCG CCC TAT GTC AAG CAC AAG GAT	247
Gln Phe Asp Thr Ile Ile Gly Asn Pro Pro Tyr Val Lys His Lys Asp	
55 60 65 70	
ATT GCG CCA AGC ACC AAA GAA AAA CTC CAT TAC AGC CTT TTT GAT GAA	295
Ile Ala Pro Ser Thr Lys Glu Lys Leu His Tyr Ser Leu Phe Asp Glu	
75 80 85	
AGG AGT AAT CTC TAC TTG TTT TTC ATA GAA AAA GCG ATC AAG CAT TTA	343
Arg Ser Asn Leu Tyr Leu Phe Phe Ile Glu Lys Ala Ile Lys His Leu	
90 95 100	
AAA CCT AAA GGC GAA TTG ATT TTC ATC ACC CCA AGG GAT TTT TTA AAA	391
Lys Pro Lys Gly Glu Leu Ile Phe Ile Thr Pro Arg Asp Phe Leu Lys	
105 110 115	
TCC ACT TCT AGC GTG AAA TTA AAC GAA TGG ATT TAT AAA GAA GGC ACG	439
Ser Thr Ser Ser Val Lys Leu Asn Glu Trp Ile Tyr Lys Glu Gly Thr	
120 125 130	
ATA ACG CAT TTT TTT GAA CTG GGC GAT CAA AAG GTT TTC CCA AAC GCC	487
Ile Thr His Phe Phe Glu Leu Gly Asp Gln Lys Val Phe Pro Asn Ala	
135 140 145 150	
ATG CCT AAT TGC GTG ATT TTT CGT TTT TGT AAG GGT AAT TTC AGT AGA	535
Met Pro Asn Cys Val Ile Phe Arg Phe Cys Lys Gly Asn Phe Ser Arg	
155 160 165	
ATC ACC AAC GAT GGT TTG CAA TTT TTG TGC AAA AAA GGC ATT TTG TAT	583
Ile Thr Asn Asp Gly Leu Gln Phe Leu Cys Lys Lys Gly Ile Leu Tyr	
170 175 180	
TTC CTC AAC CAA TCT TAC ACG CAA AAA TTA AGC GAG GTT TTT AAG GTT	631
Phe Leu Asn Gln Ser Tyr Thr Gln Lys Leu Ser Glu Val Phe Lys Val	
185 190 195	
AAA GTG GGG GCA GTG AGC GGG TGC GAT AAG ATT TTT AAA AAT GAA AAA	679
Lys Val Gly Ala Val Ser Gly Cys Asp Lys Ile Phe Lys Asn Glu Lys	
200 205 210	

Tyr	Val	Lys	His	Lys	Asp	Ile	Ala	Pro	Ser	Thr	Lys	Glu	Lys	Leu	His
65					70					75					80
Tyr	Ser	Leu	Phe	Asp	Glu	Arg	Ser	Asn	Leu	Tyr	Leu	Phe	Phe	Ile	Glu
				85					90					95	
Lys	Ala	Ile	Lys	His	Leu	Lys	Pro	Lys	Gly	Glu	Leu	Ile	Phe	Ile	Thr
			100					105					110		
Pro	Arg	Asp	Phe	Leu	Lys	Ser	Thr	Ser	Ser	Val	Lys	Leu	Asn	Glu	Trp
		115					120					125			
Ile	Tyr	Lys	Glu	Gly	Thr	Ile	Thr	His	Phe	Phe	Glu	Leu	Gly	Asp	Gln
	130					135					140				
Lys	Val	Phe	Pro	Asn	Ala	Met	Pro	Asn	Cys	Val	Ile	Phe	Arg	Phe	Cys
145					150				155						160
Lys	Gly	Asn	Phe	Ser	Arg	Ile	Thr	Asn	Asp	Gly	Leu	Gln	Phe	Leu	Cys
			165					170						175	
Lys	Lys	Gly	Ile	Leu	Tyr	Phe	Leu	Asn	Gln	Ser	Tyr	Thr	Gln	Lys	Leu
			180					185					190		
Ser	Glu	Val	Phe	Lys	Val	Lys	Val	Gly	Ala	Val	Ser	Gly	Cys	Asp	Lys
		195					200					205			
Ile	Phe	Lys	Asn	Glu	Lys	Tyr	Gly	Asn	Leu	Glu	Phe	Val	Thr	Ser	Ile
	210					215					220				
Thr	Lys	Arg	Thr	Asn	Ala	Leu	Glu	Lys	Met	Val	Phe	Val	Asn	Glu	Pro
225					230				235						240
Asn	Asp	Tyr	Leu	Leu	Gln	His	Lys	Asp	Ser	Leu	Met	Gln	Arg	Lys	Ile
			245					250						255	
Lys	Lys	Phe	Asn	Glu	Asn	Asn	Trp	Phe	Glu	Trp	Gly	Arg	Met	His	His
			260					265					270		
Ile	Ser	Pro	Lys	Lys	Arg	Ile	Tyr	Val	Asn	Ala	Lys	Thr	His	Gln	Lys
		275					280					285			
Asn	Pro	Phe	Phe	Ile	His	Gln	Cys	Pro	Asn	Tyr	Asp	Gly	Ser	Ile	Leu
	290					295					300				
Ala	Leu	Phe	Pro	Tyr	Asn	Gln	Asn	Leu	Asp	Leu	Gln	Asn	Leu	Cys	Asp
305					310				315						320
Lys	Leu	Asn	Ala	Ile	Asn	Trp	Gln	Glu	Leu	Gly	Phe	Val	Cys	Gly	Gly
			325					330						335	
Arg	Phe	Leu	Phe	Ser	Gln	Arg	Ser	Leu	Glu	Asn	Ala	Leu	Leu	Pro	Lys
			340					345					350		
Asp	Phe	Leu	Asn	Leu	Gly										
		355													

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1130
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CCTAAAGCGG AGAATAAAGT TACAGAAGTC CTAGCGAGCA AAACAATGTG ATG GCT

AAT GAT CCC AAC ATG AAC GGG CGT TGC CAA CGA AAT GGC GCT ACG GCG Asn Asp Pro Asn Met Asn Gly Arg Cys Gln Arg Asn Gly Ala Thr Ala 230 235 240	776
AAT GTG ATT GGG GTG TAT GCG CAA GCG AAT TAC ACC TTG CAT CCT ATG Asn Val Ile Gly Val Tyr Ala Gln Ala Asn Tyr Thr Leu His Pro Met 245 250 255	824
GTA ACT TTA GGG GCA GGG ACT CGT TAT GAT GTC TAT ACT TTA GTG GAT Val Thr Leu Gly Ala Gly Thr Arg Tyr Asp Val Tyr Thr Leu Val Asp 260 265 270	872
AAA GAC TGG CAA TTG CAC ATA ACC CAA GGG TTT AGC CCT AGC GCG GCT Lys Asp Trp Gln Leu His Ile Thr Gln Gly Phe Ser Pro Ser Ala Ala 275 280 285 290	920
TTA AAT GTC TCG CCT TTA GAA AAT TTG AAT TTC AGG CTT TCT TAT GCG Leu Asn Val Ser Pro Leu Glu Asn Leu Asn Phe Arg Leu Ser Tyr Ala 295 300 305	968
TAT GTA ACC AGA GGC CCT ATG CCT GGA GGT TTG GTG TGG ATG CGT CAA Tyr Val Thr Arg Gly Pro Met Pro Gly Gly Leu Val Trp Met Arg Gln 310 315 320	1016
GAT AAT TTG CGN CTA CAA CCG CAA TTT AAA GCC AGA AAT TGG GCA AAA Asp Asn Leu Xaa Leu Gln Pro Gln Phe Lys Ala Arg Asn Trp Ala Lys 325 330 335	1064
TGT GGA ATT TTA ACA CCG AAT ACA GCA GTC AGT ATT TTG ATT TTA GAG Cys Gly Ile Leu Thr Pro Asn Thr Ala Val Ser Ile Leu Ile Leu Glu 340 345 350	1112
CCG CCG GTT TTG TCC AAT TGATTTCTAA TTACATCAAT CAATTTTCTT CAACGCTT Pro Pro Val Leu Ser Asn 355 360	1168
TTTGTAACCA ACTTG	1183

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met Ala Lys Ile Asn Gly Tyr Leu Ser Glu Arg Asp Ile Leu Thr Leu 1 5 10 15
Ser Tyr Asn Met Thr Arg Asp Asn Ala Asn Arg Pro Leu Arg Ala Asn 20 25 30
Phe Thr Gly Thr Phe Leu Pro Tyr Ser Cys Gly Asp Phe Asn Ala Phe 35 40 45
Pro Asn Glu Lys Asn Pro Ser Asp Cys Leu Phe Glu Asn Asp Ala Ser 50 55 60

Leu	Phe	Lys	Thr	Tyr	Ser	Val	Asn	Leu	Val	His	Asn	Val	Ser	Leu	Asn
65					70					75					80
Tyr	Glu	Arg	Glu	Gly	Gly	Ser	Arg	Phe	Gly	Asp	Pro	Lys	Leu	Lys	Ile
			85						90					95	
Asn	Gly	Tyr	Thr	Ser	Ile	Arg	Asn	Val	Gln	Ile	Asp	Pro	Leu	Phe	Lys
			100					105					110		
Pro	Asn	Asp	Ile	Ala	Ala	Ser	Ile	Pro	Phe	Thr	Pro	Asn	Pro	Lys	Leu
			115					120					125		
Gly	Glu	Glu	Asn	Glu	Cys	Val	Ala	Gln	Gly	Gly	Ile	Tyr	Asp	Ala	Leu
			130				135						140		
Lys	Gln	Thr	Cys	Ser	Ile	Thr	Phe	Lys	Ser	Leu	Gly	Gly	Gly	Ser	Val
					150					155					160
Val	Ala	Asn	Lys	Asn	Leu	Phe	Ile	Ile	Asn	Ser	Gly	Phe	Asn	Ala	Asn
				165					170					175	
Val	Ile	His	Thr	Ile	Asp	His	Lys	Asn	Asp	Asn	Leu	Leu	Glu	Tyr	Gly
			180					185					190		
Leu	Asn	Tyr	Gln	Asn	Leu	Thr	Thr	Phe	Asp	Lys	Ala	Ile	Pro	Asn	Ser
			195				200						205		
Glu	Leu	Val	Lys	Pro	Gly	Asp	Ala	Pro	Asp	Ala	Cys	Leu	Arg	Val	Thr
			210				215					220			
Ser	Pro	Asn	Asp	Pro	Asn	Met	Asn	Gly	Arg	Cys	Gln	Arg	Asn	Gly	Ala
					230					235					240
Thr	Ala	Asn	Val	Ile	Gly	Val	Tyr	Ala	Gln	Ala	Asn	Tyr	Thr	Leu	His
				245					250					255	
Pro	Met	Val	Thr	Leu	Gly	Ala	Gly	Thr	Arg	Tyr	Asp	Val	Tyr	Thr	Leu
			260					265					270		
Val	Asp	Lys	Asp	Trp	Gln	Leu	His	Ile	Thr	Gln	Gly	Phe	Ser	Pro	Ser
			275				280					285			
Ala	Ala	Leu	Asn	Val	Ser	Pro	Leu	Glu	Asn	Leu	Asn	Phe	Arg	Leu	Ser
			290				295				300				
Tyr	Ala	Tyr	Val	Thr	Arg	Gly	Pro	Met	Pro	Gly	Gly	Leu	Val	Trp	Met
					310					315					320
Arg	Gln	Asp	Asn	Leu	Xaa	Leu	Gln	Pro	Gln	Phe	Lys	Ala	Arg	Asn	Trp
				325					330					335	
Ala	Lys	Cys	Gly	Ile	Leu	Thr	Pro	Asn	Thr	Ala	Val	Ser	Ile	Leu	Ile
			340					345					350		
Leu	Glu	Pro	Pro	Val	Leu	Ser	Asn								
			355				360								

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...387
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AGACTGAATA AAATCGCACT CGCTCCCGCA ATG ACA ACC TGG AAC ATG GGG CTG

	Met	Thr	Thr	Trp	Asn	Met	Gly	Leu										
	1				5													
CCC AAA AAC AAG TTA ATG AGC GAA CAC ACC ACC ACC ACA ATC AAA GCG																		102
Pro Lys Asn Lys Leu Met Ser Glu His Thr Thr Thr Thr Ile Lys Ala																		
10																		
ATG AAG AGC ATT TTA CCC ATA TTC GCT AGA TCG TTT TTA GTC TTA AGG																		150
Met Lys Ser Ile Leu Pro Ile Phe Ala Arg Ser Phe Leu Val Leu Arg																		
25																		40
GCA TAC ACG CTC ATC AAA CCA AAG ACA ATA GTT GTC ATG CCC AAA GCC																		198
Ala Tyr Thr Leu Ile Lys Pro Lys Thr Ile Val Val Met Pro Lys Ala																		
45																		55
TGC CAA ATC GCT CCT AAA CCA GCT TTT GCA ATC ACC ATA CCC AAC AAA																		246
Cys Gln Ile Ala Pro Lys Pro Ala Phe Ala Ile Thr Ile Pro Asn Lys																		
60																		70
GGC ACT AGC GTA ACC CCT GAT AAT GAA GTG AAA GCA AAC AGC ATG AAC																		294
Gly Thr Ser Val Thr Pro Asp Asn Glu Val Lys Ala Asn Ser Met Asn																		
75																		85
AGA TTC AAT CCG GGT TTA GAT TTA GAA AAC ATC AAA CCA AAA AAC GCC																		342
Arg Phe Asn Pro Gly Leu Asp Leu Glu Asn Ile Lys Pro Lys Asn Ala																		
90																		100
GCA ATT TCA GCG ATA AAA AAC ACC CAT TTA TAC TGC ACT ACG GCT TGAAA																		392
Ala Ile Ser Ala Ile Lys Asn Thr His Leu Tyr Cys Thr Thr Ala																		
105																		115
ATTCATTAAA CCTAGTAACG CCCCAATAGT CGCTAATAA																		431

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met	Thr	Thr	Trp	Asn	Met	Gly	Leu	Pro	Lys	Asn	Lys	Leu	Met	Ser	Glu
1				5					10					15	
His	Thr	Thr	Thr	Thr	Ile	Lys	Ala	Met	Lys	Ser	Ile	Leu	Pro	Ile	Phe
			20					25					30		
Ala	Arg	Ser	Phe	Leu	Val	Leu	Arg	Ala	Tyr	Thr	Leu	Ile	Lys	Pro	Lys
		35					40					45			
Thr	Ile	Val	Val	Met	Pro	Lys	Ala	Cys	Gln	Ile	Ala	Pro	Lys	Pro	Ala
		50				55					60				
Phe	Ala	Ile	Thr	Ile	Pro	Asn	Lys	Gly	Thr	Ser	Val	Thr	Pro	Asp	Asn
		65				70				75				80	
Glu	Val	Lys	Ala	Asn	Ser	Met	Asn	Arg	Phe	Asn	Pro	Gly	Leu	Asp	Leu
				85				90					95		
Glu	Asn	Ile	Lys	Pro	Lys	Asn	Ala	Ala	Ile	Ser	Ala	Ile	Lys	Asn	Thr

100 105 110
 His Leu Tyr Cys Thr Thr Ala
 115

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 21...599
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

AAGTTTGATA TACTAACAGA	ATG AAT ACT TAT AAA AAC AGC TTG AAT CAC	50
	Met Asn Thr Tyr Lys Asn Ser Leu Asn His	
	1 5 10	
TTT TTA AAT TTA GTG GAT TGT TTA GAA AAA ATC CCC AAT GTG GGT AAA	98	
Phe Leu Asn Leu Val Asp Cys Leu Glu Lys Ile Pro Asn Val Gly Lys		
	15 20 25	
AAG TCC GCC TTT AAA ATG GCG TAT CAT TTG GGT TTA GAA AAC CCC TAT	146	
Lys Ser Ala Phe Lys Met Ala Tyr His Leu Gly Leu Glu Asn Pro Tyr		
	30 35 40	
CTG GCG CTA AAA ATC ACG CAC GCT TTA GAG AAC GCC CTA GAA AAC CTT	194	
Leu Ala Leu Lys Ile Thr His Ala Leu Glu Asn Ala Leu Glu Asn Leu		
	45 50 55	
AAA ACA TGT TCA TCT TGT AAC GCG CTC AGC GAG AGT GAG GTT TGT GAG	242	
Lys Thr Cys Ser Ser Cys Asn Ala Leu Ser Glu Ser Glu Val Cys Glu		
	60 65 70	
ATT TGC TCT GAT GAA AGC CGA CAA AAT TCT CAG CTT TGC ATG GTT TTA	290	
Ile Cys Ser Asp Glu Ser Arg Gln Asn Ser Gln Leu Cys Met Val Leu		
	75 80 85 90	
CAC CCA AGA GAT GTG TTT ATT TTA GAA GAT TTA AAG GAT TTT TTA GGG	338	
His Pro Arg Asp Val Phe Ile Leu Glu Asp Leu Lys Asp Phe Leu Gly		
	95 100 105	
CGC TAT TAT GTG TTA AAC TCC ATA GAA GAA GTG GAT TTT AAC GCC CTA	386	
Arg Tyr Tyr Val Leu Asn Ser Ile Glu Glu Val Asp Phe Asn Ala Leu		
	110 115 120	
GAA AAA CGC CTG ATT GAA GAA AAC ATT AAA GAA ATC ATT TTT GCT TTC	434	
Glu Lys Arg Leu Ile Glu Glu Asn Ile Lys Glu Ile Ile Phe Ala Phe		
	125 130 135	

CCT CCC ACT TTA GCT AAT GAT TCT CTA ATG CTT TAT ATT GAA GAC AAA	482
Pro Pro Thr Leu Ala Asn Asp Ser Leu Met Leu Tyr Ile Glu Asp Lys	
140 145 150	
TTA CAG CAT TTC CAC CTC ACT TTC ACT AAA ATC GCT CAA GGC GTG CCT	530
Leu Gln His Phe His Leu Thr Phe Thr Lys Ile Ala Gln Gly Val Pro	
155 160 165 170	
ACT GGA GTG AAT TTT GAA AAC ATT GAC TCA GTT TCG CTC TCA AGG GCG	578
Thr Gly Val Asn Phe Glu Asn Ile Asp Ser Val Ser Leu Ser Arg Ala	
175 180 185	
TTT AAT TCA AGG ATC AAA GCA TGAATTTAAA TTTTATGCCC CTATTGCATG CTTA	633
Phe Asn Ser Arg Ile Lys Ala	
190	
TAACCATGCG AGCATTGATT TTCATTTCAA TTCTAGTG	671

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Met	Asn	Thr	Tyr	Lys	Asn	Ser	Leu	Asn	His	Phe	Leu	Asn	Leu	Val	Asp
1				5					10					15	
Cys	Leu	Glu	Lys	Ile	Pro	Asn	Val	Gly	Lys	Lys	Ser	Ala	Phe	Lys	Met
			20					25					30		
Ala	Tyr	His	Leu	Gly	Leu	Glu	Asn	Pro	Tyr	Leu	Ala	Leu	Lys	Ile	Thr
		35					40					45			
His	Ala	Leu	Glu	Asn	Ala	Leu	Glu	Asn	Leu	Lys	Thr	Cys	Ser	Ser	Cys
	50					55				60					
Asn	Ala	Leu	Ser	Glu	Ser	Glu	Val	Cys	Glu	Ile	Cys	Ser	Asp	Glu	Ser
65					70				75					80	
Arg	Gln	Asn	Ser	Gln	Leu	Cys	Met	Val	Leu	His	Pro	Arg	Asp	Val	Phe
				85					90					95	
Ile	Leu	Glu	Asp	Leu	Lys	Asp	Phe	Leu	Gly	Arg	Tyr	Tyr	Val	Leu	Asn
			100					105					110		
Ser	Ile	Glu	Glu	Val	Asp	Phe	Asn	Ala	Leu	Glu	Lys	Arg	Leu	Ile	Glu
		115					120					125			
Glu	Asn	Ile	Lys	Glu	Ile	Ile	Phe	Ala	Phe	Pro	Pro	Thr	Leu	Ala	Asn
	130					135				140					
Asp	Ser	Leu	Met	Leu	Tyr	Ile	Glu	Asp	Lys	Leu	Gln	His	Phe	His	Leu
145					150					155					160
Thr	Phe	Thr	Lys	Ile	Ala	Gln	Gly	Val	Pro	Thr	Gly	Val	Asn	Phe	Glu
				165					170					175	
Asn	Ile	Asp	Ser	Val	Ser	Leu	Ser	Arg	Ala	Phe	Asn	Ser	Arg	Ile	Lys
			180					185					190		
Ala															

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...793
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

AAAAAATTCA GGATTAAAT ATAAA ATG AAA AAA GTT TTA TTT TTG TNG GTA	52
Met Lys Lys Val Leu Phe Leu Xaa Val	
1 5	
ATA AGC TTT TTT GGG GGT TTT TTG AAC GCT TCT AGC TTG TAT GAA AAA	100
Ile Ser Phe Phe Gly Gly Phe Leu Asn Ala Ser Ser Leu Tyr Glu Lys	
10 15 20 25	
CTG ATT AAT AAA GAA ACG ATC AGC GTT GGC ACA GAA GGC ATT TAC CCC	148
Leu Ile Asn Lys Glu Thr Ile Ser Val Gly Thr Glu Gly Ile Tyr Pro	
30 35 40	
CCT TTC ACT TAC CAC AAT AAA GAA GGC AAG CTC ACC GGC TAT GAT GTG	196
Pro Phe Thr Tyr His Asn Lys Glu Gly Lys Leu Thr Gly Tyr Asp Val	
45 50 55	
GAA GTG GCT AGG GAG TTG GCC AAA GAG CTT GGC GTG AAG ATC AAA TTC	244
Glu Val Ala Arg Glu Leu Ala Lys Glu Leu Gly Val Lys Ile Lys Phe	
60 65 70	
CAC GAA ACT TCA TGG GAT ATC ATG CTG ACA GGT TTG AAA TCG GGG CGT	292
His Glu Thr Ser Trp Asp Ile Met Leu Thr Gly Leu Lys Ser Gly Arg	
75 80 85	
TTT GAT ATG GTC GCT AAC CAA GTG AGT TTG GCG ACT AAA AAA CGC CAA	340
Phe Asp Met Val Ala Asn Gln Val Ser Leu Ala Thr Lys Lys Arg Gln	
90 95 100 105	
GCG GCT TTT GAT AAA AGC TTG CCT TAT AGC TAT TCA GGC ACG ATC ATG	388
Ala Ala Phe Asp Lys Ser Leu Pro Tyr Ser Tyr Ser Gly Thr Ile Met	
110 115 120	
CTG GTC AGG AAA GAT GAA AAC CGC ATT AAA GAT ATT AAA GAC ATC AAG	436
Leu Val Arg Lys Asp Glu Asn Arg Ile Lys Asp Ile Lys Asp Ile Lys	
125 130 135	
GGT TTG AGA GCG GCT AAC ACT TTA AGC TCC ACT TAT GGG GAA ATC GCT	484
Gly Leu Arg Ala Ala Asn Thr Leu Ser Ser Thr Tyr Gly Glu Ile Ala	
140 145 150	
TTT AAA TAC GAC GCT CAA ATC GTT TCG GTG GAT TCT ATG GCG CAA GCT	532
Phe Lys Tyr Asp Ala Gln Ile Val Ser Val Asp Ser Met Ala Gln Ala	


```

Leu Ser Ser Thr Tyr Gly Glu Ile Ala Phe Lys Tyr Asp Ala Gln Ile
145          150          155          160
Val Ser Val Asp Ser Met Ala Gln Ala Leu Leu Val Ala Gln Lys
          165          170          175
Arg Ala Asp Leu Thr Leu Asn Ser Ser Leu Ala Ile Leu Asn Tyr Leu
          180          185          190
Asn Thr His Lys Asp Asn Pro Phe Lys Ile Ala Trp Glu Ser Lys Glu
          195          200          205
Lys Asp Gly Gly Ala Ser Phe Val Ile Asn Lys His Gln Glu Lys Ala
          210          215          220
Leu Glu Leu Ile Asn Gln Ala Met Gln Arg Leu Ile Asn Lys Gly Val
225          230          235          240
Leu Lys Arg Leu Gly Glu Gln Phe Phe Gly Lys Asp Val Ser Gln Pro
          245          250          255

```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 23...1372
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

CCTAGTTTAT TAAGGAGTTT TT ATG GAA ACG ATT GAT TCG GTG GTG CGT TTG      52
      Met Glu Thr Ile Asp Ser Val Val Arg Leu
              1              5              10

TTA TCT AAT TTG GTG TGG GGG ATT CCC ATG CAA ATT TTA TTA GTA GGC      100
Leu Ser Asn Leu Val Trp Gly Ile Pro Met Gln Ile Leu Leu Val Gly
              15              20              25

ACC GGC TTG TTT TTA ACC TTT TAT CTT AGG GGT TTG CAA TTC AGT AAG      148
Thr Gly Leu Phe Leu Thr Phe Tyr Leu Arg Gly Leu Gln Phe Ser Lys
              30              35              40

ATT TTT TAT GCG ATC AAA ATC CTT TTT GAC AAA GAG TCC CAA TCT AAG      196
Ile Phe Tyr Ala Ile Lys Ile Leu Phe Asp Lys Glu Ser Gln Ser Lys
              45              50              55

GGC GAC ATT TCA CAA TTT TCC GCT CTC ATG CTC TCT TTG GGG GCG ACT      244
Gly Asp Ile Ser Gln Phe Ser Ala Leu Met Leu Ser Leu Gly Ala Thr
              60              65              70

GTA GGC ATT GGG AGT ATC GTA GGC GTA GCG ACC GCT ATT AGC ATC GCA      292
Val Gly Ile Gly Ser Ile Val Gly Val Ala Thr Ala Ile Ser Ile Ala
              75              80              85              90

GGG CCA GGA GCG GTG TTT TGG ATG TGG GTT ACT GGG CTT GTT GGC ATG      340

```


(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 49...333
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

TTTAAATTAA	CCCCGAAATG	GAATTTTAAA	GGGGCTTGGT	TTTTGAGC	ATG AGC TTC	57
					Met Ser Phe	
					1	
AGG GTG TCT AAC ACC ACA CCA GGG CAT GAG AGT GGG GCT TTT TTA AAC	105					
Arg Val Ser Asn Thr Thr Pro Gly His Glu Ser Gly Ala Phe Leu Asn						
5 10 15						
GCA GAA ATA AGC CCA GCA TTC CCA AAA GAA GTG CCG TTT GCG CCA TCG	153					
Ala Glu Ile Ser Pro Ala Phe Pro Lys Glu Val Pro Phe Ala Pro Ser						
20 25 30 35						
TTT TTT TCT ATC ACG CAG ACC TTA TGC CCT AAC TTG TGC ATA GAA TAC	201					
Phe Phe Ser Ile Thr Gln Thr Leu Cys Pro Asn Leu Cys Ile Glu Tyr						
40 45 50						
GCA CAA GAA AGC CCT ACA ATC CCA CCG CCT ATG ACC ACG ACC TCT TTT	249					
Ala Gln Glu Ser Pro Thr Ile Pro Pro Pro Met Thr Thr Thr Ser Phe						
55 60 65						
TTC ATG CTG ATA GTC CCT TTA ATA AAT TAC TTA ATG GCT ATC GCT TCA	297					
Phe Met Leu Ile Val Pro Leu Ile Asn Tyr Leu Met Ala Ile Ala Ser						
70 75 80						
ATT TCT ACT AAA GCG TCT TTA GGC AGT TTA GCC ACT TGAAAGGTCG CTCTGG	349					
Ile Ser Thr Lys Ala Ser Leu Gly Ser Leu Ala Thr						
85 90 95						
CCGGATAAGG CTCTGTAA	367					

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met Ser Phe Arg Val Ser Asn Thr Thr Pro Gly His Glu Ser Gly Ala	
1 5 10 15	
Phe Leu Asn Ala Glu Ile Ser Pro Ala Phe Pro Lys Glu Val Pro Phe	
20 25 30	
Ala Pro Ser Phe Phe Ser Ile Thr Gln Thr Leu Cys Pro Asn Leu Cys	
35 40 45	
Ile Glu Tyr Ala Gln Glu Ser Pro Thr Ile Pro Pro Pro Met Thr Thr	
50 55 60	
Thr Ser Phe Phe Met Leu Ile Val Pro Leu Ile Asn Tyr Leu Met Ala	

65		70		75		80								
Ile	Ala	Ser	Ile	Ser	Thr	Lys	Ala	Ser	Leu	Gly	Ser	Leu	Ala	Thr
			85						90				95	

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 36...689
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCGCACGCTG AATTTAGGGT TTTGAAAGGT TAAAA ATG AAA TTT AAA TTT TTG	53
Met Lys Phe Lys Phe Leu	
1 5	
AAT ATG GAT AAT GAA AGC GGT TTT ATT TTG ATT GAA AAA GAA TTG AAA	101
Asn Met Asp Asn Glu Ser Gly Phe Ile Leu Ile Glu Lys Glu Leu Lys	
10 15 20	
CGA TTA AAC ATT CTC GCT CAA GTC AAA GAA GAT TGC ATT GAA TTA AAA	149
Arg Leu Asn Ile Leu Ala Gln Val Lys Glu Asp Cys Ile Glu Leu Lys	
25 30 35	
GGC GAA AAC ACA GAA CAA GCG AGA ATT TAT CTT AAA ACG CTT TTT AAC	197
Gly Glu Asn Thr Glu Gln Ala Arg Ile Tyr Leu Lys Thr Leu Phe Asn	
40 45 50	
TCC AAT ATT GTA GAA TTA GAC GAT CAT CAA AAA AGT GCA AAC GCT TTA	245
Ser Asn Ile Val Glu Leu Asp Asp His Gln Lys Ser Ala Asn Ala Leu	
55 60 65 70	
ATA GAG CGC TTG AAA TCT TTA GAT TTA AAA ATT GCG GTG GCT GAA AGC	293
Ile Glu Arg Leu Lys Ser Leu Asp Leu Lys Ile Ala Val Ala Glu Ser	
75 80 85	
TGC TCT GGG GGG CTA TTA TCG CAT GCA TTC ACT TCC ATT AGC GGG GCT	341
Cys Ser Gly Gly Leu Leu Ser His Ala Phe Thr Ser Ile Ser Gly Ala	
90 95 100	
TCA GCG GTT TTT ATG GGG GGT ATT GTG TGC TAC AAT GAA GAG GTT AAG	389
Ser Ala Val Phe Met Gly Gly Ile Val Cys Tyr Asn Glu Glu Val Lys	
105 110 115	
CGC GAA TTA TTG AAG GTC AAT GCC ACG ACT TTA AAA GTC TTT GGG GTT	437
Arg Glu Leu Leu Lys Val Asn Ala Thr Thr Leu Lys Val Phe Gly Val	
120 125 130	

Gly	Val	Ala	Gly	Pro	Asn	Gly	Gly	Asn	Lys	Ala	Asn	Pro	Val	Gly	Thr
				165					170					175	
Ile	Tyr	Ile	Gly	Ala	Gln	Lys	Leu	Gly	Ser	Gln	Ala	Leu	Ile	Asp	Arg
			180					185					190		
Cys	Phe	Phe	Glu	Gly	Asn	Arg	Glu	Ser	Ile	Gln	Asn	Lys	Ser	Val	Glu
		195					200					205			
His	Ala	Leu	Asn	Met	Leu	Ala	Arg	Met	Leu						
	210					215									

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 28...657
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

AAATTC	TCTAAA	AAAATAAA	AGG AAAATCA	ATG AAA	TTT TTG	GAT CAA	GAA AAA	AGA		54						
				Met	Lys Phe	Leu Asp	Gln Glu	Lys Arg								
				1		5										
AGA	CAA	TTA	TTA	AAC	GAG	CGC	CAT	TCT	TGC	AAG	ATG	TTT	GAT	AGC	CAT	102
Arg	Gln	Leu	Leu	Asn	Glu	Arg	His	Ser	Cys	Lys	Met	Phe	Asp	Ser	His	
10				15					20						25	
TAT	GAG	TTT	TCT	AGC	ACA	GAA	TTA	GAA	GAA	ATC	GCT	GAA	ATC	GCC	AGG	150
Tyr	Glu	Phe	Ser	Ser	Thr	Glu	Leu	Glu	Glu	Ile	Ala	Glu	Ile	Ala	Arg	
				30					35					40		
CTA	TCG	CCA	AGC	TCT	TAC	AAC	ACG	CAG	CCA	TGG	CAT	TTT	GTG	ATG	GTT	198
Leu	Ser	Pro	Ser	Ser	Tyr	Asn	Thr	Gln	Pro	Trp	His	Phe	Val	Met	Val	
			45					50					55			
ACT	GAT	AAG	GAT	TTA	AAA	AAA	CAA	ATT	GCA	GCG	CAC	AGC	TAT	TTC	AAT	246
Thr	Asp	Lys	Asp	Leu	Lys	Lys	Gln	Ile	Ala	Ala	His	Ser	Tyr	Phe	Asn	
		60					65					70				
GAA	GAG	ATG	ATT	AAA	AGC	GCT	TCA	GCG	TTA	ATG	GTG	GTA	TGC	TCT	TTA	294
Glu	Glu	Met	Ile	Lys	Ser	Ala	Ser	Ala	Leu	Met	Val	Val	Cys	Ser	Leu	
	75					80					85					
AGA	CCC	AGC	GAG	TTG	TTA	CCA	CAC	GGC	CAC	TAC	ATG	CAA	AAT	CTC	TAT	342
Arg	Pro	Ser	Glu	Leu	Leu	Pro	His	Gly	His	Tyr	Met	Gln	Asn	Leu	Tyr	
90					95					100					105	
CCG	GAG	TCT	TAT	AAA	GTT	AGA	GTG	ATC	CCC	TCT	TTT	GCT	CAA	ATG	CTT	390
Pro	Glu	Ser	Tyr	Lys	Val	Arg	Val	Ile	Pro	Ser	Phe	Ala	Gln	Met	Leu	
				110					115					120		

GGC GTG AGA TTC AAC CAC AGC ATG CAA AGA TTA GAA AGC TAT ATT TTA	438
Gly Val Arg Phe Asn His Ser Met Gln Arg Leu Glu Ser Tyr Ile Leu	
125 130 135	
GAG CAA TGC TAT ATC GCT GTG GGG CAA ATT TGC ATG GGC GTG AGC TTA	486
Glu Gln Cys Tyr Ile Ala Val Gly Gln Ile Cys Met Gly Val Ser Leu	
140 145 150	
ATG GGA TTG GAT AGT TGC ATT ATT GGA GGC TTT GAT CCT TTA AAG GTG	534
Met Gly Leu Asp Ser Cys Ile Ile Gly Gly Phe Asp Pro Leu Lys Val	
155 160 165	
GGC GAA GTT TTA GAA GAG CGT ATC AAT AAG CCT AAA ATC GCA TGC TTG	582
Gly Glu Val Leu Glu Glu Arg Ile Asn Lys Pro Lys Ile Ala Cys Leu	
170 175 180 185	
ATC GCT TTG GGC AAG AGG GTG GCA GAA GCG AGT CAA AAA TCA AGA AAA	630
Ile Ala Leu Gly Lys Arg Val Ala Glu Ala Ser Gln Lys Ser Arg Lys	
190 195 200	
TCA AAA GTT GAT GCG ATT ACT TGG TTG TGATTAAACA AAATCAAAAA CTTT	681
Ser Lys Val Asp Ala Ile Thr Trp Leu	
205 210	

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Met Lys Phe Leu Asp Gln Glu Lys Arg Arg Gln Leu Leu Asn Glu Arg	
1 5 10 15	
His Ser Cys Lys Met Phe Asp Ser His Tyr Glu Phe Ser Ser Thr Glu	
20 25 30	
Leu Glu Glu Ile Ala Glu Ile Ala Arg Leu Ser Pro Ser Ser Tyr Asn	
35 40 45	
Thr Gln Pro Trp His Phe Val Met Val Thr Asp Lys Asp Leu Lys Lys	
50 55 60	
Gln Ile Ala Ala His Ser Tyr Phe Asn Glu Glu Met Ile Lys Ser Ala	
65 70 75 80	
Ser Ala Leu Met Val Val Cys Ser Leu Arg Pro Ser Glu Leu Leu Pro	
85 90 95	
His Gly His Tyr Met Gln Asn Leu Tyr Pro Glu Ser Tyr Lys Val Arg	
100 105 110	
Val Ile Pro Ser Phe Ala Gln Met Leu Gly Val Arg Phe Asn His Ser	
115 120 125	
Met Gln Arg Leu Glu Ser Tyr Ile Leu Glu Gln Cys Tyr Ile Ala Val	
130 135 140	
Gly Gln Ile Cys Met Gly Val Ser Leu Met Gly Leu Asp Ser Cys Ile	
145 150 155 160	
Ile Gly Gly Phe Asp Pro Leu Lys Val Gly Glu Val Leu Glu Glu Arg	

AAC Asn 120	AAC Asn 120	TTG Leu 120	TTG Leu 120	GGC Gly 125	TTG Leu 125	AAA Lys 125	TTA Leu 125	AAA Lys 125	CTC Leu 130	CCT Pro 130	GAA Glu 130	GAC Asp 130	ATG Met 130	AAT Asn 130	CCC Pro 130	500
ACC Thr 135	ACA Thr 135	GCT Ala 135	ATC Ile 140	CCC Pro 140	ACT Thr 140	TAT Tyr 140	TGC Cys 145	TTA Leu 145	AAG Lys 145	GGT Gly 145	AAA Lys 145	AGA Arg 145	GAA Glu 150	GTT Val 150	TTA Leu 150	548
ATG Met 155	GGG Gly 155	TTT Phe 155	TCT Ser 155	CAA Gln 155	AAT Asn 155	GGG Gly 160	GGC Gly 160	ATG Met 160	GTG Val 160	GAA Glu 160	TTG Leu 165	CCA Pro 165	CAT His 165	CTC Leu 165	GCT Ala 165	596
TTT Phe 170	GAC Asp 170	CAT His 170	CAG Gln 170	TTT Phe 170	TTA Leu 175	AAC Asn 175	TCC Ser 175	CTT Leu 175	GGC Gly 180	TTT Phe 180	AAT Asn 180	TTG Leu 180	AAA Lys 180	GAG Glu 180	ATC Ile 180	644
ATG Met 185	CCT Pro 185	TTC Phe 185	ATG Met 185	CTT Leu 190	TTA Leu 190	AGC Ser 190	GCT Ala 190	CCT Pro 190	AGC Ser 195	GTG Val 195	CCT Pro 195	TTT Phe 195	GAA Glu 195	TTT Phe 195	TTA Leu 195	692
TGC Cys 200	TTC Phe 200	ATA Ile 200	GAC Asp 205	ACG Thr 205	CCT Pro 205	GGT Gly 205	TTT Phe 205	AAC Asn 210	TCC Ser 210	GCC Ala 210	AAG Lys 210	CAA Gln 210	GGC Gly 210	TAT Tyr 210	ACG Thr 210	740
GGT Gly 215	GGG Gly 215	GAT Asp 220	AAA Lys 220	GAA Glu 220	GCC Ala 220	TCT Ser 220	AAA Lys 220	GAA Glu 225	TCC Ser 225	CTA Leu 225	AAA Lys 225	CAC His 225	GCC Ala 225	AAA Lys 230	CAC His 230	788
ATT Ile 235	CTG Leu 235	TGG Trp 235	CTC Leu 235	ATT Ile 235	AGT Ser 240	TGC Cys 240	GAG Glu 240	AGT Ser 240	GGG Gly 240	GAG Glu 240	ATT Ile 245	CAC His 245	GAA Glu 245	GAT Asp 245	GAT Asp 245	836
TTA Leu 250	GAA Glu 250	TAT Tyr 250	TTG Leu 250	CAA Gln 250	GAA Glu 255	TTA Leu 255	TAC Tyr 255	GAA Glu 255	GAA Glu 260	GGC Gly 260	AAG Lys 260	CAG Gln 260	GTT Val 260	TTT Phe 260	ATC Ile 260	884
GTA Val 265	TTG Leu 265	AGT Ser 265	AGG Arg 270	GCT Ala 270	GAT Asp 270	AGG Arg 270	CGC Arg 270	ACA Thr 270	AAA Lys 275	AGG Arg 275	CAA Gln 275	TTA Leu 275	GAA Glu 275	GAA Glu 275	GTC Val 275	932
GTT Val 280	ATT Ile 280	AAA Lys 280	ATT Ile 285	AAA Lys 285	GAG Glu 285	ACT Thr 285	TTA Leu 285	AAA Lys 290	GAT Asp 290	AAT Asn 290	GGC Gly 290	ATT Ile 290	GAA Glu 290	TTT Phe 290	TTA Leu 290	980
GGG Gly 295	ATT Ile 295	GGT Gly 300	GCT Ala 300	TAT Tyr 300	AGT Ser 300	TCT Ser 305	ACA Thr 305	AGG Arg 305	TAT Tyr 305	CAA Gln 305	GAA Glu 305	TAT Tyr 305	AAA Lys 310	GAA Glu 310	TTC Phe 310	1028
AGC Ser 315	GAA Glu 315	AAA Lys 315	AGC Ser 315	AAA Lys 315	GTT Val 315	TTT Phe 320	AAC Asn 320	TCG Ser 320	CTT Leu 320	GAG Glu 320	GAA Glu 320	TTT Phe 325	CTA Leu 325	ATG Met 325	AAG Lys 325	1076
TTA Leu 330	AAT Asn 330	CAA Gln 330	AGG Arg 330	AGC Ser 330	GAG Glu 335	AAA Lys 335	CAA Gln 335	AAC Asn 335	GAA Glu 340	ATT Ile 340	TTA Leu 340	GGA Gly 340	TAT Tyr 340	TTA Leu 340	TAC Tyr 340	1124
GAG Glu 1172	GTG Val 1172	CAT His 1172	TCC Ser 1172	ATG Met 1172	TAT Tyr 1172	GAA Glu 1172	AAG Lys 1172	GCT Ala 1172	ATT Ile 1172	GAG Glu 1172	CAA Gln 1172	GAC Asp 1172	GCT Ala 1172	AAC Asn 1172	CAA Gln 1172	1172

Gly	Lys	Arg	Glu	Val	Leu	Met	Gly	Phe	Ser	Gln	Asn	Gly	Gly	Met	Val
145					150					155					160
Glu	Leu	Pro	His	Leu	Ala	Phe	Asp	His	Gln	Phe	Leu	Asn	Ser	Leu	Gly
				165					170					175	
Phe	Asn	Leu	Lys	Glu	Ile	Met	Pro	Phe	Met	Leu	Leu	Ser	Ala	Pro	Ser
			180					185					190		
Val	Pro	Phe	Glu	Phe	Leu	Cys	Phe	Ile	Asp	Thr	Pro	Gly	Phe	Asn	Ser
		195					200					205			
Ala	Lys	Gln	Gly	Tyr	Thr	Gly	Gly	Asp	Lys	Glu	Ala	Ser	Lys	Glu	Ser
	210					215					220				
Leu	Lys	His	Ala	Lys	His	Ile	Leu	Trp	Leu	Ile	Ser	Cys	Glu	Ser	Gly
225					230					235					240
Glu	Ile	His	Glu	Asp	Leu	Glu	Tyr	Leu	Gln	Glu	Leu	Tyr	Glu	Glu	
			245					250					255		
Gly	Lys	Gln	Val	Phe	Ile	Val	Leu	Ser	Arg	Ala	Asp	Arg	Arg	Thr	Lys
			260					265					270		
Arg	Gln	Leu	Glu	Glu	Val	Val	Ile	Lys	Ile	Lys	Glu	Thr	Leu	Lys	Asp
		275					280					285			
Asn	Gly	Ile	Glu	Phe	Leu	Gly	Ile	Gly	Ala	Tyr	Ser	Ser	Thr	Arg	Tyr
	290					295					300				
Gln	Glu	Tyr	Lys	Glu	Phe	Ser	Glu	Lys	Ser	Lys	Val	Phe	Asn	Ser	Leu
305					310					315					320
Glu	Glu	Phe	Leu	Met	Lys	Leu	Asn	Gln	Arg	Ser	Glu	Lys	Gln	Asn	Glu
			325					330					335		
Ile	Leu	Gly	Tyr	Leu	Tyr	Glu	Val	His	Ser	Met	Tyr	Glu	Lys	Ala	Ile
			340					345					350		
Glu	Gln	Asp	Ala	Asn	Gln	Phe	Lys	Arg	Tyr	Gln	Ser	Glu	Leu	His	Ser
		355					360					365			
Val	Arg	Leu	Asp	Leu	Met	Gln	Lys	Gly	Phe	Asp	Asp	Phe	Ser	Asp	Lys
	370					375					380				
Ile	Phe	Arg	Arg	Ile	Glu	Asn	Leu	Glu	Lys	Glu	Phe	Ser	Glu	Gln	Glu
385					390					395					400
Arg	Ser	Lys	Arg	Glu	Ser	Leu	Ala	Arg	Leu	Asn	Glu	Val	Ile	Asp	Leu
			405					410						415	
Phe	Lys	Glu	Gly	Ile	Asp	Lys	Val	Phe	Asp	Arg	Val	Ser	Ala	Phe	Thr
			420					425					430		
Trp	Glu	Lys	Tyr	Lys	Glu	Gln	Asn	Asp	Asp	Glu	Glu	Asp	Asp	Asp	
		435					440					445			

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...1674
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

ATTTTAGTTT TTAATTTTAA AGGATTG ATG ATG GTT TTA CGC ACA CAG ACA AAT

Met Met Val Leu Arg Thr Gln Thr Asn
1 5

TTT GTG GAG TTT TTA GAA CAG GTT TTA GAA GTT TTA AAA GAA GTG GAG	102
Phe Val Glu Phe Leu Glu Gln Val Leu Glu Val Leu Lys Glu Val Glu	
10 15 20 25	
ATC GAT AAA ACA GAA TGC TCC ACG CTT TTA GCA AGC GTT CAA AAA CAA	150
Ile Asp Lys Thr Glu Cys Ser Thr Leu Leu Ala Ser Val Gln Lys Gln	
30 35 40	
CAG CTA GTG ATA CCC GTT GTG GGG AAT TTT AGC GCA GGG AAA AGC ACG	198
Gln Leu Val Ile Pro Val Val Gly Asn Phe Ser Ala Gly Lys Ser Thr	
45 50 55	
CTA TTA AAC CGC TTT TTA GGC AGC AGC GTT TTG CCT ACC GGT ATC ACG	246
Leu Leu Asn Arg Phe Leu Gly Ser Ser Val Leu Pro Thr Gly Ile Thr	
60 65 70	
CCA GAG ACT TCT TTA GCC ACT GAG TTG CAC TAT AGC GCT AAG GAA CGC	294
Pro Glu Thr Ser Leu Ala Thr Glu Leu His Tyr Ser Ala Lys Glu Arg	
75 80 85	
ATA GAG GCT TTT TCA AAC AAT GAT GAA AAA ACA GAG AGT TTT GAA CTG	342
Ile Glu Ala Phe Ser Asn Asn Asp Glu Lys Thr Glu Ser Phe Glu Leu	
90 95 100 105	
AAT GAG CAA AGT TTT GAA GCG ATT AAA GAG AAT GCC ACG AAG TAT TCC	390
Asn Glu Gln Ser Phe Glu Ala Ile Lys Glu Asn Ala Thr Lys Tyr Ser	
110 115 120	
TAC CTT AAG GTT TAT TTG AAT AAT GAA GCT TTG AAA AAC AGC GCT CCT	438
Tyr Leu Lys Val Tyr Leu Asn Asn Glu Ala Leu Lys Asn Ser Ala Pro	
125 130 135	
TTA GTG TTT GTG GAT ATG CCA GGC TTT GAT AGC CCC ATT TCA AGC CAC	486
Leu Val Phe Val Asp Met Pro Gly Phe Asp Ser Pro Ile Ser Ser His	
140 145 150	
ACC CAT GCC ATT TTG GAA TAT TTA GAA AGG GGC GTG CAT TTT GTC ATT	534
Thr His Ala Ile Leu Glu Tyr Leu Glu Arg Gly Val His Phe Val Ile	
155 160 165	
CTC ACA AGC GTA GAA GAG GGC AAT CTC ACT AAA CGC ATG GTT AGG GAG	582
Leu Thr Ser Val Glu Glu Gly Asn Leu Thr Lys Arg Met Val Arg Glu	
170 175 180 185	
TTA AAA AAC CTT TTA GAG TTT GAC AAA GGC CTT AGC TTT ATT TTG AGT	630
Leu Lys Asn Leu Leu Glu Phe Asp Lys Gly Leu Ser Phe Ile Leu Ser	
190 195 200	
AAA ACG AAT TTA AGA ACG CCT TCG CAA GTG GGA GAA ATC TCT CAC TAC	678
Lys Thr Asn Leu Arg Thr Pro Ser Gln Val Gly Glu Ile Ser His Tyr	
205 210 215	
ATT CAA GAT CAA ATC CAG GAT CAC CTT GAT TTG ACA ACG CAC CTC ATC	726
Ile Gln Asp Gln Ile Gln Asp His Leu Asp Leu Thr Thr His Leu Ile	
220 225 230	

CAT His	TCC Ser	AAT Asn	AAA Lys	GAC Asp	AAT Asn	AAC Asn	GCC Ala	CTT Leu	TTA Leu	GAG Glu	GTA Val	GCG Ala	GAT Asp	AAA Lys	ATA Ile	774
235240245																
GAC Asp	GCT Ala	GAA Glu	AAG Lys	CTT Leu	TTT Phe	AGC Ser	GCT Ala	TTG Leu	TAT Tyr	TTG Leu	AAA Lys	CGA Arg	TTG Leu	AAG Lys	TTT Phe	822
250255260265																
TTA Leu	AAT Asn	TCT Ser	AAG Lys	TTA Leu	CAA Gln	AAT Asn	AGC Ser	CTA Leu	AAA Lys	AGC Ser	GTG Val	ATG Met	GAA Glu	AGC Ser	TTT Phe	870
270275280																
GAT Asp	TAT Tyr	TCT Ser	AAA Lys	GAA Glu	AAG Lys	GCT Ala	TTA Leu	GAA Glu	GAA Glu	ATA Ile	CAA Gln	GCT Ala	TTG Leu	GAT Asp	TTG Leu	918
285290295																
GGC Gly	GTT Val	AAA Lys	GAC Asp	ATT Ile	GAA Glu	AAA Lys	ACC Thr	TAT Tyr	GAA Glu	AAA Lys	TTA Leu	AGG Arg	GCT Ala	AAT Asn	TTA Leu	966
300305310																
GAA Glu	GAA Glu	GAA Glu	TAT Tyr	TCT Ser	AGC Ser	GTG Val	GCT Ala	GTG Val	GGA Gly	TCG Ser	GTG Val	GTT Val	AAA Lys	AAA Lys	GTA Val	1014
315320325																
GTA Val	GAA Glu	GAG Glu	GTT Val	AGG Arg	GAT Asp	CAA Gln	AAA Lys	TCC Ser	TAT Tyr	TTA Leu	GCC Ala	TCT Ser	TTA Leu	ATC Ile	AAC Asn	1062
330335340345																
AAG Lys	CCT Pro	AAC Asn	GAG Glu	TTC Phe	AAT Asn	AGC Ser	GAA Glu	ATA Ile	GAA Glu	AGC Ser	ATC Ile	ATG Met	CAA Gln	CAA Gln	AGC Ser	1110
350355360																
TTG Leu	ATC Ile	AAA Lys	AAC Asn	GCT Ala	AAA Lys	TTA Leu	GAG Glu	ATT Ile	GAA Glu	AAG Lys	ATC Ile	AAC Asn	CTT Leu	TCT Ser	TTT Phe	1158
365370375																
TCA Ser	AAA Lys	GAT Asp	TTC Phe	CAT His	GCG Ala	GAA Glu	TTT Phe	GAA Glu	AGC Ser	CTG Leu	AAC Asn	AAG Lys	CTT Leu	TCT Ser	AGC Ser	1206
380385390																
GAT Asp	CTG Leu	TCT Ser	GTG Val	AAT Asn	TTA Leu	GAG Glu	CAT His	GGG Gly	ATT Ile	GAA Glu	TTA Leu	GGG Gly	ATC Ile	AAC Asn	GCT Ala	1254
395400405																
TTA Leu	AGC Ser	GTG Val	ATT Ile	TTT Phe	TCC Ser	AAG Lys	AAT Asn	CCG Pro	GTT Val	ACA Thr	AGG Arg	CCA Pro	TTC Phe	GCG Ala	CTG Leu	1302
410415420425																
ATT Ile	TTG Leu	CAA Gln	GGG Gly	TTA Leu	AAA Lys	TCT Ser	CTT Leu	TTA Leu	AAA Lys	GAT Asp	TTA Leu	CTG Leu	ACA Thr	TTG Leu	TTG Leu	1350
430435440																
CCT Pro	AAT Asn	ATC Ile	ATC Ile	GCT Ala	TCA Ser	TTC Phe	TTT Phe	AGG Arg	AAT Asn	GAA Glu	GAA Glu	AAA Lys	GAG Glu	CGG Arg	GCG Ala	1398
445450455																
AAA Lys	TTA Leu	GAA Glu	AAT Asn	CTG Leu	ATT Ile	GAA Glu	GTC Val	AGA Arg	GTG Val	ATT Ile	CCA Pro	GAA Glu	ATC Ile	CAA Gln	TAC Tyr	1446

460	465	470	
AAG CTT AAA AAA GTT TTA CCG GGA TTG TTT AAT GAA GCT TTG CAA AAT			1494
Lys Leu Lys Lys Val Leu Pro Gly Leu Phe Asn Glu Ala Leu Gln Asn			
475	480	485	
TCC CTA AAA TCT CTA AAA GAT CGG TGC GAG CTA GAA ATC ACG CAT AAA			1542
Ser Leu Lys Ser Leu Lys Asp Arg Cys Glu Leu Glu Ile Thr His Lys			
490	495	500	505
AAA CAA GAA ATC GCG CTC GCT CAA AAG GAA AAA GAA AAA CAC CTA AAC			1590
Lys Gln Glu Ile Ala Leu Ala Gln Lys Glu Lys Glu Lys His Leu Asn			
	510	515	520
GAT TTA GAA GAT CAA AAA CAA ATC TTA GAA AAT AAG ATC AAC GCT TTA			1638
Asp Leu Glu Asp Gln Lys Gln Ile Leu Glu Asn Lys Ile Asn Ala Leu			
	525	530	535
AGC GAT TTA GAA CAA CAA TAT TTA AAG GAT CAA CAA TGAACGAGCA AGAACT			1690
Ser Asp Leu Glu Gln Gln Tyr Leu Lys Asp Gln Gln			
	540	545	
CATTCAAAAA AGCGCTTTAA TTGAAAAA			1718

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met	Met	Val	Leu	Arg	Thr	Gln	Thr	Asn	Phe	Val	Glu	Phe	Leu	Glu	Gln
1				5					10					15	
Val	Leu	Glu	Val	Leu	Lys	Glu	Val	Glu	Ile	Asp	Lys	Thr	Glu	Cys	Ser
			20					25					30		
Thr	Leu	Leu	Ala	Ser	Val	Gln	Lys	Gln	Gln	Leu	Val	Ile	Pro	Val	Val
		35				40					45				
Gly	Asn	Phe	Ser	Ala	Gly	Lys	Ser	Thr	Leu	Leu	Asn	Arg	Phe	Leu	Gly
	50				55						60				
Ser	Ser	Val	Leu	Pro	Thr	Gly	Ile	Thr	Pro	Glu	Thr	Ser	Leu	Ala	Thr
					70					75				80	
Glu	Leu	His	Tyr	Ser	Ala	Lys	Glu	Arg	Ile	Glu	Ala	Phe	Ser	Asn	Asn
			85					90						95	
Asp	Glu	Lys	Thr	Glu	Ser	Phe	Glu	Leu	Asn	Glu	Gln	Ser	Phe	Glu	Ala
			100					105					110		
Ile	Lys	Glu	Asn	Ala	Thr	Lys	Tyr	Ser	Tyr	Leu	Lys	Val	Tyr	Leu	Asn
		115				120						125			
Asn	Glu	Ala	Leu	Lys	Asn	Ser	Ala	Pro	Leu	Val	Phe	Val	Asp	Met	Pro
		130				135					140				
Gly	Phe	Asp	Ser	Pro	Ile	Ser	Ser	His	Thr	His	Ala	Ile	Leu	Glu	Tyr
					150					155				160	
Leu	Glu	Arg	Gly	Val	His	Phe	Val	Ile	Leu	Thr	Ser	Val	Glu	Glu	Gly
				165					170					175	

Asn	Leu	Thr	Lys	Arg	Met	Val	Arg	Glu	Leu	Lys	Asn	Leu	Leu	Glu	Phe
			180					185					190		
Asp	Lys	Gly	Leu	Ser	Phe	Ile	Leu	Ser	Lys	Thr	Asn	Leu	Arg	Thr	Pro
		195					200					205			
Ser	Gln	Val	Gly	Glu	Ile	Ser	His	Tyr	Ile	Gln	Asp	Gln	Ile	Gln	Asp
	210					215					220				
His	Leu	Asp	Leu	Thr	Thr	His	Leu	Ile	His	Ser	Asn	Lys	Asp	Asn	Asn
225					230					235				240	
Ala	Leu	Leu	Glu	Val	Ala	Asp	Lys	Ile	Asp	Ala	Glu	Lys	Leu	Phe	Ser
				245					250					255	
Ala	Leu	Tyr	Leu	Lys	Arg	Leu	Lys	Phe	Leu	Asn	Ser	Lys	Leu	Gln	Asn
			260					265					270		
Ser	Leu	Lys	Ser	Val	Met	Glu	Ser	Phe	Asp	Tyr	Ser	Lys	Glu	Lys	Ala
		275					280					285			
Leu	Glu	Glu	Ile	Gln	Ala	Leu	Asp	Leu	Gly	Val	Lys	Asp	Ile	Glu	Lys
	290					295					300				
Thr	Tyr	Glu	Lys	Leu	Arg	Ala	Asn	Leu	Glu	Glu	Glu	Tyr	Ser	Ser	Val
305					310					315				320	
Ala	Val	Gly	Ser	Val	Val	Lys	Lys	Val	Val	Glu	Glu	Val	Arg	Asp	Gln
				325					330					335	
Lys	Ser	Tyr	Leu	Ala	Ser	Leu	Ile	Asn	Lys	Pro	Asn	Glu	Phe	Asn	Ser
			340					345					350		
Glu	Ile	Glu	Ser	Ile	Met	Gln	Gln	Ser	Leu	Ile	Lys	Asn	Ala	Lys	Leu
		355					360					365			
Glu	Ile	Glu	Lys	Ile	Asn	Leu	Ser	Phe	Ser	Lys	Asp	Phe	His	Ala	Glu
	370					375					380				
Phe	Glu	Ser	Leu	Asn	Lys	Leu	Ser	Ser	Asp	Leu	Ser	Val	Asn	Leu	Glu
385				390						395				400	
His	Gly	Ile	Glu	Leu	Gly	Ile	Asn	Ala	Leu	Ser	Val	Ile	Phe	Ser	Lys
				405					410					415	
Asn	Pro	Val	Thr	Arg	Pro	Phe	Ala	Leu	Ile	Leu	Gln	Gly	Leu	Lys	Ser
			420					425					430		
Leu	Leu	Lys	Asp	Leu	Leu	Thr	Leu	Leu	Pro	Asn	Ile	Ile	Ala	Ser	Phe
		435					440					445			
Phe	Arg	Asn	Glu	Glu	Lys	Glu	Arg	Ala	Lys	Leu	Glu	Asn	Leu	Ile	Glu
	450					455					460				
Val	Arg	Val	Ile	Pro	Glu	Ile	Gln	Tyr	Lys	Leu	Lys	Lys	Val	Leu	Pro
465					470					475				480	
Gly	Leu	Phe	Asn	Glu	Ala	Leu	Gln	Asn	Ser	Leu	Lys	Ser	Leu	Lys	Asp
				485					490					495	
Arg	Cys	Glu	Leu	Glu	Ile	Thr	His	Lys	Lys	Gln	Glu	Ile	Ala	Leu	Ala
			500					505					510		
Gln	Lys	Glu	Lys	Glu	Lys	His	Leu	Asn	Asp	Leu	Glu	Asp	Gln	Lys	Gln
		515					520					525			

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...348
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

TCTTTTCTT CATTCTAAA GAATGAAGCG ATG ATA TTA GGC AAC AAT GTC AGT 54
Met Ile Leu Gly Asn Asn Val Ser
1 5

AAA TCT TTT AAA AGA GAT TTT AAC CCT TGC AAA ATC AGC GCG AAT GGC 102
Lys Ser Phe Lys Arg Asp Phe Asn Pro Cys Lys Ile Ser Ala Asn Gly
10 15 20

CTT GTA ACC GGA TTC TTG GAA AAA ATC ACG CTT AAA GCG TTG ATC CCT 150
Leu Val Thr Gly Phe Leu Glu Lys Ile Thr Leu Lys Ala Leu Ile Pro
25 30 35 40

AAT TCA ATC CCA TGC TCT AAA TTC ACA GAC AGA TCG CTA GAA AGC TTG 198
Asn Ser Ile Pro Cys Ser Lys Phe Thr Asp Arg Ser Leu Glu Ser Leu
45 50 55

TTC AGG CTT TCA AAT TCC GCA TGG AAA TCT TTT GAA AAA GAA AGG TTG 246
Phe Arg Leu Ser Asn Ser Ala Trp Lys Ser Phe Glu Lys Glu Arg Leu
60 65 70

ATC TTT TCA ATC TCT AAT TTA GCG TTT TTG ATC AAG CTT TGT TGC ATG 294
Ile Phe Ser Ile Ser Asn Leu Ala Phe Leu Ile Lys Leu Cys Cys Met
75 80 85

ATG CTT TCT ATT TCG CTA TTG AAC TCG TTA GGC TTG TTG ATT AAA GAG 342
Met Leu Ser Ile Ser Leu Leu Asn Ser Leu Gly Leu Leu Ile Lys Glu
90 95 100

GCT AAA TAGGATTTTT GA 360
Ala Lys
105

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Met Ile Leu Gly Asn Asn Val Ser Lys Ser Phe Lys Arg Asp Phe Asn
1 5 10 15
Pro Cys Lys Ile Ser Ala Asn Gly Leu Val Thr Gly Phe Leu Glu Lys
20 25 30

GAG Glu	CGC Arg	TTG Leu	AGC Ser	AGC Ser	GTG Val	ATG Met	AAA Lys	GAT Asp	TTA Leu	CCC Pro	GTG Val	GGG Gly	GTT Val	GAG Glu	GGG Gly	444
115120125																
GGC Gly	ATG Met	GCG Ala	CCC Pro	ATT Ile	GTT Val	ACG Thr	CCG Pro	CTA Leu	TCA Ser	GAT Asp	ATC Ile	TTT Phe	ATG Met	TTC Phe	ACT Thr	492
130135140																
ATT Ile	GAT Asp	GGC Gly	AAT Asn	ATC Ile	ACT Thr	GAG Glu	ATA Ile	GAA Glu	AAA Lys	CGA Arg	CAG Gln	CTT Leu	TTA Leu	GAT Asp	TTT Phe	540
145150155160																
GTG Val	ATC Ile	CGC Arg	CCA Pro	CAA Gln	TTA Leu	AGA Arg	ATG Met	ATT Ile	AGC Ser	GGC Gly	GTA Val	GCA Ala	GAT Asp	GTC Val	AAT Asn	588
165170175																
TCC Ser	ATT Ile	GGA Gly	GGC Gly	TTT Phe	AGC Ser	AGA Arg	GCG Ala	TTT Phe	GTG Val	ATC Ile	GTG Val	CCG Pro	GAT Asp	TTT Phe	AAT Asn	636
180185190																
GAC Asp	ATG Met	GCA Ala	AGG Arg	CTT Leu	GGG Gly	GTG Val	AGT Ser	ATT Ile	TCT Ser	GAT Asp	TTA Leu	GAA Glu	TCG Ser	GCT Ala	GTG Val	684
195200205																
AGA Arg	GTG Val	AAT Asn	TTA Leu	AGA Arg	AAC Asn	AGC Ser	GGA Gly	GCG Ala	GGG Gly	CGC Arg	GTG Val	GAT Asp	AGA Arg	GAT Asp	GGC Gly	732
210215220																
GAA Glu	ACC Thr	TTT Phe	TTA Leu	GTC Val	AAA Lys	ATC Ile	CAA Gln	ACC Thr	GCT Ala	TCT Ser	TTG Leu	AGT Ser	TTA Leu	GAA Glu	GAC Asp	780
225230235240																
ATT Ile	GGC Gly	AAA Lys	ATC Ile	ACC Thr	GTT Val	TCC Ser	ACT Thr	AAT Asn	TTA Leu	GGG Gly	CAT His	TTG Leu	CAC His	ATT Ile	AAG Lys	828
245250255																
GAT Asp	TTT Phe	GCG Ala	AAA Lys	GTC Val	ATC Ile	AGC Ser	CAG Gln	TCT Ser	CGC Arg	ACC Thr	CGT Arg	TTG Leu	GGG Gly	TTT Phe	GTT Val	876
260265270																
ACT Thr	AAA Lys	GAT Asp	GGC Gly	GTG Val	GGC Gly	GAG Glu	ACC Thr	ACA Thr	GAA Glu	GGC Gly	TTG Leu	GTG Val	CTT Leu	TCT Ser	TTA Leu	924
275280285																
AAA Lys	GAC Asp	GCT Ala	AAC Asn	ACC Thr	AAA Lys	GAA Glu	ATC Ile	ATC Ile	ACT Thr	CAA Gln	GTG Val	TAT Tyr	CAA Gln	AAA Lys	CTA Leu	972
290295300																
GAA Glu	GAA Glu	TTA Leu	AAA Lys	CCC Pro	TTT Phe	TTA Leu	CCG Pro	AAT Asn	GGC Gly	GTG Val	TCC Ser	ATT Ile	AAT Asn	GTT Val	TTT Phe	1020
305310315320																
TAT Tyr	GAT Asp	CGC Arg	TCA Ser	GAA Glu	TTT Phe	ACG Thr	CAA Gln	AAA Lys	GCC Ala	ATT Ile	GCC Ala	ACC Thr	GTT Val	TCT Ser	AAA Lys	1068
325330335																
ACC Thr	CTC Leu	ATT Ile	GAA Glu	GCC Ala	GTT Val	GTT Val	TTA Leu	ATC Ile	ATC Ile	ATC Ile	ACG Thr	CTC Leu	TTT Phe	TTA Leu	TTT Phe	1116

340								345				350						
TTA Leu	GGG Gly	AAT Asn 355	TTG Leu	AGG Arg	GCG Ala	AGC Ser	GTG Val 360	GCT Ala	GTG Val	GGG Gly	GTG Val	ATT Ile 365	TTA Leu	CCT Pro	TTA Leu	1164		
AGC Ser	TTG Leu 370	TCC Ser	GTG Val	GCG Ala	TTT Phe 375	ATT Ile	TTT Phe	ATC Ile	AAG Lys	TTT Phe 380	AGC Ser	GAT Asp	CTG Leu	ACT Thr	TTA Leu	1212		
AAT Asn 385	TTG Leu	ATG Met	AGT Ser	TTA Leu	GGG Gly 390	GGA Gly	TTG Leu	GTT Val	ATC Ile	GCT Ala 395	ATA Ile	GGC Gly	ATG Met	CTC Leu	ATT Ile 400	1260		
GAC Asp	TCA Ser	GCC Ala	GTG Val 405	GTG Val	GTG Val	GTG Val	GAA Glu	AAC Asn	GCT Ala 410	TTT Phe	GAA Glu	AAA Lys	TTA Leu	AGC Ser 415	GCT Ala	1308		
AAC Asn	ACT Thr	AAA Lys	ACC Thr 420	ACT Thr	AAA Lys	CTC Leu	CAT His	GCA Ala 425	ATC Ile	TAT Tyr	CGT Arg	TCG Ser	TGT Cys 430	AAA Lys	GAA Glu	1356		
ATC Ile	GCT Ala 435	GTT Val	TCA Ser	GTG Val	GTG Val	AGC Ser	GGG Gly 440	GTG Val	GTG Val	ATC Ile	ATC Ile	ATT Ile 445	GTG Val	TTT Phe	TTT Phe	1404		
GTG Val 450	CCG Pro	ATT Ile	TTA Leu	ACC Thr	TTA Leu	CAG Gln 455	GGG Gly	TTA Leu	GAG Glu	GGT Gly	AAG Lys 460	ATG Met	TTT Phe	AGG Arg	CCT Pro	1452		
TTA Leu 465	GCG Ala	CAA Gln	AGC Ser	ATT Ile	GTG Val 470	TAT Tyr	GCG Ala	CTT Leu	TTA Leu	GGC Gly 475	ACT Thr	TTA Leu	GTT Val	CTA Leu	TCT Ser 480	1500		
ATT Ile	ACA Thr	ATC Ile	ATT Ile	CCT Pro 485	GTA Val	GTC Val	AGC Ser	TCT Ser	CTT Leu 490	GTC Val	TTA Leu	AAA Lys	GCC Ala	ACG Thr 495	CCC Pro	1548		
CAT His	AGC Ser	GAA Glu	ACC Thr 500	TTT Phe	TTA Leu	ACG Thr	AGG Arg	TTT Phe 505	TTA Leu	AAC Asn	AGA Arg	ATC Ile	TAC Tyr 510	GCC Ala	CCT Pro	1596		
TTA Leu	TTG Leu	GAA Glu 515	TTT Phe	TTT Phe	GTG Val	CAT His	AAC Asn 520	CCT Pro	AAA Lys	AAA Lys	GTG Val	ATT Ile 525	TTA Leu	GGA Gly	GCG Ala	1644		
TTT Phe 530	GTT Val	TTT Phe	TTA Leu	ATC Ile	GCA Ala	AGC Ser 535	CTT Leu	TCT Ser	TTA Leu	TTC Phe	CCT Pro 540	TTT Phe	GTG Val	GGG Gly	AAG Lys	1692		
AAT Asn 545	TTC Phe	ATG Met	CCC Pro	GTT Val	TTA Leu 550	GAT Asp	GAG Glu	GGC Gly	GAT Asp	GTG Val 555	GTT Val	TTG Leu	AGC Ser	GTG Val	GAA Glu 560	1740		
ACC Thr	ACC Thr	CCT Pro	TCT Ser 565	ATT Ile	TCT Ser	TTA Leu	GAT Asp	CAA Gln	TCT Ser 570	AGG Arg	GAT Asp	CTC Leu	ATG Met	CTA Leu	AAC Asn 575	1788		

ATT Ile	GAG Glu	AGC Ser	GCG Ala 580	ATT Ile	AAA Lys	AAG Lys	CAT His	GTC Val 585	AAG Lys	GAA Glu	GTT Val	AAA Lys	AGC Ser 590	ATT Ile	GTC Val	1836
GCG Ala	CGC Arg	ACA Thr 595	GGG Gly	AGC Ser	GAT Asp	GAA Glu	TTG Leu 600	GGG Gly	CTG Leu	GAT Asp	TTA Leu	GGA Gly 605	GGT Gly	TTG Leu	AAT Asn	1884
CAA Gln 610	ACC Thr	GAT Asp	ACT Thr	TTT Phe	ATT Ile	TCT Ser 615	TTT Phe	ATT Ile	CCT Pro	AAA Lys	AAA Lys 620	GAA Glu	TGG Trp	AGC Ser	GTT Val	1932
AAA Lys 625	ACC Thr	AAA Lys	GAT Asp	GAA Glu	TTA Leu 630	TTA Leu	GAA Glu	AAA Lys	ATC Ile	ATG Met 635	GAT Asp	TCT Ser	TTA Leu	AAA Lys	GAC Asp 640	1980
TTT Phe	AAG Lys	GGG Gly	ATT Ile	AAC Asn 645	TTT Phe	TCT Ser	TTC Phe	ACC Thr	CAA Gln 650	CCC Pro	ATT Ile	GAA Glu	ATG Met	AGA Arg 655	ATT Ile	2028
TCT Ser	GAA Glu	ATG Met	CTG Leu 660	ACA Thr	GGG Gly	GTT Val	AGG Arg	GGG Gly 665	GAT Asp	TTA Leu	GCG Ala	GTT Val 670	AAG Lys	ATT Ile	TTT Phe	2076
GGA Gly	GAT Asp	GGT Gly 675	ATT Ile	AGC Ser	GAA Glu	TTG Leu	AAT Asn 680	GAA Glu	TTG Leu	AGT Ser	TTT Phe	CAA Gln 685	ATC Ile	GCG Ala	CAA Gln	2124
GCT Ala 690	CTA Leu	AAA Lys	GGG Gly	ATT Ile	AAA Lys	GGA Gly 695	TCT Ser	AGT Ser	GAA Glu	GTT Val	TTA Leu 700	ACC Thr	ACG Thr	CTT Leu	AAT Asn	2172
GAG Glu 705	GGC Gly	GTG Val	AAT Asn	TAT Tyr	TTG Leu 710	TAT Tyr	GTA Val	ACC Thr	CCT Pro	AAT Asn 715	AAA Lys	GAA Glu	TCG Ser	ATG Met	GCG Ala 720	2220
GAT Asp	GTG Val	GGG Gly	ATC Ile	ACT Thr 725	AGC Ser	GAT Asp	GAA Glu	TTT Phe	TCC Ser 730	AAG Lys	TTT Phe	TTA Leu	AAA Lys	TCC Ser 735	GCT Ala	2268
TTA Leu	GAG Glu	GGC Gly	TTG Leu 740	GTT Val	GTA Val	GAT Asp	GTG Val	ATC Ile 745	CCT Pro	ACA Thr	GGG Gly	ATT Ile 750	TCA Ser	CGC Arg	ACG Thr	2316
CCA Pro	GTG Val	ATG Met 755	ATC Ile	CGC Arg	CAA Gln	GAG Glu	AGC Ser 760	GAT Asp	TTT Phe	GCA Ala	AGC Ser 765	TCT Ser 770	ATC Ile	ACT Thr	AAA Lys	2364
ATC Ile 770	AAA Lys	AGT Ser	TTA Leu	GCC Ala	TTG Leu	ACT Thr 775	TCA Ser	AAA Lys	TAT Tyr	GGC Gly	GTT Val 780	TTA Leu	GTG Val	CCT Pro	ATC Ile	2412
ACT Thr 785	TCT Ser	ATC Ile	GCC Ala	AAA Lys	ATT Ile 790	GAA Glu	GAA Glu	GTG Val	GAT Asp	GGC Gly 795	CCT Pro	GTT Val	TCT Ser	GTT Val	GTG Val 800	2460
CGT Arg	GAA Glu	AAT Asn	TCA Ser	ATG Met	CGC Arg	ATG Met	AGC Ser	GTG Val	GTT Val	CGC Arg	AGT Ser	AAT Asn	GTG Val	GTG Val	GGG Gly	2508

805																810																815																																																
CGC	GAT	TTG	AAA	TCT	TTT	GTA	GAA	GAG	GCT	AAA	AAA	GTG	ATC	GCT	CAA	2556	Arg	Asp	Leu	Lys	Ser	Phe	Val	Glu	Glu	Ala	Lys	Lys	Val	Ile	Ala	Gln																																																
820																825																830																																																
AAC	ATC	AAA	CTC	CCT	CCC	AGC	TAC	TAT	ATC	ACT	TAT	GGG	GGG	CAG	TTT	2604	Asn	Ile	Lys	Leu	Pro	Pro	Ser	Tyr	Tyr	Ile	Thr	Tyr	Gly	Gly	Gln	Phe																																																
835																840																845																																																
GAA	AAC	CAG	CAA	CGG	GCC	AAT	AAA	AGG	CTC	TCC	ACC	GTT	ATC	CCT	TTA	2652	Glu	Asn	Gln	Gln	Arg	Ala	Asn	Lys	Arg	Leu	Ser	Thr	Val	Ile	Pro	Leu																																																
850																855																860																																																
AGC	ATC	TTA	GCG	ATT	TTT	TTC	ATT	CTT	TTT	TTC	ACT	TTT	AAA	AGC	ATT	2700	Ser	Ile	Leu	Ala	Ile	Phe	Phe	Ile	Leu	Phe	Phe	Thr	Phe	Lys	Ser	Ile																																																
865																870																875																880																																
CCT	TTA	GCC	TTG	CTC	ATT	CTT	TTG	AAT	ATC	CCT	TTT	GCG	GTT	ACC	GGA	2748	Pro	Leu	Ala	Leu	Leu	Ile	Leu	Leu	Asn	Ile	Pro	Phe	Ala	Val	Thr	Gly																																																
885																890																895																																																
GGC	CTT	ATT	GCG	TTG	TTT	GCG	GTC	GGG	GAG	TAT	ATT	TCA	GTG	CCA	GCG	2796	Gly	Leu	Ile	Ala	Leu	Phe	Ala	Val	Gly	Glu	Tyr	Ile	Ser	Val	Pro	Ala																																																
900																905																910																																																
AGC	GTG	GGC	TTT	ATC	GCT	CTT	TTT	GGG	ATT	GCG	GTT	TTA	AAT	GGC	GTG	2844	Ser	Val	Gly	Phe	Ile	Ala	Leu	Phe	Gly	Ile	Ala	Val	Leu	Asn	Gly	Val																																																
915																920																925																																																
GTG	ATG	ATA	GGC	TAT	TTT	AAA	GAG	CTT	CTC	TTG	CAA	GGG	AAA	AGC	GTA	2892	Val	Met	Ile	Gly	Tyr	Phe	Lys	Glu	Leu	Leu	Leu	Gln	Gly	Lys	Ser	Val																																																
930																935																940																																																
GAA	GAA	TGC	GTT	TTA	TTG	GGC	GCT	AAA	AGG	CGT	TTG	AGA	CCG	GTT	TTA	2940	Glu	Glu	Cys	Val	Leu	Leu	Gly	Ala	Lys	Arg	Leu	Arg	Pro	Val	Leu																																																	
945																950																955																																																
ATG	ACC	GCT	TGC	ATT	GCC	GGT	TTG	GGT	TTG	CTC	CCT	TTA	TTA	TTT	TCT	2988	Met	Thr	Ala	Cys	Ile	Ala	Gly	Leu	Gly	Leu	Leu	Pro	Leu	Leu	Phe	Ser																																																
965																970																975																																																
CAT	AGC	GTG	GGA	TCA	GAA	GTC	CAA	AAA	CCT	TTA	GCG	ATC	GTG	GTG	CTT	3036	His	Ser	Val	Gly	Ser	Glu	Val	Gln	Lys	Pro	Leu	Ala	Ile	Val	Val	Leu																																																
980																985																990																																																
GGA	GGC	TTG	GTT	ACC	TCA	AGC	GCT	CTA	ACC	TTA	CTC	CTA	CTG	CCG	CCA	3084	Gly	Gly	Leu	Val	Thr	Ser	Ser	Ala	Leu	Thr	Leu	Leu	Leu	Leu	Pro	Pro																																																
995																1000																1005																																																
ATG	TTT	ATG	CTC	ATC	GCT	AAA	AAG	ATT	AAA	ATC	GTT	TGAGTTAAAG	GATTTC	3136	Met	Phe	Met	Leu	Ile	Ala	Lys	Lys	Ile	Lys	Ile	Val																																																						
1010																1015																1020																																																
ACATGCTCGC																TTTAGAAATT																TATATTGATA																TTTGTTTGAA																AGA																3179

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1020 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Met	Met	Leu	Ala	Ser	Ile	Ile	Glu	Phe	Ser	Leu	Arg	Gln	Arg	Val	Ile
1				5					10					15	
Val	Ile	Val	Gly	Ala	Ile	Leu	Ile	Leu	Phe	Phe	Gly	Thr	Tyr	Ser	Phe
			20					25					30		
Ile	Asn	Thr	Pro	Val	Asp	Ala	Phe	Pro	Asp	Ile	Ser	Pro	Thr	Gln	Val
		35				40					45				
Lys	Ile	Ile	Leu	Lys	Leu	Pro	Gly	Ser	Ser	Pro	Glu	Glu	Met	Glu	Asn
	50				55					60					
Asn	Ile	Val	Arg	Pro	Leu	Glu	Leu	Glu	Leu	Gly	Leu	Lys	Gly	Gln	
65				70				75						80	
Lys	Ser	Leu	Arg	Ser	Val	Ser	Lys	Tyr	Ser	Ile	Ser	Asp	Ile	Thr	Ile
			85					90					95		
Asp	Phe	Asp	Asp	Ser	Val	Asp	Ile	Tyr	Leu	Ala	Arg	Asn	Ile	Val	Asn
			100					105					110		
Glu	Arg	Leu	Ser	Ser	Val	Met	Lys	Asp	Leu	Pro	Val	Gly	Val	Glu	Gly
		115					120					125			
Gly	Met	Ala	Pro	Ile	Val	Thr	Pro	Leu	Ser	Asp	Ile	Phe	Met	Phe	Thr
	130					135					140				
Ile	Asp	Gly	Asn	Ile	Thr	Glu	Ile	Glu	Lys	Arg	Gln	Leu	Leu	Asp	Phe
145				150					155					160	
Val	Ile	Arg	Pro	Gln	Leu	Arg	Met	Ile	Ser	Gly	Val	Ala	Asp	Val	Asn
			165					170						175	
Ser	Ile	Gly	Gly	Phe	Ser	Arg	Ala	Phe	Val	Ile	Val	Pro	Asp	Phe	Asn
			180					185					190		
Asp	Met	Ala	Arg	Leu	Gly	Val	Ser	Ile	Ser	Asp	Leu	Glu	Ser	Ala	Val
	195						200					205			
Arg	Val	Asn	Leu	Arg	Asn	Ser	Gly	Ala	Gly	Arg	Val	Asp	Arg	Asp	Gly
	210				215						220				
Glu	Thr	Phe	Leu	Val	Lys	Ile	Gln	Thr	Ala	Ser	Leu	Ser	Leu	Glu	Asp
225					230					235				240	
Ile	Gly	Lys	Ile	Thr	Val	Ser	Thr	Asn	Leu	Gly	His	Leu	His	Ile	Lys
			245					250					255		
Asp	Phe	Ala	Lys	Val	Ile	Ser	Gln	Ser	Arg	Thr	Arg	Leu	Gly	Phe	Val
			260					265					270		
Thr	Lys	Asp	Gly	Val	Gly	Glu	Thr	Thr	Glu	Gly	Leu	Val	Leu	Ser	Leu
		275					280					285			
Lys	Asp	Ala	Asn	Thr	Lys	Glu	Ile	Ile	Thr	Gln	Val	Tyr	Gln	Lys	Leu
	290					295					300				
Glu	Glu	Leu	Lys	Pro	Phe	Leu	Pro	Asn	Gly	Val	Ser	Ile	Asn	Val	Phe
305					310					315				320	
Tyr	Asp	Arg	Ser	Glu	Phe	Thr	Gln	Lys	Ala	Ile	Ala	Thr	Val	Ser	Lys
			325					330					335		
Thr	Leu	Ile	Glu	Ala	Val	Val	Leu	Ile	Ile	Ile	Thr	Leu	Phe	Leu	Phe
			340					345					350		
Leu	Gly	Asn	Leu	Arg	Ala	Ser	Val	Ala	Val	Gly	Val	Ile	Leu	Pro	Leu
		355				360						365			
Ser	Leu	Ser	Val	Ala	Phe	Ile	Phe	Ile	Lys	Phe	Ser	Asp	Leu	Thr	Leu
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...638
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

AAGCTTATAA AATCATCAAA AAGAGTGCTG AA	ATG AAT GTT TTA ATC AGA TTG	53
	Met Asn Val Leu Ile Arg Leu	
	1 5	
TGC TTT ATT TTT TTG ATT GGG TTT TTT GGC GCG AAT AAA ACC CTA AAC		101
Cys Phe Ile Phe Leu Ile Gly Phe Phe Gly Ala Asn Lys Thr Leu Asn		
10 15 20		
GCA ACA GCC ATT CTT TCT CTT GAC TTT GGC TCT TTT TCC ATG CCA ATC		149
Ala Thr Ala Ile Leu Ser Leu Asp Phe Gly Ser Phe Ser Met Pro Ile		
25 30 35		
ACT GCC AAT TTC TCA GAT GGT GCG TTA AAT GTA TTC AAA TGG TTT GAA		197
Thr Ala Asn Phe Ser Asp Gly Ala Leu Asn Val Phe Lys Trp Phe Glu		
40 45 50 55		
AAA CAC CCA TCA GTG GGT GTT AAA GTT GGT CGG CTT GCA AAT CAA GAC		245
Lys His Pro Ser Val Gly Val Lys Val Gly Arg Leu Ala Asn Gln Asp		
60 65 70		
GAC ACT ATC TTT ACT CTA GTT TTC ATT GTG ATA GTT GTC GCA ATA ATT		293
Asp Thr Ile Phe Thr Leu Val Phe Ile Val Ile Val Val Ala Ile Ile		
75 80 85		
GCC CTT ATC GCT ATT TTT ATA AGG AGT ATA TTA CTA AAC ACA ATT TTT		341
Ala Leu Ile Ala Ile Phe Ile Arg Ser Ile Leu Leu Asn Thr Ile Phe		
90 95 100		
GTA GGA TCG CTC ATA GGA TCC TTA TGG TTG TAT ATG GTA GGG TTT TAT		389
Val Gly Ser Leu Ile Gly Ser Leu Trp Leu Tyr Met Val Gly Phe Tyr		
105 110 115		
TAT TTT TAT GGT GTT CCC TTT TTG AGT TAT TTG AGC GGT TGT TAT GAA		437
Tyr Phe Tyr Gly Val Pro Phe Leu Ser Tyr Leu Ser Gly Cys Tyr Glu		
120 125 130 135		
TCG TTT TCT TTC TCC GCA TGC TAT CCT CAT AGT TTG CAG CTA CTC CCC		485
Ser Phe Ser Phe Ser Ala Cys Tyr Pro His Ser Leu Gln Leu Leu Pro		
140 145 150		

ACC CTT ATG CAG TAT TCG CCC ATT TAC TCC ATA ATC AAA CTT CTT GCT	533
Thr Leu Met Gln Tyr Ser Pro Ile Tyr Ser Ile Ile Lys Leu Leu Ala	
155 160 165	
CAT TTT AAT ATA GAG ATC ACT TCT AAG ATT ATC ATT TCT CTT GTT TGG	581
His Phe Asn Ile Glu Ile Thr Ser Lys Ile Ile Ile Ser Leu Val Trp	
170 175 180	
GTG TGT ATA GGG CTG TAT TTT TTG TTA TTG CAA GCG TTT TTT AGT CTT	629
Val Cys Ile Gly Leu Tyr Phe Leu Leu Leu Gln Ala Phe Phe Ser Leu	
185 190 195	
ACA AAT TAT TAGTTGCAGA AAATTCAAGA AGGCAAAAAA TTATCTTTTT TCCTCGAAT	687
Thr Asn Tyr	
200	
CAATCATTAG GTTATTTTTT GGTTTTATGA TAG	720

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met	Asn	Val	Leu	Ile	Arg	Leu	Cys	Phe	Ile	Phe	Leu	Ile	Gly	Phe	Phe
1				5					10					15	
Gly	Ala	Asn	Lys	Thr	Leu	Asn	Ala	Thr	Ala	Ile	Leu	Ser	Leu	Asp	Phe
			20					25					30		
Gly	Ser	Phe	Ser	Met	Pro	Ile	Thr	Ala	Asn	Phe	Ser	Asp	Gly	Ala	Leu
		35					40					45			
Asn	Val	Phe	Lys	Trp	Phe	Glu	Lys	His	Pro	Ser	Val	Gly	Val	Lys	Val
	50					55				60					
Gly	Arg	Leu	Ala	Asn	Gln	Asp	Asp	Thr	Ile	Phe	Thr	Leu	Val	Phe	Ile
65					70				75					80	
Val	Ile	Val	Val	Ala	Ile	Ile	Ala	Leu	Ile	Ala	Ile	Phe	Ile	Arg	Ser
				85				90					95		
Ile	Leu	Leu	Asn	Thr	Ile	Phe	Val	Gly	Ser	Leu	Ile	Gly	Ser	Leu	Trp
			100					105					110		
Leu	Tyr	Met	Val	Gly	Phe	Tyr	Tyr	Phe	Tyr	Gly	Val	Pro	Phe	Leu	Ser
		115					120					125			
Tyr	Leu	Ser	Gly	Cys	Tyr	Glu	Ser	Phe	Ser	Phe	Ser	Ala	Cys	Tyr	Pro
		130				135				140					
His	Ser	Leu	Gln	Leu	Leu	Pro	Thr	Leu	Met	Gln	Tyr	Ser	Pro	Ile	Tyr
145					150					155					160
Ser	Ile	Ile	Lys	Leu	Leu	Ala	His	Phe	Asn	Ile	Glu	Ile	Thr	Ser	Lys
			165					170					175		
Ile	Ile	Ile	Ser	Leu	Val	Trp	Val	Cys	Ile	Gly	Leu	Tyr	Phe	Leu	Leu
			180					185					190		
Leu	Gln	Ala	Phe	Phe	Ser	Leu	Thr	Asn	Tyr						
		195					200								

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 65...280
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```
AATTCAGAA GGCAAAAAT TATCTTTTTT CCTCGAATCA ATCATTAGGT TATTTTTTGG      60
TTTT ATG ATA GTT TCT TTT ATT GCC GTT CCA TGC TAC TAT GTT TTA TTG      109
Met Ile Val Ser Phe Ile Ala Val Pro Cys Tyr Tyr Val Leu Leu
  1             5             10             15

GCG ATG GAA TAC CAA ATA GCC TAT GAA CAC CCA GGA GAA TTA ATA AGC      157
Ala Met Glu Tyr Gln Ile Ala Tyr Glu His Pro Gly Glu Leu Ile Ser
      20             25             30

ACG ATT GGT TTT GTT GCG TTA GCA GTG CTT GTG TAT TAC TTA TGG GGT      205
Thr Ile Gly Phe Val Ala Leu Ala Val Leu Val Tyr Tyr Leu Trp Gly
      35             40             45

AAA TGG GAG AAG TTG CTA TGG GGC GCA CCT TCC AAT CAA GAG CAA CAA      253
Lys Trp Glu Lys Leu Leu Trp Gly Ala Pro Ser Asn Gln Glu Gln Gln
      50             55             60

CTC TCC AAT CAA GGC AAC CAA AAT CAA TGATTGTGAT TGATCGCTAG GTCAATC      307
Leu Ser Asn Gln Gly Asn Gln Asn Gln
      65             70

TGA                                                                    310
```

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```
Met Ile Val Ser Phe Ile Ala Val Pro Cys Tyr Tyr Val Leu Leu Ala
  1             5             10             15
Met Glu Tyr Gln Ile Ala Tyr Glu His Pro Gly Glu Leu Ile Ser Thr
      20             25             30
Ile Gly Phe Val Ala Leu Ala Val Leu Val Tyr Tyr Leu Trp Gly Lys
      35             40             45
Trp Glu Lys Leu Leu Trp Gly Ala Pro Ser Asn Gln Glu Gln Gln Leu
```


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Met	Val	Val	Ser	Met	Asn	Cys	Ile	Gly	Ser	Lys	Tyr	Lys	Leu	Ile	Ala
1				5					10					15	
Phe	Ile	Gln	Glu	Asn	Ile	His	Ala	Val	Val	Gly	Gln	Pro	Phe	Gly	Cys
			20					25					30		
Asp	Phe	Leu	Arg	Ser	Val	Arg	Trp	Asp	Gly	Tyr	Arg	Gly	Val	Cys	Val
		35					40					45			
Lys	Trp	Ser	Leu	Gly	Ser	Thr	Leu	Lys	Asn	Ile	Phe	Ser	Leu	Asp	Ser
	50					55					60				
Val	Leu	Lys	Ala	Asn	Gln	Val	Ile	Pro	Lys	Asp	Ala				
65					70					75					

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...872
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

AAAATTAAGT	TGTTTGATCG	CTTTTAAACG	ATTTTAAAA	GGAAAAATTT	ATG GAT	56
					Met Asp	
					1	
GAA ATT AAA ACG CTG TTA GTG GAT TTT TTT CCG CAG GCA AAG CAT TTT						104
Glu Ile Lys Thr Leu Leu Val Asp Phe Phe Pro Gln Ala Lys His Phe						
	5		10		15	
GGG ATA ATC TTA ATC AAG GCT ATT GTT GTC TTT TGT ATA GGT TTT TAT						152
Gly Ile Ile Leu Ile Lys Ala Ile Val Val Phe Cys Ile Gly Phe Tyr						
	20		25		30	
TTT TCA TTT TTC TTA CAA AAA AAA ACC ATG AAA TTT TTA TCC AAA AAG						200
Phe Ser Phe Phe Leu Gln Lys Lys Thr Met Lys Phe Leu Ser Lys Lys						
	35		40		45	50
GAT GAG ATT TTA GCG AAT TTT GTC GCA CAG GTT ACT TTT ATC TTA ATC						248
Asp Glu Ile Leu Ala Asn Phe Val Ala Gln Val Thr Phe Ile Leu Ile						
		55		60		65
CTT ATC ATC ACC ACA ATC ATT GCG CTC AGC ACG CTA GGC GTG CAA ACC						296
Leu Ile Ile Thr Thr Ile Ile Ala Leu Ser Thr Leu Gly Val Gln Thr						
	70		75		80	
ACC TCT ATT ATC ACT GTT TTA GGA ACG GTA GGG ATT GCT GTG GCG TTG						344
Thr Ser Ile Ile Thr Val Leu Gly Thr Val Gly Ile Ala Val Ala Leu						
	85		90		95	

ATAGAATAAG TATTTTTTTTTT CCAAAC TATT CCTATTTTAG TGGTAGTGTT G

833

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Met	Gln	Ser	Leu	Ala	Gly	Gly	Leu	Ser	Gly	Arg	Ala	Trp	Gly	Glu	Met
1				5					10					15	
Leu	Cys	Lys	Met	Val	Asn	Asp	Ser	Asn	Tyr	Glu	Ser	Glu	Gln	Ala	Leu
			20					25					30		
Leu	Ala	Thr	Gly	Asn	Ser	Ser	Glu	Gln	Lys	Arg	Arg	Phe	Leu	Leu	
		35					40				45				
Arg	Val	Lys	Lys	Lys	Val	Asn	Asp	Asn	Arg	Gln	Leu	Lys	Lys	Lys	Leu
	50					55				60					
Asp	Pro	Phe	Leu	Lys	Arg	Leu	Asp	Val	Leu	Gln	Thr	Glu	Phe	Gly	Val
65					70				75						80
Thr	Asp	Pro	Thr	Ala	Asn	His	Asn	Lys	Gln	Gly	Ile	His	Tyr	Cys	Thr
				85				90						95	
Glu	Asn	Lys	Lys	Thr	Gly	Lys	Cys	Asp	Pro	Ile	Asp	Asn	Val	Phe	Arg
			100				105						110		
Thr	Thr	Arg	Leu	Asp	Asn	Glu	Leu	Glu	Gln	Glu	Ile	Gln	Thr	Leu	Thr
		115				120						125			
Leu	Asp	Leu	Thr	Lys	Ala	Pro	Asn	Lys	Asp	Ala	Gln	Ser	Gln	Ala	Tyr
		130				135				140					
Ala	Asn	Phe	Asn	Gln	Arg	Ile	Lys	Leu	Leu	Thr	Leu	Lys	Tyr	Leu	Lys
145					150				155						160
Glu	Ile	Thr	Asn	Gln	Met	Leu	Phe	Leu	Asn	Gln	Thr	Met	Ala	Met	Gln
				165				170						175	
Ser	Glu	Ile	Met	Ala	Asp	Asp	Tyr	Phe	Arg	Gln	Asn	Asn	Asp	Gly	Phe
			180				185						190		
Gly	Lys	Glu	Glu	Asn	His	Ile	Asp	Lys	Gln	Leu	Thr	Gln	Lys	Arg	Ile
		195				200						205			
Asn	Glu	Arg	Glu	Arg	Ala	Arg	Ile	Tyr	Phe	Gln	Asn	Pro	Asn	Val	Lys
	210					215					220				
Phe	Asp	Gln	Phe	Gly	Phe	Pro	Ile	Phe	Ser	Ile	Trp	Asp			
225					230					235					

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 63...311
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```

TCAAACCAAA ACCAACACAA AATTTGCTAA ACTACAATCA AATCAATTTA GGGAGGATAA      60
AA ATG TCA TTT GCC CCT ATG TTA TTA GCT ACA ATC AAT AAC TCT ATT      107
  Met Ser Phe Ala Pro Met Leu Leu Ala Thr Ile Asn Asn Ser Ile
    1             5             10             15

GGC AAT AAA GAT AAG CAT GTG AGT TTA GAG TAT CTT ATA GGG CTT TTT      155
Gly Asn Lys Asp Lys His Val Ser Leu Glu Tyr Leu Ile Gly Leu Phe
      20             25             30

ATG GAT AAA AAA ACA ACT AAT CTA AGC AAT ACT GAC AAG TAT ATT ATA      203
Met Asp Lys Lys Thr Thr Asn Leu Ser Asn Thr Asp Lys Tyr Ile Ile
      35             40             45

GGC ACA ATT CAA ACA GAG GCA CTA GAG CAA GAA ATA GAA TGG TTT TCA      251
Gly Thr Ile Gln Thr Glu Ala Leu Glu Gln Glu Ile Glu Trp Phe Ser
      50             55             60

CAA GAC TAT CAC ATT CCT ATG GAG AAT ATT TTA CAT GTC CTT TCT ATC      299
Gln Asp Tyr His Ile Pro Met Glu Asn Ile Leu His Val Leu Ser Ile
      65             70             75

AAT CCC TAT CAA TGAAAAGAGC CTTAGTTTTA TCAAAAACAA CTTTCAAGCT      351
Asn Pro Tyr Gln
80
  
```

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```

Met Ser Phe Ala Pro Met Leu Leu Ala Thr Ile Asn Asn Ser Ile Gly
  1             5             10             15
Asn Lys Asp Lys His Val Ser Leu Glu Tyr Leu Ile Gly Leu Phe Met
      20             25             30
Asp Lys Lys Thr Thr Asn Leu Ser Asn Thr Asp Lys Tyr Ile Ile Gly
      35             40             45
Thr Ile Gln Thr Glu Ala Leu Glu Gln Glu Ile Glu Trp Phe Ser Gln
      50             55             60
Asp Tyr His Ile Pro Met Glu Asn Ile Leu His Val Leu Ser Ile Asn
      65             70             75             80
Pro Tyr Gln
  
```

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1934 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 67...1866
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```
AAACATAGGG CAAATCTAGT TGGCACAAAA ACAGCTAGTC CTGTGCTTAT TAAAAACATA      60
GGGCAA ATG AAA CGC TCC CAC TTA GAA AAT GCC CTA AAT TAT GCT TTA      108
Met Lys Arg Ser His Leu Glu Asn Ala Leu Asn Tyr Ala Leu
   1             5             10

GAA AAT AGC GAA ACA GCT TAC AAT GAA ATG TTT TTA GAA TGC GAT AAG      156
Glu Asn Ser Glu Thr Ala Tyr Asn Glu Met Phe Leu Glu Cys Asp Lys
  15             20             25             30

CAA TTC ATC TTA GAG AGT TGG CTC AAT GAC TTT GAT TTG ACT AAA GAT      204
Gln Phe Ile Leu Glu Ser Trp Leu Asn Asp Phe Asp Leu Thr Lys Asp
             35             40             45

TAT AAC GAG ACT ATG CAC TTA GTT TTT TCT ATC AAA GAT AAG CCA GAT      252
Tyr Asn Glu Thr Met His Leu Val Phe Ser Ile Lys Asp Lys Pro Asp
             50             55             60

GAA GAG ACA ATG CAA GGG CTT TTA CAT TCT ACT TGG GAG AGC TTA AAA      300
Glu Glu Thr Met Gln Gly Leu Leu His Ser Thr Trp Glu Ser Leu Lys
             65             70             75

ATA AGA TTG CCT GAA TAC AAG TTT GCC CTT GTG CCA CAC GCT CAT CAA      348
Ile Arg Leu Pro Glu Tyr Lys Phe Ala Leu Val Pro His Ala His Gln
             80             85             90

GAC CAT GCC CAT ATC CAT TGT TTT ATC AAT AAG ACT AAT CAG CTC ACA      396
Asp His Ala His Ile His Cys Phe Ile Asn Lys Thr Asn Gln Leu Thr
             95             100             105             110

CGA AGA AGA CTG CGT TTT AAG GGG CAT GAA GAT TGT AAA GAA TTT TTT      444
Arg Arg Arg Leu Arg Phe Lys Gly His Glu Asp Cys Lys Glu Phe Phe
             115             120             125

AAT GAA TTA AGA AGT GAG TTT GCT TAT AGG TTG AAT GAC CAC TTA TTG      492
Asn Glu Leu Arg Ser Glu Phe Ala Tyr Arg Leu Asn Asp His Leu Leu
             130             135             140

AGC GAA GAA TAC TTG TAT GTC AAT GAG CCA AAA CTT AAA GAG CTA GAC      540
Ser Glu Glu Tyr Leu Tyr Val Asn Glu Pro Lys Leu Lys Glu Leu Asp
             145             150             155
```

AAT ATC AAA CAA CAA TTA CAA GAC TTG GAA AAA GAA GAA AAA GCC TTA	588
Asn Ile Lys Gln Gln Leu Gln Asp Leu Glu Lys Glu Glu Lys Ala Leu	
160 165 170	
GAA CAA ATC AAA TCC CCA CAA GAT GAG TGG GAC TTA AAC AAG GCT TTA	636
Glu Gln Ile Lys Ser Pro Gln Asp Glu Trp Asp Leu Asn Lys Ala Leu	
175 180 185 190	
CAA AGC GAG TAT TTA CAA GAA CTC AAA TAT AAA AAC AAA GCA AAA GCC	684
Gln Ser Glu Tyr Leu Gln Glu Leu Lys Tyr Lys Asn Lys Ala Lys Ala	
195 200 205	
CTA GAC ATT CAA AAT AAC CAC AGC ACC CCT TTA AAA CAA AAG ATT TCT	732
Leu Asp Ile Gln Asn Asn His Ser Thr Pro Leu Lys Gln Lys Ile Ser	
210 215 220	
GAA TTT AAA ATC GCT CTG TTT AAT CAC AAA GAC ACA AGC GAT GAT GAA	780
Glu Phe Lys Ile Ala Leu Phe Asn His Lys Asp Thr Ser Asp Asp Glu	
225 230 235	
AAA GAA CAG CTA GAT ATT GAC AGG ATA GAT AAG AGA AAA CCA GTA AGC	828
Lys Glu Gln Leu Asp Ile Asp Arg Ile Asp Lys Arg Lys Pro Val Ser	
240 245 250	
GAA CAC TTA AAA AAC ACT AAC AAA CAC GAG CTA TAC GAA CTC TTA GGC	876
Glu His Leu Lys Asn Thr Asn Lys His Glu Leu Tyr Glu Leu Leu Gly	
255 260 265 270	
TTT TAT CAA AAA GAA TTA GAT AAA AAA CAA AAC CAT TCA GCC TTT AAG	924
Phe Tyr Gln Lys Glu Leu Asp Lys Lys Gln Asn His Ser Ala Phe Lys	
275 280 285	
AAT TTT GCT ATT CTC AAT GGT TTA GAC AGA GAC TTT GAA AGA GAG ACT	972
Asn Phe Ala Ile Leu Asn Gly Leu Asp Arg Asp Phe Glu Arg Glu Thr	
290 295 300	
AAT GGC TAT TCT GTT TTA AAG AAA AAA GAA ATG CTT TTA AAT AAG CTT	1020
Asn Gly Tyr Ser Val Leu Lys Lys Lys Glu Met Leu Leu Asn Lys Leu	
305 310 315	
GAA CAC CTA GAC AAA CGC CTT TTA GAT AAA AAC TCA CAC TTA CTA TTA	1068
Glu His Leu Asp Lys Arg Leu Leu Asp Lys Asn Ser His Leu Leu Leu	
320 325 330	
GCC CAG CTA AGA AAT GAA GTT AAA ACC AAG CAA AAC ATC CAA TAC AAC	1116
Ala Gln Leu Arg Asn Glu Val Lys Thr Lys Gln Asn Ile Gln Tyr Asn	
335 340 345 350	
ACT CTA ACT AAT CCT ATT CTT TTA GCC AAA GCC TTA GAA CTT TCT AAA	1164
Thr Leu Thr Asn Pro Ile Leu Leu Ala Lys Ala Leu Glu Leu Ser Lys	
355 360 365	
GAT AAA CGC CCC ACT CTC AAA ACT TTT AAA AAC GCT TAT TTT AGT GCT	1212
Asp Lys Arg Pro Thr Leu Lys Thr Phe Lys Asn Ala Tyr Phe Ser Ala	
370 375 380	
AGA AAA TAT CAA TTC ATG CTA GAG AGC TTT AAA ACT AAG CAA AAT GAC	1260
Arg Lys Tyr Gln Phe Met Leu Glu Ser Phe Lys Thr Lys Gln Asn Asp	

385	390	395	
CCC ACT TAC AAG CTT AAT GAT AAC ACT TAT GAG CTA GTG AGT AAG CAA Pro Thr Tyr Lys Leu Asn Asp Asn Thr Tyr Glu Leu Val Ser Lys Gln 400 405 410			1308
CTA CAA GAC TAT CAA AAC ACC ATG CTT TTA TTA GCC AAA GAG AGA TTA Leu Gln Asp Tyr Gln Asn Thr Met Leu Leu Leu Ala Lys Glu Arg Leu 415 420 425 430			1356
CTT TTT TTA GAA CAA GAT TTA AAA CAA AAA GAA GAA GAG TTT GAA AGA Leu Phe Leu Glu Gln Asp Leu Lys Gln Lys Glu Glu Glu Phe Glu Arg 435 440 445			1404
GCC AAA GAA CAT TAT GTG AAA TCT TCA AAA CAT TAT AGA GAA ACT TCA Ala Lys Glu His Tyr Val Lys Ser Ser Lys His Tyr Arg Glu Thr Ser 450 455 460			1452
TTG TCT CCA AAA GAA AAA CAA GGC TTT CTC AAA CAA ATT AAA CAA TTT Leu Ser Pro Lys Glu Lys Gln Gly Phe Leu Lys Gln Ile Lys Gln Phe 465 470 475			1500
TCT AAA ATT TCT AAG GAT ATT CTC TAT ACT TGT AAT GAG ATC ATA GGA Ser Lys Ile Ser Lys Asp Ile Leu Tyr Thr Cys Asn Glu Ile Ile Gly 480 485 490			1548
GCT AAT AGG TTT TTA ACC CAC TAT GAC AAC CTA AAC CTT GAA AAA GTC Ala Asn Arg Phe Leu Thr His Tyr Asp Asn Leu Asn Leu Glu Lys Val 495 500 505 510			1596
CTA GAA CAC GCT AAA GAT ACT AAG CTA GAG CAA AAA GAA ATT CAA GCT Leu Glu His Ala Lys Asp Thr Lys Leu Glu Gln Lys Glu Ile Gln Ala 515 520 525			1644
ATC ACA AAA GAG CCT AAT AAC GAT GAG CCT TGG ATT GAG TTT GGT AAA Ile Thr Lys Glu Pro Asn Asn Asp Glu Pro Trp Ile Glu Phe Gly Lys 530 535 540			1692
AAA GAA CAA GCT AGA GCT AAA GCA CAC TAT CAA GCT ATG CTA GAA AAA Lys Glu Gln Ala Arg Ala Lys Ala His Tyr Gln Ala Met Leu Glu Lys 545 550 555			1740
GAA AAA GCT AAA GAA TTA GCT AAA CAA CAA GCT AAC ACC TTG CAC TCT Glu Lys Ala Lys Glu Leu Ala Lys Gln Gln Ala Asn Thr Leu His Ser 560 565 570			1788
AAT GAG CTT GAT GAT GAC CCT AAA GCT CAT GCT GGA TTA AAA CAA AAT Asn Glu Leu Asp Asp Asp Pro Lys Ala His Ala Gly Leu Lys Gln Asn 575 580 585 590			1836
GAC AAC ACA AAC TTT AAA GGG CGT AAT AGA TAATGCTCTC AAGCGATGAT TGC Asp Asn Thr Asn Phe Lys Gly Arg Asn Arg 595 600			1889
CTTTAATGTT CTTAATAAAG AATATACCCT TTGAAAGGGG TTTAT			1934

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 600 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Met	Lys	Arg	Ser	His	Leu	Glu	Asn	Ala	Leu	Asn	Tyr	Ala	Leu	Glu	Asn
1				5					10					15	
Ser	Glu	Thr	Ala	Tyr	Asn	Glu	Met	Phe	Leu	Glu	Cys	Asp	Lys	Gln	Phe
			20					25					30		
Ile	Leu	Glu	Ser	Trp	Leu	Asn	Asp	Phe	Asp	Leu	Thr	Lys	Asp	Tyr	Asn
		35					40					45			
Glu	Thr	Met	His	Leu	Val	Phe	Ser	Ile	Lys	Asp	Lys	Pro	Asp	Glu	Glu
	50					55					60				
Thr	Met	Gln	Gly	Leu	Leu	His	Ser	Thr	Trp	Glu	Ser	Leu	Lys	Ile	Arg
65					70					75					80
Leu	Pro	Glu	Tyr	Lys	Phe	Ala	Leu	Val	Pro	His	Ala	His	Gln	Asp	His
				85					90					95	
Ala	His	Ile	His	Cys	Phe	Ile	Asn	Lys	Thr	Asn	Gln	Leu	Thr	Arg	Arg
			100					105					110		
Arg	Leu	Arg	Phe	Lys	Gly	His	Glu	Asp	Cys	Lys	Glu	Phe	Phe	Asn	Glu
		115					120					125			
Leu	Arg	Ser	Glu	Phe	Ala	Tyr	Arg	Leu	Asn	Asp	His	Leu	Leu	Ser	Glu
	130					135					140				
Glu	Tyr	Leu	Tyr	Val	Asn	Glu	Pro	Lys	Leu	Lys	Glu	Leu	Asp	Asn	Ile
145					150					155					160
Lys	Gln	Gln	Leu	Gln	Asp	Leu	Glu	Lys	Glu	Glu	Lys	Ala	Leu	Glu	Gln
				165					170					175	
Ile	Lys	Ser	Pro	Gln	Asp	Glu	Trp	Asp	Leu	Asn	Lys	Ala	Leu	Gln	Ser
			180					185					190		
Glu	Tyr	Leu	Gln	Glu	Leu	Lys	Tyr	Lys	Asn	Lys	Ala	Lys	Ala	Leu	Asp
		195					200				205				
Ile	Gln	Asn	Asn	His	Ser	Thr	Pro	Leu	Lys	Gln	Lys	Ile	Ser	Glu	Phe
	210					215					220				
Lys	Ile	Ala	Leu	Phe	Asn	His	Lys	Asp	Thr	Ser	Asp	Asp	Glu	Lys	Glu
225					230					235					240
Gln	Leu	Asp	Ile	Asp	Arg	Ile	Asp	Lys	Arg	Lys	Pro	Val	Ser	Glu	His
				245					250					255	
Leu	Lys	Asn	Thr	Asn	Lys	His	Glu	Leu	Tyr	Glu	Leu	Leu	Gly	Phe	Tyr
			260				265						270		
Gln	Lys	Glu	Leu	Asp	Lys	Lys	Gln	Asn	His	Ser	Ala	Phe	Lys	Asn	Phe
		275					280					285			
Ala	Ile	Leu	Asn	Gly	Leu	Asp	Arg	Asp	Phe	Glu	Arg	Glu	Thr	Asn	Gly
	290					295					300				
Tyr	Ser	Val	Leu	Lys	Lys	Lys	Glu	Met	Leu	Leu	Asn	Lys	Leu	Glu	His
305					310					315					320
Leu	Asp	Lys	Arg	Leu	Asp	Lys	Asn	Ser	His	Leu	Leu	Leu	Ala	Gln	
				325				330					335		
Leu	Arg	Asn	Glu	Val	Lys	Thr	Lys	Gln	Asn	Ile	Gln	Tyr	Asn	Thr	Leu
			340				345						350		
Thr	Asn	Pro	Ile	Leu	Leu	Ala	Lys	Ala	Leu	Glu	Leu	Ser	Lys	Asp	Lys
		355				360						365			
Arg	Pro	Thr	Leu	Lys	Thr	Phe	Lys	Asn	Ala	Tyr	Phe	Ser	Ala	Arg	Lys
	370					375					380				

0950027-061504

GAA AAG TTT GCT AAA AAT TTA ACC CAA CTG ACA CAA GAA GAA TTC ATG Glu Lys Phe Ala Lys Asn Leu Thr Gln Leu Thr Gln Glu Glu Phe Met 45 50 55	195
CGT TTA AGA GAG CCA CAA AAA CAA GTG GTC ATC AAA AAC ATA GGC AAT Arg Leu Arg Glu Pro Gln Lys Gln Val Val Ile Lys Asn Ile Gly Asn 60 65 70	243
ATG ACA CGC CTG CAT TCA AAA AGA GCG ATG GAT TAT ATC GCT AAA CAT Met Thr Arg Leu His Ser Lys Arg Ala Met Asp Tyr Ile Ala Lys His 75 80 85 90	291
GGT GAG CTA GTG AGA GAT GAA TTT TTT AAT GAA GTT AAT TAT AAT GAC Gly Glu Leu Val Arg Asp Glu Phe Phe Asn Glu Val Asn Tyr Asn Asp 95 100 105	339
ATA GCA GAG CAA TGG AAT GAG CAA TTT GAA AAA TTA TTA GAA AAT AAG Ile Ala Glu Gln Trp Asn Glu Gln Phe Glu Lys Leu Leu Glu Asn Lys 110 115 120	387
AGC CGT GTT AAA AAT TGC GCT TTA CAT CTA GTG TTT AGC ATT GAT GAA Ser Arg Val Lys Asn Cys Ala Leu His Leu Val Phe Ser Ile Asp Glu 125 130 135	435
AAT TGT AAT GAA AAA AAT TTA AAA GCT TTG GAA TTA AGC GTG TAT CAA Asn Cys Asn Glu Lys Asn Leu Lys Ala Leu Glu Leu Ser Val Tyr Gln 140 145 150	483
ACA CTC ACT AAC ACG CTA GGT TAT GAT TAT CCT TTT ATA ATG AAA CTC Thr Leu Thr Asn Thr Leu Gly Tyr Asp Tyr Pro Phe Ile Met Lys Leu 155 160 165 170	531
CAT ACA CAC CAA AAC AAT CCG CAT GCG CAT GTG ATT ATC AAC AAA ACT His Thr His Gln Asn Asn Pro His Ala His Val Ile Ile Asn Lys Thr 175 180 185	579
AAC AAA ATT ACC AAT AAG CAA CTA TGC TTT AAT TCT AAA GAC AGC TGT Asn Lys Ile Thr Asn Lys Gln Leu Cys Phe Asn Ser Lys Asp Ser Cys 190 195 200	627
AAA GAG TTT TAC CAC ACA CTA AGA GAA ACA TTT AAA GAT TAT TTA TTT Lys Glu Phe Tyr His Thr Leu Arg Glu Thr Phe Lys Asp Tyr Leu Phe 205 210 215	675
GCT AAC TCA AAA GGC GAA TTG CAA TAT TCT AAC ACG CCT AAT ATT TAT Ala Asn Ser Lys Gly Glu Leu Gln Tyr Ser Asn Thr Pro Asn Ile Tyr 220 225 230	723
AAG GCG ATT AAA GAC ATA GAA ACA GAG CTA GAT GCA CTA GAA AAC AGG Lys Ala Ile Lys Asp Ile Glu Thr Glu Leu Asp Ala Leu Glu Asn Arg 235 240 245 250	771
CTA GAA ACA ATA AGA GTT TTA GGC ATG AAA ACT ATT TTT ATA AAG TTT Leu Glu Thr Ile Arg Val Leu Gly Met Lys Thr Ile Phe Ile Lys Phe 255 260 265	819
TGG GTA GTG CAA CTT CTC AAA TAGAAAGTTT GAAAAAAGA GAAAATGCCC TATT Trp Val Val Gln Leu Leu Lys	874

TGATCATTTA

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```

Met Ala Leu Glu Lys Ser Tyr Ser Lys Asn Phe Glu Ser Asp Glu Leu
 1           5           10           15
Phe Asp Tyr Glu Ile Ile Lys Pro Lys Lys Thr Leu Lys Ile Gln Tyr
          20           25           30
Thr Tyr Ala Lys Arg Tyr Tyr Lys Glu Val Glu Lys Phe Ala Lys Asn
          35           40           45
Leu Thr Gln Leu Thr Gln Glu Phe Met Arg Leu Arg Glu Pro Gln
          50           55           60
Lys Gln Val Val Ile Lys Asn Ile Gly Asn Met Thr Arg Leu His Ser
65           70           75           80
Lys Arg Ala Met Asp Tyr Ile Ala Lys His Gly Glu Leu Val Arg Asp
          85           90           95
Glu Phe Phe Asn Glu Val Asn Tyr Asn Asp Ile Ala Glu Gln Trp Asn
          100          105          110
Glu Gln Phe Glu Lys Leu Leu Glu Asn Lys Ser Arg Val Lys Asn Cys
          115          120          125
Ala Leu His Leu Val Phe Ser Ile Asp Glu Asn Cys Asn Glu Lys Asn
          130          135          140
Leu Lys Ala Leu Glu Leu Ser Val Tyr Gln Thr Leu Thr Asn Thr Leu
145          150          155          160
Gly Tyr Asp Tyr Pro Phe Ile Met Lys Leu His Thr His Gln Asn Asn
          165          170          175
Pro His Ala His Val Ile Ile Asn Lys Thr Asn Lys Ile Thr Asn Lys
          180          185          190
Gln Leu Cys Phe Asn Ser Lys Asp Ser Cys Lys Glu Phe Tyr His Thr
          195          200          205
Leu Arg Glu Thr Phe Lys Asp Tyr Leu Phe Ala Asn Ser Lys Gly Glu
          210          215          220
Leu Gln Tyr Ser Asn Thr Pro Asn Ile Tyr Lys Ala Ile Lys Asp Ile
225          230          235          240
Glu Thr Glu Leu Asp Ala Leu Glu Asn Arg Leu Glu Thr Ile Arg Val
          245          250          255
Leu Gly Met Lys Thr Ile Phe Ile Lys Phe Trp Val Val Gln Leu Leu
          260          265          270
Lys

```

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 49...519
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

ATAAACAACC ATGACAAACT AACGGACTTT AAGCAATACC AAACAGAC ATG AAA GAA	57
Met Lys Glu	
1	
TTA CTA GGG ATA GAA ATA GAT GAA GAG CTG GAT ACT AAA CGA CTT ATC	105
Leu Leu Gly Ile Glu Ile Asp Glu Glu Leu Asp Thr Lys Arg Leu Ile	
5 10 15	
CCT ACT TAT TCC AAA TTG TAT TCT TTA AAA AAA TAC TCT AAA AAA TTT	153
Pro Thr Tyr Ser Lys Leu Tyr Ser Leu Lys Lys Tyr Ser Lys Lys Phe	
20 25 30 35	
AAA AGA TTA CAA AGA AAA CAA AGC CGT AGG GTG TTA AAG TCT AAA CAA	201
Lys Arg Leu Gln Arg Lys Gln Ser Arg Arg Val Leu Lys Ser Lys Gln	
40 45 50	
AAC AAA ACC AAA TTA GGA GGT AAT TTT TAC AAA ACC CAA AAG AAA TTA	249
Asn Lys Thr Lys Leu Gly Gly Asn Phe Tyr Lys Thr Gln Lys Lys Leu	
55 60 65	
AAC CAA GCC TTT GAC AAG TCT AGT CAT CAA AAA ACA GAC AGA TAC CAT	297
Asn Gln Ala Phe Asp Lys Ser Ser His Gln Lys Thr Asp Arg Tyr His	
70 75 80	
AAA ATC ACA AGC GAA CTT TCA AAG CAA TTT GAA TTG ATA GTA GTT GAA	345
Lys Ile Thr Ser Glu Leu Ser Lys Gln Phe Glu Leu Ile Val Val Glu	
85 90 95	
GAT TTG CAA GTA AAA AAC ATG ACT AAA AGA GCT AAA CTC AAA AAT GTT	393
Asp Leu Gln Val Lys Asn Met Thr Lys Arg Ala Lys Leu Lys Asn Val	
100 105 110 115	
AAA CAA AAG AGT GGG CTT AAT CAA TCT ATT TTA AAC GCT TCA TTC TAT	441
Lys Gln Lys Ser Gly Leu Asn Gln Ser Ile Leu Asn Ala Ser Phe Tyr	
120 125 130	
CAA ATC ATC TCT TTT TTA GAC TAC AAA CAA CAG CAT AAT GGC AAA TTG	489
Gln Ile Ile Ser Phe Leu Asp Tyr Lys Gln Gln His Asn Gly Lys Leu	
135 140 145	
TTA GTG AAA GTT TCC CCC ACA ATA TAC GAG TAAAACTTGC CATTGTTGTG GGA	542
Leu Val Lys Val Ser Pro Thr Ile Tyr Glu	
150 155	
ATATCAACCA CAAGC	557

245

250

255

AAA AAT CTT TTA TCC CAC TAGCGCGAAA AACTCCGTCC TTTAGGGCGG AGATGTAA 881
 Lys Asn Leu Leu Ser His
 260

GCGTTTAG

889

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Met Lys Lys Ser Asn Asp Asn Asn Ala Leu Ala Arg Ser Gln Arg Glu
 1 5 10 15
 Leu Phe Val Gly Ile Arg Asp Phe Ile Val Phe Lys Phe Lys Arg Met
 20 25 30
 Val Val Phe Asn Gly Val Arg Asp Phe Thr Lys Met Arg Phe Leu Ser
 35 40 45
 Ile Glu Leu Glu Lys Cys Glu Asn Ile Lys Asp Leu Glu Lys Leu Cys
 50 55 60
 His Thr Ile Tyr Asn Gln Gly Thr Lys His Ile Leu Met Met Arg Val
 65 70 75 80
 Leu Phe Leu Phe Phe Asp Tyr Phe Cys Lys His Leu Lys Val Lys Arg
 85 90 95
 Leu Arg Leu Leu Asn Glu Glu Met Leu Val Asn Phe Leu Phe Glu Leu
 100 105 110
 Ala Lys Gln Arg Lys Ile Asn Ser Met Ala Lys Tyr Val Met Tyr Ile
 115 120 125
 Arg Gln Phe Phe Asp Tyr Leu Asp Arg Thr Lys His Tyr Glu Phe Tyr
 130 135 140
 Phe Ser Leu Lys Asn Ile Ala Phe Ala Lys His Lys Asp Asn Leu Pro
 145 150 155 160
 Lys His Leu Asn Ser Lys Asp Leu Lys Ser Phe Ile Tyr Thr Leu Ile
 165 170 175
 Asn Tyr Arg Thr Arg Ser Ser Tyr Glu Lys Arg Asn Lys Cys Ile Leu
 180 185 190
 Leu Leu Ile Ile Leu Gly Gly Leu Arg Lys Ser Glu Val Phe Asn Leu
 195 200 205
 Glu Leu Arg Asn Ile Val Leu Glu Lys Glu His Tyr Ile Leu Leu Ile
 210 215 220
 Lys Gly Lys Asn Asn Lys Glu Arg Lys Ala Phe Ile Lys Ile Ala Gln
 225 230 235 240
 Thr Asp Ile Asp Thr Leu Ala Pro Leu Ile Arg Ile Leu Leu Glu Ser
 245 250 255
 Ile Ala Lys Asn Leu Leu Ser His
 260

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 546 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 75...530
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

TTGACAGAGT GGATTTTTTT ATTTCTAACG CTATTATTTA TGGGCGTTCT GTCGTGGGGG	60
GATTTCACACC GTTT ATG CGA TTA AAA CCT AAG GGG TTA AAC AAC ATT TAC	110
Met Arg Leu Lys Pro Lys Gly Leu Asn Asn Ile Tyr	
1 5 10	
ACA GCC ACC GTG TTA GCG TTC GTC GTA GGG GCT CAA GAA GCG GCA AAA	158
Thr Ala Thr Val Leu Ala Phe Val Val Gly Ala Gln Glu Ala Ala Lys	
15 20 25	
CGC ATG CAA AAA ATA GGC GGT GGG GCG ATC GTG AGC TTA AGT TCT ACC	206
Arg Met Gln Lys Ile Gly Gly Gly Ala Ile Val Ser Leu Ser Ser Thr	
30 35 40	
GGG AAT CTA GTT TAT ATG CCT AAT TAC GCC GGG CAT GGC AAT TCC AAA	254
Gly Asn Leu Val Tyr Met Pro Asn Tyr Ala Gly His Gly Asn Ser Lys	
45 50 55 60	
AAC GCC GTA GAA ACC ATG GTC AAA TAC GCT GCC GTG GAT TTA GGC GAA	302
Asn Ala Val Glu Thr Met Val Lys Tyr Ala Ala Val Asp Leu Gly Glu	
65 70 75	
TTT AAC ATT AGA GTG AAT GCG GTT AGT GGC GGG CCT ATT GAT ACG GAC	350
Phe Asn Ile Arg Val Asn Ala Val Ser Gly Gly Pro Ile Asp Thr Asp	
80 85 90	
GCT TTG AAA GCC TTC CCT GAT TAT GTG GAG ATT AAA GAA AAA GTA GAA	398
Ala Leu Lys Ala Phe Pro Asp Tyr Val Glu Ile Lys Glu Lys Val Glu	
95 100 105	
GAG CAA TCG CCC CTA AAA CGC ATG GGC AAT CCT AAC GAT CTA GCC GGA	446
Glu Gln Ser Pro Leu Lys Arg Met Gly Asn Pro Asn Asp Leu Ala Gly	
110 115 120	
GCG GCT TAT TTT TTA TGC GAT GAG ACC CAA AGC GGT TGG CTT ACA GGG	494
Ala Ala Tyr Phe Leu Cys Asp Glu Thr Gln Ser Gly Trp Leu Thr Gly	
125 130 135 140	
CAA ACG ATC GTT GTA GAT GGC GGG ACT ACT TTT AAA TAAAGATATT TCTTGC	546
Gln Thr Ile Val Val Asp Gly Gly Thr Thr Phe Lys	
145 150	
	546

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```

Met Arg Leu Lys Pro Lys Gly Leu Asn Asn Ile Tyr Thr Ala Thr Val
 1          5          10          15
Leu Ala Phe Val Val Gly Ala Gln Glu Ala Ala Lys Arg Met Gln Lys
 20          25          30
Ile Gly Gly Gly Ala Ile Val Ser Leu Ser Ser Thr Gly Asn Leu Val
 35          40          45
Tyr Met Pro Asn Tyr Ala Gly His Gly Asn Ser Lys Asn Ala Val Glu
 50          55          60
Thr Met Val Lys Tyr Ala Ala Val Asp Leu Gly Glu Phe Asn Ile Arg
 65          70          75          80
Val Asn Ala Val Ser Gly Gly Pro Ile Asp Thr Asp Ala Leu Lys Ala
 85          90          95
Phe Pro Asp Tyr Val Glu Ile Lys Glu Lys Val Glu Glu Gln Ser Pro
100          105          110
Leu Lys Arg Met Gly Asn Pro Asn Asp Leu Ala Gly Ala Ala Tyr Phe
115          120          125
Leu Cys Asp Glu Thr Gln Ser Gly Trp Leu Thr Gly Gln Thr Ile Val
130          135          140
Val Asp Gly Gly Thr Thr Phe Lys
145          150

```

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 2...616
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

A AGA TAT TTC TTG CAA AAC ATT ATC CAC ATC CAC CAA AAC AAA GAG TTG      49
  Arg Tyr Phe Leu Gln Asn Ile Ile His Ile His Gln Asn Lys Glu Leu
  1          5          10          15

CAA TTC ATT AAA AAA TGC TTG TTG GGC TAT TTT TTC GCC CCT TTG TGT      97
  Gln Phe Ile Lys Lys Cys Leu Leu Gly Tyr Phe Phe Ala Pro Leu Cys
  20          25          30

```

GGG GCT ATT CTG TTA GTG CTT TTT ATT GTT TCA AGC GGG GCA AAA TCG	145
Gly Ala Ile Leu Leu Val Leu Phe Ile Val Ser Ser Gly Ala Lys Ser	
35 40 45	
TTT CAA ATT TCT AAT CTC TTT AAC AAT CAA CTA GCC TAT ATC GTT TTG	193
Phe Gln Ile Ser Asn Leu Phe Asn Asn Gln Leu Ala Tyr Ile Val Leu	
50 55 60	
TTG TCT CTT TTT TTG TGC GCG CTT GGG TTT ATT GCC GGA GCG ATT GGT	241
Leu Ser Leu Phe Leu Cys Ala Leu Gly Phe Ile Ala Gly Ala Ile Gly	
65 70 75 80	
TTT TAT AGG CTT TCT AAA ATC ACA CGC CAT CTG AGT TTT TTT GAA AAT	289
Phe Tyr Arg Leu Ser Lys Ile Thr Arg His Leu Ser Phe Phe Glu Asn	
85 90 95	
TTC GCT TTC AGT TTT TTA GCG GTG ATT TTA TGC GCT ATT TTA AGC TAT	337
Phe Ala Phe Ser Phe Leu Ala Val Ile Leu Cys Ala Ile Leu Ser Tyr	
100 105 110	
CTT GTC CCT AAC GCC AGT AAC GCT CTT TCG CTA ATC GGT AAT GGC GTT	385
Leu Val Pro Asn Ala Ser Asn Ala Leu Ser Leu Ile Gly Asn Gly Val	
115 120 125	
TCT ATT TTT TAT TTG CAC AAA CTC TAT AGA GAA TTG AGC CTT TAC ACG	433
Ser Ile Phe Tyr Leu His Lys Leu Tyr Arg Glu Leu Ser Leu Tyr Thr	
130 135 140	
CAA GAA AGG TTT TTT TTA AGC GGG TTT AGG TTG TTG CTT TTT AGT TTC	481
Gln Glu Arg Phe Phe Leu Ser Gly Phe Arg Leu Leu Leu Phe Ser Phe	
145 150 155 160	
ATG CTG GCT CTT TTA GGG ATT TTA GTG CAA GCG TTA GTT ATC ATT TTT	529
Met Leu Ala Leu Leu Gly Ile Leu Val Gln Ala Leu Val Ile Ile Phe	
165 170 175	
TTA ACG ACC GCT GTG GTT TTA ATG TGT GTG GCG CTT GGT TTT TTG GCG	577
Leu Thr Thr Ala Val Val Leu Met Cys Val Ala Leu Gly Phe Leu Ala	
180 185 190	
CGC GCG TTT TTG AAT TTT TCA CAA GTC TTT TTG AAA GCA TGAAAGTTTT AA	628
Arg Ala Phe Leu Asn Phe Ser Gln Val Phe Leu Lys Ala	
195 200 205	
AACTCCTGCC TAATTT	644

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Arg	Tyr	Phe	Leu	Gln	Asn	Ile	Ile	His	Ile	His	Gln	Asn	Lys	Glu	Leu
1				5					10					15	
Gln	Phe	Ile	Lys	Lys	Cys	Leu	Leu	Gly	Tyr	Phe	Phe	Ala	Pro	Leu	Cys
			20					25					30		
Gly	Ala	Ile	Leu	Leu	Val	Leu	Phe	Ile	Val	Ser	Ser	Gly	Ala	Lys	Ser
		35					40					45			
Phe	Gln	Ile	Ser	Asn	Leu	Phe	Asn	Asn	Gln	Leu	Ala	Tyr	Ile	Val	Leu
	50					55					60				
Leu	Ser	Leu	Phe	Leu	Cys	Ala	Leu	Gly	Phe	Ile	Ala	Gly	Ala	Ile	Gly
65					70					75					80
Phe	Tyr	Arg	Leu	Ser	Lys	Ile	Thr	Arg	His	Leu	Ser	Phe	Phe	Glu	Asn
			85					90						95	
Phe	Ala	Phe	Ser	Phe	Leu	Ala	Val	Ile	Leu	Cys	Ala	Ile	Leu	Ser	Tyr
			100					105					110		
Leu	Val	Pro	Asn	Ala	Ser	Asn	Ala	Leu	Ser	Leu	Ile	Gly	Asn	Gly	Val
		115					120					125			
Ser	Ile	Phe	Tyr	Leu	His	Lys	Leu	Tyr	Arg	Glu	Leu	Ser	Leu	Tyr	Thr
	130					135					140				
Gln	Glu	Arg	Phe	Phe	Leu	Ser	Gly	Phe	Arg	Leu	Leu	Leu	Phe	Ser	Phe
145					150					155					160
Met	Leu	Ala	Leu	Leu	Gly	Ile	Leu	Val	Gln	Ala	Leu	Val	Ile	Ile	Phe
			165					170					175		
Leu	Thr	Thr	Ala	Val	Val	Leu	Met	Cys	Val	Ala	Leu	Gly	Phe	Leu	Ala
			180					185					190		
Arg	Ala	Phe	Leu	Asn	Phe	Ser	Gln	Val	Phe	Leu	Lys	Ala			
	195						200					205			

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 62...598
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GTGTGGCGCT	TGGTTTTTTG	GCGCGCGCGT	TTTTGAATTT	TTCACAAGTC	TTTTTGAAAG	60
C ATG AAA GTT TTA AAA CTC CTG CCT AAT TTT TTA ACA ATT TTA CGC ATT						109
Met Lys Val Leu Lys Leu Leu Pro Asn Phe Leu Thr Ile Leu Arg Ile						
1	5	10	15			
GTC TTA TCC TTA TTT TTA TTA TTT TTA TTG TTA AAC ACG CGC ACT TAT						157
Val Leu Ser Leu Phe Leu Leu Phe Leu Leu Asn Thr Arg Thr Tyr						
20	25	30				
TTT AGT TTT TTA ACC CCC TTT CAA ACC AAT ATG ATC TCT TCA TTG GTT						205
Phe Ser Phe Leu Thr Pro Phe Gln Thr Asn Met Ile Ser Ser Leu Val						
35	40	45				

TTT TTG TTT GCC GCG CTC ACG GAT TTA TTG GAC GGC TAC ATC GCT AGA	253
Phe Leu Phe Ala Ala Leu Thr Asp Leu Leu Asp Gly Tyr Ile Ala Arg	
50 55 60	
AGC TAT AAA GCC AAA TCG CGC TTT GGG GAA ATC TTT GAT CCT TTA GCG	301
Ser Tyr Lys Ala Lys Ser Arg Phe Gly Glu Ile Phe Asp Pro Leu Ala	
65 70 75 80	
GAT AAA ATC CTT ATT TTG AGC GCG TTT TTA GGG TTA GTT TAT TTG GAT	349
Asp Lys Ile Leu Ile Leu Ser Ala Phe Leu Gly Leu Val Tyr Leu Asp	
85 90 95	
CGT GTG AAT GCG TGG ATC CCG TTT GTG ATT TTA GGG CGT GAA TTT TTT	397
Arg Val Asn Ala Trp Ile Pro Phe Val Ile Leu Gly Arg Glu Phe Phe	
100 105 110	
ATT TCA GGG CTT AGA GTC TTA GCC GCT AAT GAG AAA AAG GAT ATT CCT	445
Ile Ser Gly Leu Arg Val Leu Ala Ala Asn Glu Lys Lys Asp Ile Pro	
115 120 125	
GTC AAT GCG TTA GGC AAG TAT AAA ACC GTT TCT CAA GTC GTG GCG ATT	493
Val Asn Ala Leu Gly Lys Tyr Lys Thr Val Ser Gln Val Val Ala Ile	
130 135 140	
GGT GCT TTA TTG GCT GAT GTA ACT TAC TCT TAT GCG CTT GTG GCT ATA	541
Gly Ala Leu Leu Ala Asp Val Thr Tyr Ser Tyr Ala Leu Val Ala Ile	
145 150 155 160	
GCG GTT TTT TTA ACC CTT TAT TCG GGG ATA GAT TAC ACC ATT AAA TAT	589
Ala Val Phe Leu Thr Leu Tyr Ser Gly Ile Asp Tyr Thr Ile Lys Tyr	
165 170 175	
TAT AAA TCT TAATATTTTA AAAGAAGTTT TTAGCGTTCT TT	630
Tyr Lys Ser	

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Lys Val Leu Lys Leu Leu Pro Asn Phe Leu Thr Ile Leu Arg Ile	
1 5 10 15	
Val Leu Ser Leu Phe Leu Leu Phe Leu Leu Asn Thr Arg Thr Tyr	
20 25 30	
Phe Ser Phe Leu Thr Pro Phe Gln Thr Asn Met Ile Ser Ser Leu Val	
35 40 45	
Phe Leu Phe Ala Ala Leu Thr Asp Leu Leu Asp Gly Tyr Ile Ala Arg	
50 55 60	
Ser Tyr Lys Ala Lys Ser Arg Phe Gly Glu Ile Phe Asp Pro Leu Ala	

65 70 75 80
 Asp Lys Ile Leu Ile Leu Ser Ala Phe Leu Gly Leu Val Tyr Leu Asp
 85 90 95
 Arg Val Asn Ala Trp Ile Pro Phe Val Ile Leu Gly Arg Glu Phe Phe
 100 105 110
 Ile Ser Gly Leu Arg Val Leu Ala Ala Asn Glu Lys Lys Asp Ile Pro
 115 120 125
 Val Asn Ala Leu Gly Lys Tyr Lys Thr Val Ser Gln Val Val Ala Ile
 130 135 140
 Gly Ala Leu Leu Ala Asp Val Thr Tyr Ser Tyr Ala Leu Val Ala Ile
 145 150 155 160
 Ala Val Phe Leu Thr Leu Tyr Ser Gly Ile Asp Tyr Thr Ile Lys Tyr
 165 170 175
 Tyr Lys Ser

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 913 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...879
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ATAGAAGAAG AGTGAGAA ATG CAA GAT TTT ATT AAG ATT TTT ATT CAA GAG	51
Met Gln Asp Phe Ile Lys Ile Phe Ile Gln Glu	
1 5 10	
GTT GTC TCT ACT TTA GAA GGG TTA GTG GGT AAG GCT CCA AGC GTG GGA	99
Val Val Ser Thr Leu Glu Gly Leu Val Gly Lys Ala Pro Ser Val Gly	
15 20 25	
TTA GAA AAA GAA ATT TCT AGT AGC GAC GAA TCT TTT TTG AAA TTA ATC	147
Leu Glu Lys Glu Ile Ser Ser Ser Asp Glu Ser Phe Leu Lys Leu Ile	
30 35 40	
AGC ACG CCT TAT GCA AGA GTT GTG ATA AGC GCG ATT GAA AAA GAA GAG	195
Ser Thr Pro Tyr Ala Arg Val Val Ile Ser Ala Ile Glu Lys Glu Glu	
45 50 55	
AGC TCT ATT GAA TTA CTG GCT CCG GTA GTT TTA GTT ACC TCT TTA AGC	243
Ser Ser Ile Glu Leu Leu Ala Pro Val Val Leu Val Thr Ser Leu Ser	
60 65 70 75	
GAT TTG ATG CTA GGA GGT GAG GGA GCG AGT AAG GAA GAA ATG GAT AAT	291
Asp Leu Met Leu Gly Gly Glu Gly Ala Ser Lys Glu Glu Met Asp Asn	
80 85 90	

GAC GAT TTA GAC GCT TTT AAA GAA ATG GCT TCT AAT ATT TTT GGC GCG Asp Asp Leu Asp Ala Phe Lys Glu Met Ala Ser Asn Ile Phe Gly Ala 95 100 105	339
ATC GCT ACA AGC TTG AAG TCT CAA GAA TTG CTC CCT AAA CTC AAT TTC Ile Ala Thr Ser Leu Lys Ser Gln Glu Leu Leu Pro Lys Leu Asn Phe 110 115 120	387
ACC ACT ATA AAC GCT GAA ATC GCT AAA GAG CTT CCT AAA AAA GAA GAT Thr Thr Ile Asn Ala Glu Ile Ala Lys Glu Leu Pro Lys Lys Glu Asp 125 130 135	435
TAC GCT AAA GCG ATG GTG TTT TCT TTT AAA ATG GAA GCC ATC AAA GAA Tyr Ala Lys Ala Met Val Phe Ser Phe Lys Met Glu Ala Ile Lys Glu 140 145 150 155	483
AGC CAA ATC ATT TTA TTG ACT ACG GCG GCT TTT GAG GGC CAA TTT GAA Ser Gln Ile Ile Leu Leu Thr Thr Ala Ala Phe Glu Gly Gln Phe Glu 160 165 170	531
AAA ACG CAT AAA GAA GAA AAA GAA GAA ACG ACA GAG GGC GTT GCT GAA Lys Thr His Lys Glu Glu Lys Glu Glu Thr Thr Glu Gly Val Ala Glu 175 180 185	579
GAG GTT AAA ACC CAT GAT GCG TCT TTA GAA AAC ATA GAA ATC CGC AAT Glu Val Lys Thr His Asp Ala Ser Leu Glu Asn Ile Glu Ile Arg Asn 190 195 200	627
ATC AGC ATG CTT TTA GAC GTG AAA TTG AAC GTT AAG GTG CGC ATC GGG Ile Ser Met Leu Leu Asp Val Lys Leu Asn Val Lys Val Arg Ile Gly 205 210 215	675
CAA AAA AAA ATG ATT TTA AAA GAC GTG GTC TCT ATG GAT ATA GGG AGC Gln Lys Lys Met Ile Leu Lys Asp Val Val Ser Met Asp Ile Gly Ser 220 225 230 235	723
GTG GTA GAG CTG GAT CAA TTG GTG AAT GAC CCT TTG GAA ATT CTT GTA Val Val Glu Leu Asp Gln Leu Val Asn Asp Pro Leu Glu Ile Leu Val 240 245 250	771
GAT GAC AAG GTG ATC GCT AAG GGC GAA GTG GTG ATT GTG GAT GGG AAT Asp Asp Lys Val Ile Ala Lys Gly Glu Val Val Ile Val Asp Gly Asn 255 260 265	819
TTT GGC ATT CAA ATC ACG GAT ATT GGC ACT AAA AAA GAA CGC TTA GAA Phe Gly Ile Gln Ile Thr Asp Ile Gly Thr Lys Lys Glu Arg Leu Glu 270 275 280	867
CAA TTG AAA CAT TAAATCTTTT TATCATAAAA AGGAAAGGGA TATG Gln Leu Lys His 285	913

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Met	Gln	Asp	Phe	Ile	Lys	Ile	Phe	Ile	Gln	Glu	Val	Val	Ser	Thr	Leu
1				5					10					15	
Glu	Gly	Leu	Val	Gly	Lys	Ala	Pro	Ser	Val	Gly	Leu	Glu	Lys	Glu	Ile
		20						25					30		
Ser	Ser	Ser	Asp	Glu	Ser	Phe	Leu	Lys	Leu	Ile	Ser	Thr	Pro	Tyr	Ala
		35					40					45			
Arg	Val	Val	Ile	Ser	Ala	Ile	Glu	Lys	Glu	Glu	Ser	Ser	Ile	Glu	Leu
	50					55					60				
Leu	Ala	Pro	Val	Val	Leu	Val	Thr	Ser	Leu	Ser	Asp	Leu	Met	Leu	Gly
65					70					75					80
Gly	Glu	Gly	Ala	Ser	Lys	Glu	Glu	Met	Asp	Asn	Asp	Asp	Leu	Asp	Ala
				85					90					95	
Phe	Lys	Glu	Met	Ala	Ser	Asn	Ile	Phe	Gly	Ala	Ile	Ala	Thr	Ser	Leu
			100					105					110		
Lys	Ser	Gln	Glu	Leu	Leu	Pro	Lys	Leu	Asn	Phe	Thr	Thr	Ile	Asn	Ala
		115					120					125			
Glu	Ile	Ala	Lys	Glu	Leu	Pro	Lys	Lys	Glu	Asp	Tyr	Ala	Lys	Ala	Met
	130					135				140					
Val	Phe	Ser	Phe	Lys	Met	Glu	Ala	Ile	Lys	Glu	Ser	Gln	Ile	Ile	Leu
145					150					155					160
Leu	Thr	Thr	Ala	Ala	Phe	Glu	Gly	Gln	Phe	Glu	Lys	Thr	His	Lys	Glu
				165					170					175	
Glu	Lys	Glu	Glu	Thr	Thr	Glu	Gly	Val	Ala	Glu	Glu	Val	Lys	Thr	His
			180					185					190		
Asp	Ala	Ser	Leu	Glu	Asn	Ile	Glu	Ile	Arg	Asn	Ile	Ser	Met	Leu	Leu
		195					200					205			
Asp	Val	Lys	Leu	Asn	Val	Lys	Val	Arg	Ile	Gly	Gln	Lys	Lys	Met	Ile
	210					215					220				
Leu	Lys	Asp	Val	Val	Ser	Met	Asp	Ile	Gly	Ser	Val	Val	Glu	Leu	Asp
225					230					235					240
Gln	Leu	Val	Asn	Asp	Pro	Leu	Glu	Ile	Leu	Val	Asp	Asp	Lys	Val	Ile
			245						250					255	
Ala	Lys	Gly	Glu	Val	Val	Ile	Val	Asp	Gly	Asn	Phe	Gly	Ile	Gln	Ile
		260						265					270		
Thr	Asp	Ile	Gly	Thr	Lys	Lys	Glu	Arg	Leu	Glu	Gln	Leu	Lys	His	
		275					280					285			

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 13...1056
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

TAAAAAAGGA	GA	ATG	ATG	CAA	GTT	TAC	CAC	CTT	TCA	CAC	ATT	GAT	TTA	GAC	51	
	Met	Met	Gln	Val	Tyr	His	Leu	Ser	His	Ile	Asp	Leu	Asp			
	1				5						10					
GGC	TAT	GCA	TGC	CAG	CTT	GTT	TCA	AAA	CAA	TTT	TTT	AAA	AAT	ATC	CAA	99
Gly	Tyr	Ala	Cys	Gln	Leu	Val	Ser	Lys	Gln	Phe	Phe	Lys	Asn	Ile	Gln	
	15					20					25					
TGC	TAT	AAC	GCT	AAT	TAC	GGG	CGT	GAA	GTC	TCA	GCG	AGA	ATT	TAT	GAG	147
Cys	Tyr	Asn	Ala	Asn	Tyr	Gly	Arg	Glu	Val	Ser	Ala	Arg	Ile	Tyr	Glu	
	30				35					40					45	
ATT	TTA	AAC	GCA	ATC	GCT	CAG	TCT	AAA	GAG	AGT	GAA	TTC	CTT	ATT	TTG	195
Ile	Leu	Asn	Ala	Ile	Ala	Gln	Ser	Lys	Glu	Ser	Glu	Phe	Leu	Ile	Leu	
				50					55					60		
GTT	AGC	GAT	TTG	AAT	CTG	AAT	TTG	AAT	GAA	GCA	GAG	TAT	TTG	CAG	GAT	243
Val	Ser	Asp	Leu	Asn	Leu	Asn	Leu	Asn	Glu	Ala	Glu	Tyr	Leu	Gln	Asp	
			65				70						75			
AAG	ATC	CAA	GAA	CAC	CGC	TTG	CAA	AAT	AAA	AAC	ATT	CAA	ATC	CAG	CTT	291
Lys	Ile	Gln	Glu	His	Arg	Leu	Gln	Asn	Lys	Asn	Ile	Gln	Ile	Gln	Leu	
		80					85					90				
TTA	GAT	CAC	CAT	ATC	AGC	GGT	AAG	GAA	GTG	GCT	GAG	AGT	TTC	CAT	TGG	339
Leu	Asp	His	His	Ile	Ser	Gly	Lys	Glu	Val	Ala	Glu	Ser	Phe	His	Trp	
	95					100					105					
TAT	TTT	TTA	GAC	ATT	AAC	CGT	TGC	GCG	ACT	AAA	ATC	GTG	TAT	GAA	TTT	387
Tyr	Phe	Leu	Asp	Ile	Asn	Arg	Cys	Ala	Thr	Lys	Ile	Val	Tyr	Glu	Phe	
	110				115					120				125		
TTG	AAA	AAG	CAT	TAC	GCT	ATT	TTA	GAG	CCA	AAA	AAC	ACA	ACA	TGG	CTA	435
Leu	Lys	Lys	His	Tyr	Ala	Ile	Leu	Glu	Pro	Lys	Asn	Thr	Thr	Trp	Leu	
				130					135					140		
GAG	CCT	TTA	GTG	GAA	ATG	GTC	AAT	TCT	GTG	GAT	ATT	TGG	GAC	ACG	CAA	483
Glu	Pro	Leu	Val	Glu	Met	Val	Asn	Ser	Val	Asp	Ile	Trp	Asp	Thr	Gln	
			145					150					155			
GGT	TAT	GGC	TTT	GAA	TTA	GGC	AAG	GTG	TGC	ATG	CGC	ATG	ATT	AAC	CAA	531
Gly	Tyr	Gly	Phe	Glu	Leu	Gly	Lys	Val	Cys	Met	Arg	Met	Ile	Asn	Gln	
	160						165					170				
AGC	TCT	GAA	TTG	AAT	CGT	TTC	ATG	TTT	GAT	GAT	GAA	AAC	CGC	AAC	TAT	579
Ser	Ser	Glu	Leu	Asn	Arg	Phe	Met	Phe	Asp	Asp	Glu	Asn	Arg	Asn	Tyr	
	175				180						185					
AAA	TTA	AAG	CTT	TTA	GAA	GAA	GTT	AAA	AAC	TAT	TTG	TTT	TTA	GAA	AAT	627
Lys	Leu	Lys	Leu	Leu	Glu	Glu	Val	Lys	Asn	Tyr	Leu	Phe	Leu	Glu	Asn	
	190				195				200					205		
GCC	CCT	GTA	GCC	TAT	GAT	AAC	GAT	TTG	TTC	AAA	CTC	AAA	AAA	ATC	GCT	675
Ala	Pro	Val	Ala	Tyr	Asp	Asn	Asp	Leu	Phe	Lys	Leu	Lys	Lys	Ile	Ala	

210										215					220					
TTA	GGG	GGC	GAC	CCT	GAT	GCA	GAA	ACG	ATG	GAC	AAT	ATC	TCT	TCA	AAC	723				
Leu	Gly	Gly	Asp	Pro	Asp	Ala	Glu	Thr	Met	Asp	Asn	Ile	Ser	Ser	Asn					
			225					230					235							
GCG	CAA	ACG	CAT	TTG	CTC	TCT	TTA	AAA	AAG	CAT	GAT	TGC	AGC	GTT	TAT	771				
Ala	Gln	Thr	His	Leu	Leu	Ser	Leu	Lys	Lys	His	Asp	Cys	Ser	Val	Tyr					
		240					245					250								
TAC	CAG	GAT	AAA	AAA	GGG	TTT	TTA	AGT	TAT	TCT	ATG	GGG	GGC	ATT	AGC	819				
Tyr	Gln	Asp	Lys	Lys	Gly	Phe	Leu	Ser	Tyr	Ser	Met	Gly	Gly	Ile	Ser					
	255					260					265									
GTG	TTG	GCT	AAC	CTT	TTT	TTA	ACG	CAA	AAT	CCG	GAT	TTT	GAT	TTT	TAT	867				
Val	Leu	Ala	Asn	Leu	Phe	Leu	Thr	Gln	Asn	Pro	Asp	Phe	Asp	Phe	Tyr					
270					275					280					285					
ATG	GAT	GTG	AAC	GCT	AAA	GGG	AAT	GTG	AGC	TTA	AGG	GCG	AAT	GGG	AAT	915				
Met	Asp	Val	Asn	Ala	Lys	Gly	Asn	Val	Ser	Leu	Arg	Ala	Asn	Gly	Asn					
			290					295					300							
TGC	GAT	GTG	TGC	GAA	CTC	AGT	CAA	ATG	TGT	TTT	AAT	GGG	GGT	GGG	CAT	963				
Cys	Asp	Val	Cys	Glu	Leu	Ser	Gln	Met	Cys	Phe	Asn	Gly	Gly	Gly	His					
			305				310					315								
AGG	AAT	GCG	AGC	GGA	GGC	AAG	ATT	GAT	GGT	TTT	AGG	GAG	AGT	TTC	AAT	1011				
Arg	Asn	Ala	Ser	Gly	Gly	Lys	Ile	Asp	Gly	Phe	Arg	Glu	Ser	Phe	Asn					
		320				325					330									
TAT	AGG	GAT	ATT	AAA	GAA	CAA	ATT	GAA	GAA	ATC	TTC	AAC	AAC	GCT	TAAAA	1061				
Tyr	Arg	Asp	Ile	Lys	Glu	Gln	Ile	Glu	Glu	Ile	Phe	Asn	Asn	Ala						
	335				340					345										
CTAAGCTGTT TAGAAAAAAC TAACAAAAAC TGAAAAGAGT TTAAAAGCTC															1111					

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met	Met	Gln	Val	Tyr	His	Leu	Ser	His	Ile	Asp	Leu	Asp	Gly	Tyr	Ala
1				5					10					15	
Cys	Gln	Leu	Val	Ser	Lys	Gln	Phe	Phe	Lys	Asn	Ile	Gln	Cys	Tyr	Asn
			20					25					30		
Ala	Asn	Tyr	Gly	Arg	Glu	Val	Ser	Ala	Arg	Ile	Tyr	Glu	Ile	Leu	Asn
		35					40					45			
Ala	Ile	Ala	Gln	Ser	Lys	Glu	Ser	Glu	Phe	Leu	Ile	Leu	Val	Ser	Asp
	50					55					60				
Leu	Asn	Leu	Asn	Leu	Asn	Glu	Ala	Glu	Tyr	Leu	Gln	Asp	Lys	Ile	Gln
65					70				75					80	

Glu His Arg Leu Gln Asn Lys Asn Ile Gln Ile Gln Leu Leu Asp His
85 90 95
His Ile Ser Gly Lys Glu Val Ala Glu Ser Phe His Trp Tyr Phe Leu
100 105 110
Asp Ile Asn Arg Cys Ala Thr Lys Ile Val Tyr Glu Phe Leu Lys Lys
115 120 125
His Tyr Ala Ile Leu Glu Pro Lys Asn Thr Thr Trp Leu Glu Pro Leu
130 135 140
Val Glu Met Val Asn Ser Val Asp Ile Trp Asp Thr Gln Gly Tyr Gly
145 150 155 160
Phe Glu Leu Gly Lys Val Cys Met Arg Met Ile Asn Gln Ser Ser Glu
165 170 175
Leu Asn Arg Phe Met Phe Asp Asp Glu Asn Arg Asn Tyr Lys Leu Lys
180 185 190
Leu Leu Glu Glu Val Lys Asn Tyr Leu Phe Leu Glu Asn Ala Pro Val
195 200 205
Ala Tyr Asp Asn Asp Leu Phe Lys Leu Lys Lys Ile Ala Leu Gly Gly
210 215 220
Asp Pro Asp Ala Glu Thr Met Asp Asn Ile Ser Ser Asn Ala Gln Thr
225 230 235 240
His Leu Leu Ser Leu Lys Lys His Asp Cys Ser Val Tyr Tyr Gln Asp
245 250 255
Lys Lys Gly Phe Leu Ser Tyr Ser Met Gly Gly Ile Ser Val Leu Ala
260 265 270
Asn Leu Phe Leu Thr Gln Asn Pro Asp Phe Asp Phe Tyr Met Asp Val
275 280 285
Asn Ala Lys Gly Asn Val Ser Leu Arg Ala Asn Gly Asn Cys Asp Val
290 295 300
Cys Glu Leu Ser Gln Met Cys Phe Asn Gly Gly Gly His Arg Asn Ala
305 310 315 320
Ser Gly Gly Lys Ile Asp Gly Phe Arg Glu Ser Phe Asn Tyr Arg Asp
325 330 335
Ile Lys Glu Gln Ile Glu Glu Ile Phe Asn Asn Ala
340 345

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2070 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...2024
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

ATAAAAAATG CGCTTAAAAC CATGAAAAAG GAGATGCG ATG CAA TTA GAC GAA GAT 56
Met Gln Leu Asp Glu Asp
1 5
TTA GAA TTC GCT AAA AAA ATC TTT AAC CCT AAC AGA GCG TTT GCC AAG 104

Leu	Glu	Phe	Ala	Lys	Lys	Ile	Phe	Asn	Pro	Asn	Arg	Ala	Phe	Ala	Lys	
			10				15						20			
CAA	GCC	AGG	ATT	AAA	AAC	ATG	TGC	GAA	TAT	AAA	GAT	TTA	GTG	CAT	GAA	152
Gln	Ala	Arg	Ile	Lys	Asn	Met	Cys	Glu	Tyr	Lys	Asp	Leu	Val	His	Glu	
			25				30						35			
GCC	AAT	GAA	GAT	TAT	GAA	CAT	TTT	TGG	GGC	GAT	TTA	GCC	AAG	CAG	AAA	200
Ala	Asn	Glu	Asp	Tyr	Glu	His	Phe	Trp	Gly	Asp	Leu	Ala	Lys	Gln	Lys	
			40				45						50			
CTC	ACA	TGG	TTT	AAA	CCT	TTT	GAT	AAG	GTT	TTA	AAC	AGC	GAT	AAC	GCC	248
Leu	Thr	Trp	Phe	Lys	Pro	Phe	Asp	Lys	Val	Leu	Asn	Ser	Asp	Asn	Ala	
			55				60						65			70
CCT	TTT	TTC	AAA	TGG	TTT	GAA	AAC	GGC	AAA	ATC	AAT	GTT	TCT	TAC	AAT	296
Pro	Phe	Phe	Lys	Trp	Phe	Glu	Asn	Gly	Lys	Ile	Asn	Val	Ser	Tyr	Asn	
			75				80						85			
TGC	ATA	GAC	AGG	CAT	TTA	AAA	GAC	AAA	AAA	AAT	AAA	GTG	GCG	ATC	ATT	344
Cys	Ile	Asp	Arg	His	Leu	Lys	Asp	Lys	Lys	Asn	Lys	Val	Ala	Ile	Ile	
			90				95						100			
TTT	GAA	GGG	GAA	ATG	GGG	GAT	TAT	AAT	GTC	ATC	ACT	TAC	AGA	AAA	CTC	392
Phe	Glu	Gly	Glu	Met	Gly	Asp	Tyr	Asn	Val	Ile	Thr	Tyr	Arg	Lys	Leu	
			105				110						115			
CAC	TCT	GAA	GTC	AAT	AAA	ACA	GCC	AAC	CTT	TTA	AAA	AAC	GAA	TTC	AAT	440
His	Ser	Glu	Val	Asn	Lys	Thr	Ala	Asn	Leu	Leu	Lys	Asn	Glu	Phe	Asn	
			120				125						130			
GTC	AAA	AAA	GGC	GAT	AGG	GTC	ATT	ATC	TAT	ATG	CCC	ATG	ATT	GTA	GAA	488
Val	Lys	Lys	Gly	Asp	Arg	Val	Ile	Ile	Tyr	Met	Pro	Met	Ile	Val	Glu	
			135				140						145			150
AGC	GTT	TAT	ATG	ATG	CTC	GCA	TGC	ACT	AGG	ATT	GGA	GCG	ATC	CAT	AGC	536
Ser	Val	Tyr	Met	Met	Leu	Ala	Cys	Thr	Arg	Ile	Gly	Ala	Ile	His	Ser	
			155				160						165			
ATC	GTT	TTT	GCT	GGG	TTT	AGC	CCT	GAA	GCC	TTA	AGG	GAT	AGG	ATC	AAC	584
Ile	Val	Phe	Ala	Gly	Phe	Ser	Pro	Glu	Ala	Leu	Arg	Asp	Arg	Ile	Asn	
			170				175						180			
GAC	GCT	CAA	GCT	AAA	TTA	GTT	ATC	ACA	GCG	GAT	GGG	ACT	TTT	AGA	AAA	632
Asp	Ala	Gln	Ala	Lys	Leu	Val	Ile	Thr	Ala	Asp	Gly	Thr	Phe	Arg	Lys	
			185				190						195			
GGC	AAA	CCT	TAC	ATG	CTC	AAG	CCA	GCC	CTT	GAC	AAG	GCT	CTA	GAA	AAT	680
Gly	Lys	Pro	Tyr	Met	Leu	Lys	Pro	Ala	Leu	Asp	Lys	Ala	Leu	Glu	Asn	
			200				205						210			
AAC	GCC	TGC	CCT	AGC	GTG	GAA	AAA	GCG	CTC	ATT	GTG	ATA	CGA	AAC	GCC	728
Asn	Ala	Cys	Pro	Ser	Val	Glu	Lys	Ala	Leu	Ile	Val	Ile	Arg	Asn	Ala	
			215				220						225			230
AAA	GAG	ATT	GAC	TAT	GTG	AGA	GGG	CGC	GAT	TTT	GTC	TAT	AAT	GAA	ATG	776
Lys	Glu	Ile	Asp	Tyr	Val	Arg	Gly	Arg	Asp	Phe	Val	Tyr	Asn	Glu	Met	
			235				240						245			

GTC Val	AAT Asn	TAC Tyr	CAA Gln 250	TCC Ser	GAC Asp	AAA Lys	TGC Cys	GAA Glu 255	CCT Pro	GAA Glu	ATG Met	ATG Met	GAC Asp 260	TCT Ser	GAA Glu	824
GAT Asp	CCT Pro	TTA Leu 265	TTC Phe	TTG Leu	CTC Leu	TAT Tyr	ACA Thr 270	AGC Ser	GGA Gly	TCA Ser	ACC Thr	GGA Gly 275	AAG Lys	CCT Pro	AAA Lys	872
GGC Gly	GTT Val 280	CAA Gln	CAC His	AGC Ser	AGT Ser	GCG Ala 285	GGG Gly	TAT Tyr	TTG Leu	TTA Leu	TGG Trp 290	GCG Ala	CAA Gln	ATG Met	ACG Thr	920
ATG Met 295	GAG Glu	TGG Trp	GTT Val	TTT Phe	GAT Asp 300	ATT Ile	AGA Arg	GAT Asp	AAC Asn	GAT Asp 305	AAT Asn	TTT Phe	TGG Trp	TGC Cys	ACC Thr 310	968
GCC Ala	GAT Asp	ATT Ile	GGC Gly	TGG Trp 315	ATC Ile	ACA Thr	GGG Gly	CAC His	ACT Thr 320	TAT Tyr	GTG Val	GTT Val	TAT Tyr	GGA Gly 325	CCT Pro	1016
TTA Leu	GCT Ala	TGT Cys	GGG Gly 330	GCG Ala	ACG Thr	ACT Thr	TTG Leu	ATA Ile 335	CTA Leu	GAA Glu	GGC Gly	ACG Thr	ATG Met 340	TCT Ser	TAT Tyr	1064
CCG Pro	GAT Asp	TAT Tyr 345	GGG Gly	AGA Arg	TGG Trp	TGG Trp	AGG Arg 350	ATG Met	ATA Ile	GAA Glu	GAA Glu	TAC Tyr 355	CGT Arg	GTG Val	GAT Asp	1112
AAA Lys	TTC Phe 360	TAC Tyr	ACT Thr	TCC Ser	CCT Pro	ACC Thr 365	GCT Ala	ATA Ile	AGA Arg	ATG Met	TTG Leu 370	CAT His	GCC Ala	AAA Lys	GGT Gly	1160
GAA Glu 375	AAC Asn	GAA Glu	CCC Pro	TCA Ser	AAG Lys 380	TAT Tyr	AAT Asn	TTA Leu	GAG Glu	TCG Ser 385	CTC Leu	AAA Lys	GTT Val	TTA Leu	GGA Gly 390	1208
ACG Thr	GTG Val	GGA Gly	GAG Glu	CCC Pro 395	ATT Ile	AAC Asn	CCT Pro	ACA Thr	GCA Ala 400	TGG Trp	AAA Lys	TGG Trp	TTT Phe	TAT Tyr 405	GAA Glu	1256
AAA Lys	ATC Ile	GGC Gly	AAC Asn 410	TCA Ser	AAA Lys	TGC Cys	AGC Ser	ATC Ile 415	GTG Val	GAT Asp	ACT Thr	TGG Trp	TGG Trp	CAG Gln	ACA Thr	1304
GAA Glu	ACA Thr	GGC Gly 425	GGG Gly	CAC His	ATC Ile	ATC Ile	AGC Ser 430	CCT Pro	TTA Leu	CCG Pro	GGA Gly	GCT Ala 435	ACG Thr	CCT Pro	ATA Ile	1352
AGG Arg	GCC Ala 440	AGT Ser	TGC Cys	GCG Ala	ACT Thr	TTA Leu 445	CCT Pro	TTG Leu	CCT Pro	GGA Gly	ATC Ile 450	CAT His	GCG Ala	GAA Glu	GTT Val	1400
TTA Leu 455	AAC Asn	GAA Glu	GAC Asp	GGC Gly	ACT Thr 460	AAA Lys	ACA Thr	AAG Lys	CCT Pro	GGA Gly 465	GAG Glu	CAA Gln	GGG Gly	TTT Phe	TTA Leu 470	1448
TGC Cys	ATC Ile	ACT Thr	AAG Lys	CCA Pro	TGG Trp	CCT Pro	TCT Ser	ATG Met	ATA Ile	AGA Arg	AAC Asn	ATT Ile	TGG Trp	GGC Gly	GAT Asp	1496

475										480					485					
GAA	AAA	CGA	TAC	ATT	GAT	AGC	TAT	TTT	TCT	CAG	ATC	AAG	TTG	AAT	GGG	1544				
Glu	Lys	Arg	Tyr	Ile	Asp	Ser	Tyr	Phe	Ser	Gln	Ile	Lys	Leu	Asn	Gly					
			490					495					500							
GAA	TAT	GTC	TAC	CTC	TCT	GGA	GAT	GGC	GCT	ATC	GTG	GAT	GAA	AAC	GGA	1592				
Glu	Tyr	Val	Tyr	Leu	Ser	Gly	Asp	Gly	Ala	Ile	Val	Asp	Glu	Asn	Gly					
		505					510					515								
TAC	ATT	ACT	ATT	ATT	GGG	CGC	ACA	GAT	GAT	ATT	GTG	AAT	GTG	AGT	GGG	1640				
Tyr	Ile	Thr	Ile	Ile	Gly	Arg	Thr	Asp	Asp	Ile	Val	Asn	Val	Ser	Gly					
	520					525					530									
CAT	AGG	ATT	GGC	ACG	GCT	GAA	GTG	GAG	AGC	GCT	ATT	TCC	AAG	CAT	GAA	1688				
His	Arg	Ile	Gly	Thr	Ala	Glu	Val	Glu	Ser	Ala	Ile	Ser	Lys	His	Glu					
	535				540					545					550					
ATG	GTG	GCT	GAA	TGC	GCG	GTG	GTG	GGT	ATC	CCT	GAT	GCG	ATT	AAA	GGA	1736				
Met	Val	Ala	Glu	Cys	Ala	Val	Val	Gly	Ile	Pro	Asp	Ala	Ile	Lys	Gly					
				555					560					565						
GAG	GGC	TTG	TTT	GCG	TTT	GTG	GTG	CTG	TGC	GAT	GGG	GCT	AAA	TGC	AAT	1784				
Glu	Gly	Leu	Phe	Ala	Phe	Val	Val	Leu	Cys	Asp	Gly	Ala	Lys	Cys	Asn					
			570					575					580							
CTT	GGC	GAG	AGT	TTA	GAA	TTG	CTA	AAA	GAA	ATG	AAC	CAT	ATC	TTA	TCC	1832				
Leu	Gly	Glu	Ser	Leu	Glu	Leu	Leu	Lys	Glu	Met	Asn	His	Ile	Leu	Ser					
		585					590					595								
ATT	GAG	ATT	GGA	AAG	ATC	GCG	AAA	TTA	GAC	AAT	GTC	ATG	TAT	GTG	CCA	1880				
Ile	Glu	Ile	Gly	Lys	Ile	Ala	Lys	Leu	Asp	Asn	Val	Met	Tyr	Val	Pro					
	600					605					610									
GGT	TTG	CCT	AAA	ACC	AGG	AGC	GGG	AAA	ATC	ATG	AGA	AGG	CTT	TTG	AAA	1928				
Gly	Leu	Pro	Lys	Thr	Arg	Ser	Gly	Lys	Ile	Met	Arg	Arg	Leu	Leu	Lys					
	615				620					625					630					
TCC	ATC	GCC	AAA	AAA	GAG	CCT	ATC	ACT	CAA	GAT	TTA	AGC	ACG	CTA	GAA	1976				
Ser	Ile	Ala	Lys	Lys	Glu	Pro	Ile	Thr	Gln	Asp	Leu	Ser	Thr	Leu	Glu					
			635						640					645						
GAT	GTG	AAT	GTG	GTT	AAA	GAA	ATA	ATG	AGC	ATC	GCT	CAA	ATG	GAG	GAG	T 2025				
Asp	Val	Asn	Val	Val	Lys	Glu	Ile	Met	Ser	Ile	Ala	Gln	Met	Glu	Glu					
			650					655					660							
AAAATCTAAA AAATGCTTTT TAGCGTTTTT TAGCCAAATA ATAAG																2070				

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```

Met Gln Leu Asp Glu Asp Leu Glu Phe Ala Lys Lys Ile Phe Asn Pro
1      5      10      15
Asn Arg Ala Phe Ala Lys Gln Ala Arg Ile Lys Asn Met Cys Glu Tyr
20      25      30
Lys Asp Leu Val His Glu Ala Asn Glu Asp Tyr Glu His Phe Trp Gly
35      40      45
Asp Leu Ala Lys Gln Lys Leu Thr Trp Phe Lys Pro Phe Asp Lys Val
50      55      60
Leu Asn Ser Asp Asn Ala Pro Phe Phe Lys Trp Phe Glu Asn Gly Lys
65      70      75      80
Ile Asn Val Ser Tyr Asn Cys Ile Asp Arg His Leu Lys Asp Lys Lys
85      90      95
Asn Lys Val Ala Ile Ile Phe Glu Gly Glu Met Gly Asp Tyr Asn Val
100     105     110
Ile Thr Tyr Arg Lys Leu His Ser Glu Val Asn Lys Thr Ala Asn Leu
115     120     125
Leu Lys Asn Glu Phe Asn Val Lys Lys Gly Asp Arg Val Ile Ile Tyr
130     135     140
Met Pro Met Ile Val Glu Ser Val Tyr Met Met Leu Ala Cys Thr Arg
145     150     155     160
Ile Gly Ala Ile His Ser Ile Val Phe Ala Gly Phe Ser Pro Glu Ala
165     170     175
Leu Arg Asp Arg Ile Asn Asp Ala Gln Ala Lys Leu Val Ile Thr Ala
180     185     190
Asp Gly Thr Phe Arg Lys Gly Lys Pro Tyr Met Leu Lys Pro Ala Leu
195     200     205
Asp Lys Ala Leu Glu Asn Asn Ala Cys Pro Ser Val Glu Lys Ala Leu
210     215     220
Ile Val Ile Arg Asn Ala Lys Glu Ile Asp Tyr Val Arg Gly Arg Asp
225     230     235     240
Phe Val Tyr Asn Glu Met Val Asn Tyr Gln Ser Asp Lys Cys Glu Pro
245     250     255
Glu Met Met Asp Ser Glu Asp Pro Leu Phe Leu Leu Tyr Thr Ser Gly
260     265     270
Ser Thr Gly Lys Pro Lys Gly Val Gln His Ser Ser Ala Gly Tyr Leu
275     280     285
Leu Trp Ala Gln Met Thr Met Glu Trp Val Phe Asp Ile Arg Asp Asn
290     295     300
Asp Asn Phe Trp Cys Thr Ala Asp Ile Gly Trp Ile Thr Gly His Thr
305     310     315     320
Tyr Val Val Tyr Gly Pro Leu Ala Cys Gly Ala Thr Thr Leu Ile Leu
325     330     335
Glu Gly Thr Met Ser Tyr Pro Asp Tyr Gly Arg Trp Trp Arg Met Ile
340     345     350
Glu Glu Tyr Arg Val Asp Lys Phe Tyr Thr Ser Pro Thr Ala Ile Arg
355     360     365
Met Leu His Ala Lys Gly Glu Asn Glu Pro Ser Lys Tyr Asn Leu Glu
370     375     380
Ser Leu Lys Val Leu Gly Thr Val Gly Glu Pro Ile Asn Pro Thr Ala
385     390     395     400
Trp Lys Trp Phe Tyr Glu Lys Ile Gly Asn Ser Lys Cys Ser Ile Val
405     410     415
Asp Thr Trp Trp Gln Thr Glu Thr Gly Gly His Ile Ile Ser Pro Leu
420     425     430
Pro Gly Ala Thr Pro Ile Arg Ala Ser Cys Ala Thr Leu Pro Leu Pro
435     440     445

```


GTC ATA GGG TTT TTA GAA AAA AAC CAT GCC CTT TTG CAA TAT TTT CTT Val Ile Gly Phe Leu Glu Lys Asn His Ala Leu Leu Gln Tyr Phe Leu 45 50 55	195
ATT ATT TTT AAA TAC GAT ATT GAA TCA GAA GTC AAA GCC GTT TTG CGC Ile Ile Phe Lys Tyr Asp Ile Glu Ser Glu Val Lys Ala Val Leu Arg 60 65 70 75	243
AAA CAC CAG CTT TTG TTT TTA GAA ACG AAT CGC GTT TTA AAC GGA CGC Lys His Gln Leu Leu Phe Leu Glu Thr Asn Arg Val Leu Asn Gly Arg 80 85 90	291
CAT ATC AAA ACC ATG CCT TTA AAA GAC GAA ACC GAT CAT CCA AAA CCC His Ile Lys Thr Met Pro Leu Lys Asp Glu Thr Asp His Pro Lys Pro 95 100 105	339
AAT CAT TCT AAA ACA GAA CCT AAA ACA ACG ATT TAT GAG CGC CAT ATC Asn His Ser Lys Thr Glu Pro Lys Thr Thr Ile Tyr Glu Arg His Ile 110 115 120	387
AGG AGT GGG GAA GAG ATT TAT AGC ACT AAT CAC CTT ATT TTT TTG GGT Arg Ser Gly Glu Glu Ile Tyr Ser Thr Asn His Leu Ile Phe Leu Gly 125 130 135	435
AAT ATC CAT AAT GGA GCC AAG ATT ATT TCA GAG GGC TGT GTG TCT GTT Asn Ile His Asn Gly Ala Lys Ile Ile Ser Glu Gly Cys Val Ser Val 140 145 150 155	483
TAT GGG GTT TGC GAA GGG GCG ATT GTG TGC TTT GGA GAG TGT TTG ATC Tyr Gly Val Cys Glu Gly Ala Ile Val Cys Phe Gly Glu Cys Leu Ile 160 165 170	531
TTA AAA GAA GTC AAG AGC GCT CAA ATC GTT TTT CAA AAC AAA ATT TTG Leu Lys Glu Val Lys Ser Ala Gln Ile Val Phe Gln Asn Lys Ile Leu 175 180 185	579
TCT CTA AAA GAG GTT GAA CCG CTT TTG GTA AAT AAA AAT ATT AAA ATA Ser Leu Lys Glu Val Glu Pro Leu Leu Val Asn Lys Asn Ile Lys Ile 190 195 200	627
ATC ACT AAA AAT GAC GAT ATA CTA GAC ATA AAG GAA GTA TTA TGAAACAAA Ile Thr Lys Asn Asp Asp Ile Leu Asp Ile Lys Glu Val Leu 205 210 215	678
CAACCATTA CCACTCTGTG GAATTAGTAG GGATAGGCTT GCACAAG	725

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Met	Asp	Lys	Asn	Gln	Tyr	His	Arg	Pro	His	Arg	Ala	Ser	Gln	Thr	Ala
1				5					10					15	
Phe	Asn	Glu	Arg	Ile	Val	Met	Leu	Lys	Thr	Asn	Gln	Lys	Asn	Val	His
			20					25					30		
Ala	Phe	Glu	Ile	Glu	Lys	Gln	Glu	Pro	Glu	Ala	Val	Ile	Gly	Phe	Leu
		35					40					45			
Glu	Lys	Asn	His	Ala	Leu	Leu	Gln	Tyr	Phe	Leu	Ile	Ile	Phe	Lys	Tyr
	50					55					60				
Asp	Ile	Glu	Ser	Glu	Val	Lys	Ala	Val	Leu	Arg	Lys	His	Gln	Leu	Leu
65					70					75				80	
Phe	Leu	Glu	Thr	Asn	Arg	Val	Leu	Asn	Gly	Arg	His	Ile	Lys	Thr	Met
				85					90					95	
Pro	Leu	Lys	Asp	Glu	Thr	Asp	His	Pro	Lys	Pro	Asn	His	Ser	Lys	Thr
			100					105					110		
Glu	Pro	Lys	Thr	Thr	Ile	Tyr	Glu	Arg	His	Ile	Arg	Ser	Gly	Glu	Glu
		115					120					125			
Ile	Tyr	Ser	Thr	Asn	His	Leu	Ile	Phe	Leu	Gly	Asn	Ile	His	Asn	Gly
	130					135					140				
Ala	Lys	Ile	Ile	Ser	Glu	Gly	Cys	Val	Ser	Val	Tyr	Gly	Val	Cys	Glu
145					150					155				160	
Gly	Ala	Ile	Val	Cys	Phe	Gly	Glu	Cys	Leu	Ile	Leu	Lys	Glu	Val	Lys
				165					170					175	
Ser	Ala	Gln	Ile	Val	Phe	Gln	Asn	Lys	Ile	Leu	Ser	Leu	Lys	Glu	Val
		180						185					190		
Glu	Pro	Leu	Leu	Val	Asn	Lys	Asn	Ile	Lys	Ile	Ile	Thr	Lys	Asn	Asp
		195				200						205			
Asp	Ile	Leu	Asp	Ile	Lys	Glu	Val	Leu							
	210					215									

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 64...1068
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAGAAAATC	TGTTATTGGA	TAAACCCAAG	TCTTTAGAAG	TGCCTTTGAC	TAGGCCCGAA	60
ATC ATG GGG CTA GAA GAC AAG TGC CTT TTA TAT GAA ATT AAA GCT AAT	108					
Met Gly Leu Glu Asp Lys Cys Leu Leu Tyr Glu Ile Lys Ala Asn						
1	5		10		15	
GAT TGG AGT TAT GCT AAT TTT TTC AAT GGC AAT AAA GCG TCT TTC AAA	156					
Asp Trp Ser Tyr Ala Asn Phe Phe Asn Gly Asn Lys Ala Ser Phe Lys						
	20		25		30	
CAA GAA GTG TGT GTT GAT ACG ATA AAA CCC TCA ATC ACT ATT TTA TCT	204					
Gln Glu Val Cys Val Asp Thr Ile Lys Pro Ser Ile Thr Ile Leu Ser						

35							40					45					
CGA Arg	TCC Ser	CCA Pro 50	AGC Ser	ATC Ile	GCT Ala	TAT Tyr	GGG Gly 55	GGG Gly	AGC Ser	GCG Ala	ATA Ile	GTC Val 60	GTT Val	TTT Phe	GAA Glu	252	
GCT Ala	TTG Leu 65	GAT Asp	AAG Lys	AAT Asn	TTG Leu	TCT Ser 70	CAA Gln	GCG Ala	TTT Phe	GTG Val	CGC Arg 75	GTC Val	AAA Lys	AAA Lys	AAG Lys	300	
GAT Asp 80	TTT Phe	GAA Glu	GCT Ala	TTC Phe	AGG Arg 85	CTT Leu	TTA Leu	GAA Glu	TTC Phe	AAA Lys 90	CAG Gln	CGT Arg	AAT Asn	GTT Val	TTT Phe 95	348	
ATC Ile	GCT Ala	CTA Leu	GTG Val	CCT Pro 100	TGG Trp	TCT Ser	TAT Tyr	AAA Lys	AAT Asn 105	AAG Lys	GAT Asp	TTT Phe	AAG Lys	GCG Ala 110	TTC Phe	396	
ATT Ile	GTC Val	GCT Ala	AAA Lys 115	GAT Asp	AAA Lys	GCC Ala	TAT Tyr	AAC Asn 120	TTT Phe	AAT Asn	ACC Thr	GCC Ala	CCT Pro 125	TTA Leu	TTG Leu	444	
TTC Phe	AAG Lys	CGA Arg 130	AAA Lys	ATC Ile	CAT His	CGT Arg	TTG Leu 135	AGG Arg	GAA Glu	AAA Lys	GAT Asp	ATA Ile 140	GAC Asp	TTA Leu	AGC Ser	492	
GCC Ala	TTA Leu 145	AAA Lys	GAT Asp	AAG Lys	ATT Ile	GCA Ala 150	AAG Lys	CAA Gln	GAA Glu	AAA Lys	TTT Phe 155	CAA Gln	AAC Asn	GAC Asp	ACT Thr	540	
GAA Glu 160	CAA Gln	GCT Ala	TTA Leu	TTA Leu	GAA Glu 165	AGA Arg	TTT Phe	TCC Ser	AAT Asn	GCG Ala 170	CGC Arg	CCA Pro	AAA Lys	GAT Asp	TTA Leu 175	588	
GAA Glu	AAA Lys	ATC Ile	CAA Gln	AAG Lys 180	ATC Ile	GCT Ala	TTA Leu	GAG Glu	CAA Gln 185	GGG Gly	GAT Asp	TTT Phe	TAT Tyr	AAG Lys 190	GAT Asp	636	
TTT Phe	TCT Ser	CAT His	TTT Phe 195	CAA Gln	GCG Ala	CTA Leu	AAA Lys	CCC Pro 200	TTG Leu	AAC Asn	GGG Gly	CCT Pro	TTT Phe 205	AAA Lys	ATG Met	684	
GCA Ala	AGC Ser	AAT Asn 210	TTT Phe	TTA Leu	GAA Glu	AAT Asn	CGG Arg 215	CGT Arg	ATC Ile	TTA Leu	AAG Lys	AAT Asn 220	AAT Asn	CAG Gln	GTG Val	732	
TTG Leu	TTT Phe 225	AAA Lys	TTC Phe	TTG Leu	CAT His	TTA Leu 230	GGG Gly	GTG Val	GAT Asp	TTG Leu	ATA Ile 235	CCT Pro	GGC Gly	AAG Lys	GAT Asp	780	
TTA Leu 240	TCT Ser	TTA Leu	GCG Ala	TTT Phe	GAT Asp 245	TTG Leu	TCT Ser	GTG Val	AAG Lys	AGG Arg 250	GTT Val	TTT Phe	AAG Lys	GGG Gly	GAG Glu 255	828	
TTC Phe	GAT Asp	TTT Phe	TAT Tyr	GGT Gly 260	AAT Asn	AGT Ser	TTA Leu	ATC Ile	CAT His 265	TGC Cys	TAT Tyr	GGG Gly	TTA Leu	GGT Gly 270	TTG Leu	876	

TGC GTT TTT TTA GCC CAT TTA AAA GAT GAT AAA AGC GTG GGG AGT AGT	924
Cys Val Phe Leu Ala His Leu Lys Asp Asp Lys Ser Val Gly Ser Ser	
275 280 285	
GGT TTG AAA TTA GGG AGC GGG TTG CAT TTA GGG ATG CTT TTG CAA GGG	972
Gly Leu Lys Leu Gly Ser Gly Leu His Leu Gly Met Leu Leu Gln Gly	
290 295 300	
GTT TTT GTC CGG CCC AAT GAA TGG CTT AAT GAG CAA TGG ATA AAA ACC	1020
Val Phe Val Arg Pro Asn Glu Trp Leu Asn Glu Gln Trp Ile Lys Thr	
305 310 315	
AAT ATC ACC GCC CCC ATA GAG CAA GCC AAA CGG CTT TTA ATG AAA GGA T	1069
Asn Ile Thr Ala Pro Ile Glu Gln Ala Lys Arg Leu Leu Met Lys Gly	
320 325 330 335	
AGTCATGTTA AAAACGAATC AAAAAAATGT GCATGCGTTT GAAATTGAAA AG	1121

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Met	Gly	Leu	Glu	Asp	Lys	Cys	Leu	Leu	Tyr	Glu	Ile	Lys	Ala	Asn	Asp
1				5					10					15	
Trp	Ser	Tyr	Ala	Asn	Phe	Phe	Asn	Gly	Asn	Lys	Ala	Ser	Phe	Lys	Gln
			20					25					30		
Glu	Val	Cys	Val	Asp	Thr	Ile	Lys	Pro	Ser	Ile	Thr	Ile	Leu	Ser	Arg
		35					40				45				
Ser	Pro	Ser	Ile	Ala	Tyr	Gly	Gly	Ser	Ala	Ile	Val	Val	Phe	Glu	Ala
	50					55				60					
Leu	Asp	Lys	Asn	Leu	Ser	Gln	Ala	Phe	Val	Arg	Val	Lys	Lys	Lys	Asp
65				70					75						80
Phe	Glu	Ala	Phe	Arg	Leu	Leu	Glu	Phe	Lys	Gln	Arg	Asn	Val	Phe	Ile
			85					90					95		
Ala	Leu	Val	Pro	Trp	Ser	Tyr	Lys	Asn	Lys	Asp	Phe	Lys	Ala	Phe	Ile
			100					105					110		
Val	Ala	Lys	Asp	Lys	Ala	Tyr	Asn	Phe	Asn	Thr	Ala	Pro	Leu	Leu	Phe
		115					120				125				
Lys	Arg	Lys	Ile	His	Arg	Leu	Arg	Glu	Lys	Asp	Ile	Asp	Leu	Ser	Ala
	130					135				140					
Leu	Lys	Asp	Lys	Ile	Ala	Lys	Gln	Glu	Lys	Phe	Gln	Asn	Asp	Thr	Glu
145				150					155						160
Gln	Ala	Leu	Leu	Glu	Arg	Phe	Ser	Asn	Ala	Arg	Pro	Lys	Asp	Leu	Glu
			165					170						175	
Lys	Ile	Gln	Lys	Ile	Ala	Leu	Glu	Gln	Gly	Asp	Phe	Tyr	Lys	Asp	Phe
		180						185				190			
Ser	His	Phe	Gln	Ala	Leu	Lys	Pro	Leu	Asn	Gly	Pro	Phe	Lys	Met	Ala
		195					200				205				
Ser	Asn	Phe	Leu	Glu	Asn	Arg	Arg	Ile	Leu	Lys	Asn	Asn	Gln	Val	Leu
	210					215					220				

Phe	Lys	Phe	Leu	His	Leu	Gly	Val	Asp	Leu	Ile	Pro	Gly	Lys	Asp	Leu
225					230					235					240
Ser	Leu	Ala	Phe	Asp	Leu	Ser	Val	Lys	Arg	Val	Phe	Lys	Gly	Glu	Phe
				245					250					255	
Asp	Phe	Tyr	Gly	Asn	Ser	Leu	Ile	His	Cys	Tyr	Gly	Leu	Gly	Leu	Cys
			260					265					270		
Val	Phe	Leu	Ala	His	Leu	Lys	Asp	Asp	Lys	Ser	Val	Gly	Ser	Ser	Gly
		275					280					285			
Leu	Lys	Leu	Gly	Ser	Gly	Leu	His	Leu	Gly	Met	Leu	Leu	Gln	Gly	Val
	290					295				300					
Phe	Val	Arg	Pro	Asn	Glu	Trp	Leu	Asn	Glu	Gln	Trp	Ile	Lys	Thr	Asn
305				310					315						320
Ile	Thr	Ala	Pro	Ile	Glu	Gln	Ala	Lys	Arg	Leu	Leu	Met	Lys	Gly	
			325						330					335	

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...969
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

TTACA	ACTAT	TTATT	GTAAA	GGCTAAA	ATG	TTG	AAA	TTT	AAA	TAT	GGT	TTG	ATT		54
					Met	Leu	Lys	Phe	Lys	Tyr	Gly	Leu	Ile		
					1					5					
TAT	ATC	GCG	CTC	ATA	CTA	GGA	CTT	CAA	GCG	ACA	GAT	TAT	GAC	AAT	TTA
Tyr	Ile	Ala	Leu	Ile	Leu	Gly	Leu	Gln	Ala	Thr	Asp	Tyr	Asp	Asn	Leu
10					15				20					25	102
GAA	GAA	GAA	AAC	CAA	CAA	TTA	GAT	GAA	AAA	ATA	AAC	CAT	TTA	AAG	CAA
Glu	Glu	Glu	Asn	Gln	Gln	Leu	Asp	Glu	Lys	Ile	Asn	His	Leu	Lys	Gln
			30						35					40	150
CAG	CTC	ACC	GAA	AAA	GGG	GTT	TCG	CCC	AAA	GAG	ATG	GAT	AAG	GAT	AAG
Gln	Leu	Thr	Glu	Lys	Gly	Val	Ser	Pro	Lys	Glu	Met	Asp	Lys	Asp	Lys
			45					50					55		198
TTT	GAA	GAA	GAA	TAC	ATC	AAT	CGA	TCT	TAT	CCT	AAA	ATT	TCT	TCC	AAG
Phe	Glu	Glu	Glu	Tyr	Ile	Asn	Arg	Ser	Tyr	Pro	Lys	Ile	Ser	Ser	Lys
			60				65					70			246
AAA	AAA	GAG	AAA	TTG	CTC	AAA	TCT	TTT	TCC	ATA	GCC	GAT	GAT	AAG	AGT
Lys	Lys	Glu	Lys	Leu	Leu	Lys	Ser	Phe	Ser	Ile	Ala	Asp	Asp	Lys	Ser
		75				80					85				294
GGG	GTT	TTT	TTA	GGG	GGT	GGG	TAT	GCT	TAT	GGG	GAA	CTT	AAC	TTG	TCT
															342

Gly 90	Val	Phe	Leu	Gly 95	Gly	Gly	Tyr	Ala	Tyr	Gly 100	Glu	Leu	Asn	Leu	Ser 105	
TAT	CAA	GGG	GAA	ATG	TTA	GAC	AGA	TAC	GGC	GCG	AAT	GCC	CCT	AGC	GCG	390
Tyr	Gln	Gly	Glu	Met 110	Leu	Asp	Arg	Tyr	Gly 115	Ala	Asn	Ala	Pro	Ser 120	Ala	
TTT	AAA	AAC	AAT	ATC	AAT	ATT	AAC	GCT	CCT	GTT	TCT	ATG	ATT	AGC	GCT	438
Phe	Lys	Asn	Asn	Ile 125	Asn	Ile	Asn	Ala 130	Pro	Val	Ser	Met	Ile 135	Ser	Ala	
AAA	TTT	GGG	TAT	CAA	AAA	TAC	TTT	GTG	TCT	TAT	TTT	GGG	ACA	CGA	TTT	486
Lys	Phe	Gly 140	Tyr	Gln	Lys	Tyr	Phe 145	Val	Ser	Tyr	Phe	Gly 150	Thr	Arg	Phe	
TAT	GGG	GAT	TTA	TTG	CTT	GGG	GGT	GGG	GCA	TTA	AAA	GAG	GAT	GCA	ATC	534
Tyr	Gly 155	Asp	Leu	Leu	Leu	Gly 160	Gly	Gly	Ala	Leu	Lys	Glu	Asp	Ala	Ile	
AAG	CAG	CCT	GTA	GGC	TCG	TTT	ATT	TAT	GTT	TTA	GGG	GCT	GTC	AAT	ACC	582
Lys 170	Gln	Pro	Val	Gly	Ser 175	Phe	Ile	Tyr	Val	Leu	Gly 180	Ala	Val	Asn	Thr 185	
GAT	TTA	TTG	TTT	GAT	ATG	CCT	TTA	GAT	TTT	AAA	ACT	AAA	AAG	CAT	TTT	630
Asp	Leu	Leu	Phe	Asp 190	Met	Pro	Leu	Asp	Phe 195	Lys	Thr	Lys	Lys	His	Phe 200	
TTA	GGC	GTT	TAT	GCG	GGT	TTT	GGG	ATA	GGG	CTT	ATG	CTC	TAT	CAA	GAC	678
Leu	Gly	Val	Tyr	Ala 205	Gly	Phe	Gly	Ile 210	Gly	Leu	Met	Leu	Tyr	Gln	Asp 215	
AGG	CCT	AAT	CAA	AAC	GGG	AGG	AAT	TTA	GTA	GTG	GGG	GGC	TAT	TCA	AGC	726
Arg	Pro	Asn 220	Gln	Asn	Gly	Arg	Asn 225	Leu	Val	Val	Gly	Gly	Tyr	Ser	Ser 230	
CCT	AAT	TTT	TTA	TGG	AAA	TCT	TTG	ATT	GAA	GTG	GAT	TAC	ACT	TTT	AAT	774
Pro	Asn	Phe 235	Leu	Trp	Lys	Ser 240	Leu	Ile	Glu	Val	Asp	Tyr	Thr	Phe	Asn 245	
GTG	GGC	GTG	AGT	TTA	ACG	CTT	TAT	AGG	AAA	CAC	CGT	TTA	GAG	ATT	GGC	822
Val 250	Gly	Val	Ser	Leu	Thr 255	Leu	Tyr	Arg	Lys	His 260	Arg	Leu	Glu	Ile	Gly 265	
ACA	AAA	TTG	CCG	ATT	AGC	TAT	TTG	AGA	ATG	GGA	GTG	GAA	GAG	GGA	GCG	870
Thr	Lys	Leu	Pro	Ile 270	Ser	Tyr	Leu	Arg	Met 275	Gly	Val	Glu	Glu	Gly	Ala 280	
ATT	TAT	CAA	AAT	AAA	GAA	GAT	GAT	GAG	CGT	TTG	TTG	GTT	TCG	GCT	AAC	918
Ile	Tyr	Gln	Asn	Lys 285	Glu	Asp	Asp	Glu 290	Arg	Leu	Leu	Val	Ser	Ala	Asn 295	
AAC	CAG	TTC	AAG	CGA	TCC	AGT	TTT	TTA	TTA	GTG	AAT	TAT	GCG	TTT	ATT	966
Asn	Gln	Phe 300	Lys	Arg	Ser	Ser	Phe 305	Leu	Leu	Val	Asn	Tyr	Ala	Phe	Ile 310	
TTT	TAAGGCTTGA	TCTTGAGTT	AAGGTTTAAA	ATTTT												1004
Phe																

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Met	Leu	Lys	Phe	Lys	Tyr	Gly	Leu	Ile	Tyr	Ile	Ala	Leu	Ile	Leu	Gly	1	5	10	15
Leu	Gln	Ala	Thr	Asp	Tyr	Asp	Asn	Leu	Glu	Glu	Glu	Asn	Gln	Gln	Leu	20	25	30	
Asp	Glu	Lys	Ile	Asn	His	Leu	Lys	Gln	Gln	Leu	Thr	Glu	Lys	Gly	Val	35	40	45	
Ser	Pro	Lys	Glu	Met	Asp	Lys	Asp	Lys	Phe	Glu	Glu	Glu	Tyr	Ile	Asn	50	55	60	
Arg	Ser	Tyr	Pro	Lys	Ile	Ser	Ser	Lys	Lys	Lys	Glu	Lys	Leu	Leu	Lys	65	70	75	
Ser	Phe	Ser	Ile	Ala	Asp	Asp	Lys	Ser	Gly	Val	Phe	Leu	Gly	Gly	Gly	85	90	95	
Tyr	Ala	Tyr	Gly	Glu	Leu	Asn	Leu	Ser	Tyr	Gln	Gly	Glu	Met	Leu	Asp	100	105	110	
Arg	Tyr	Gly	Ala	Asn	Ala	Pro	Ser	Ala	Phe	Lys	Asn	Asn	Ile	Asn	Ile	115	120	125	
Asn	Ala	Pro	Val	Ser	Met	Ile	Ser	Ala	Lys	Phe	Gly	Tyr	Gln	Lys	Tyr	130	135	140	
Phe	Val	Ser	Tyr	Phe	Gly	Thr	Arg	Phe	Tyr	Gly	Asp	Leu	Leu	Leu	Gly	145	150	155	
Gly	Gly	Ala	Leu	Lys	Glu	Asp	Ala	Ile	Lys	Gln	Pro	Val	Gly	Ser	Phe	165	170	175	
Ile	Tyr	Val	Leu	Gly	Ala	Val	Asn	Thr	Asp	Leu	Leu	Phe	Asp	Met	Pro	180	185	190	
Leu	Asp	Phe	Lys	Thr	Lys	Lys	His	Phe	Leu	Gly	Val	Tyr	Ala	Gly	Phe	195	200	205	
Gly	Ile	Gly	Leu	Met	Leu	Tyr	Gln	Asp	Arg	Pro	Asn	Gln	Asn	Gly	Arg	210	215	220	
Asn	Leu	Val	Val	Gly	Gly	Tyr	Ser	Ser	Pro	Asn	Phe	Leu	Trp	Lys	Ser	225	230	235	
Leu	Ile	Glu	Val	Asp	Tyr	Thr	Phe	Asn	Val	Gly	Val	Ser	Leu	Thr	Leu	245	250	255	
Tyr	Arg	Lys	His	Arg	Leu	Glu	Ile	Gly	Thr	Lys	Leu	Pro	Ile	Ser	Tyr	260	265	270	
Leu	Arg	Met	Gly	Val	Glu	Glu	Gly	Ala	Ile	Tyr	Gln	Asn	Lys	Glu	Asp	275	280	285	
Asp	Glu	Arg	Leu	Leu	Val	Ser	Ala	Asn	Asn	Gln	Phe	Lys	Arg	Ser	Ser	290	295	300	
Phe	Leu	Leu	Val	Asn	Tyr	Ala	Phe	Ile	Phe							305	310		

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 18...827
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

AACACTTAGG ATTTTATA ATG AGC ATG CAA ACC GCC CCA ATT AAA AAG ATC	50
Met Ser Met Gln Thr Ala Pro Ile Lys Lys Ile	
1 5 10	
ACT CTC AAC CAC CTC CAA GCT AAA AAA AAT CAA GAA AAA ATC ATC GCT	98
Thr Leu Asn His Leu Gln Ala Lys Lys Asn Gln Glu Lys Ile Ile Ala	
15 20 25	
ATT ACC GCT TAT GAT GCG CTG TTC GCT CAA ATA TTT GAT CCG CTA GTG	146
Ile Thr Ala Tyr Asp Ala Leu Phe Ala Gln Ile Phe Asp Pro Leu Val	
30 35 40	
GAT GTG ATT TTA GTG GGC GAT AGT TTG AAT ATG AGT TTT TTC AAT CAA	194
Asp Val Ile Leu Val Gly Asp Ser Leu Asn Met Ser Phe Phe Asn Gln	
45 50 55	
AAC GAC ACT TTA AGC GCG AGT GTG GAA ATG ATG CTC TAT CAC ACC AAA	242
Asn Asp Thr Leu Ser Ala Ser Val Glu Met Met Leu Tyr His Thr Lys	
60 65 70 75	
GCC GTG TGC GCG GGC GCT AAG ACT CCT TTT ATC ATC ACA GAC ATG CCT	290
Ala Val Cys Ala Gly Ala Lys Thr Pro Phe Ile Ile Thr Asp Met Pro	
80 85 90	
TTT GGA AGC TAT AAA GAT GAA AAA ACA GCC CTA AAA AAC GCC ATT AGG	338
Phe Gly Ser Tyr Lys Asp Glu Lys Thr Ala Leu Lys Asn Ala Ile Arg	
95 100 105	
GTT TAT AAA GAA ACC CAA GCG AGC GCA ATC AAA TTA GAG GGG GGG AAA	386
Val Tyr Lys Glu Thr Gln Ala Ser Ala Ile Lys Leu Glu Gly Gly Lys	
110 115 120	
GAA AAA GCG AAA CTG GTT AAA ACG CTC ACT AAT GAG GGC GTT ATT GTG	434
Glu Lys Ala Lys Leu Val Lys Thr Leu Thr Asn Glu Gly Val Ile Val	
125 130 135	
GTA GGG CAT ATT GGC TTG ATG CCC CAA TTC GTG CGC CTT GAT GGA GGT	482
Val Gly His Ile Gly Leu Met Pro Gln Phe Val Arg Leu Asp Gly Gly	
140 145 150 155	
TAT AAG ATT AAG GGC AAA AAT GAA GAA CAA CAA AAA AAG CTT TTA GAA	530
Tyr Lys Ile Lys Gly Lys Asn Glu Glu Gln Gln Lys Lys Leu Leu Glu	
160 165 170	

GAC GCC TTG AGT TTA GAA GAA GCT GGG GTG GGT TTG TTG GTT TTA GAG	578
Asp Ala Leu Ser Leu Glu Glu Ala Gly Val Gly Leu Leu Val Leu Glu	
175 180 185	
GGT ATA ACC ACC CCT ATC GCT CAA AAA ATC ACG CAA AAA ATC AAA ATC	626
Gly Ile Thr Thr Pro Ile Ala Gln Lys Ile Thr Gln Lys Ile Lys Ile	
190 195 200	
CCC ACG ATC GGC ATA GGG AGC GGT AAA GAT TGC GAT GGG CAG ATT TTA	674
Pro Thr Ile Gly Ile Gly Ser Gly Lys Asp Cys Asp Gly Gln Ile Leu	
205 210 215	
GTG TGG AGC GAT ATG TTA GGC TTT TTT GAT AGC TTT AAG CCT AAA TTC	722
Val Trp Ser Asp Met Leu Gly Phe Phe Asp Ser Phe Lys Pro Lys Phe	
220 225 230 235	
GTG CGA GAA TAC CTT AAG GGG AAA GAA TTG ATT CAA AAC GCT ATC AAA	770
Val Arg Glu Tyr Leu Lys Gly Lys Glu Leu Ile Gln Asn Ala Ile Lys	
240 245 250	
CAA TAC GCT GAT GAT GTG AAA AAG GGA AAC TTC CCT AAC GAA TTA GAA	818
Gln Tyr Ala Asp Asp Val Lys Lys Gly Asn Phe Pro Asn Glu Leu Glu	
255 260 265	
AGT TAT CAT TAATGAAAGA ACGGATAGTC AATTTAGAAA CTTTGGATTT TGAAATT	874
Ser Tyr His	
270	

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Met	Ser	Met	Gln	Thr	Ala	Pro	Ile	Lys	Lys	Ile	Thr	Leu	Asn	His	Leu
1				5				10						15	
Gln	Ala	Lys	Lys	Asn	Gln	Glu	Lys	Ile	Ile	Ala	Ile	Thr	Ala	Tyr	Asp
			20					25					30		
Ala	Leu	Phe	Ala	Gln	Ile	Phe	Asp	Pro	Leu	Val	Asp	Val	Ile	Leu	Val
			35				40					45			
Gly	Asp	Ser	Leu	Asn	Met	Ser	Phe	Phe	Asn	Gln	Asn	Asp	Thr	Leu	Ser
	50					55					60				
Ala	Ser	Val	Glu	Met	Met	Leu	Tyr	His	Thr	Lys	Ala	Val	Cys	Ala	Gly
65					70					75					80
Ala	Lys	Thr	Pro	Phe	Ile	Ile	Thr	Asp	Met	Pro	Phe	Gly	Ser	Tyr	Lys
				85				90						95	
Asp	Glu	Lys	Thr	Ala	Leu	Lys	Asn	Ala	Ile	Arg	Val	Tyr	Lys	Glu	Thr
			100					105				110			
Gln	Ala	Ser	Ala	Ile	Lys	Leu	Glu	Gly	Gly	Lys	Glu	Lys	Ala	Lys	Leu
			115				120					125			
Val	Lys	Thr	Leu	Thr	Asn	Glu	Gly	Val	Ile	Val	Val	Gly	His	Ile	Gly

130		135		140	
Leu Met Pro Gln Phe Val Arg Leu Asp Gly Gly Tyr Lys Ile Lys Gly					
145		150		155	160
Lys Asn Glu Glu Gln Lys Lys Leu Leu Glu Asp Ala Leu Ser Leu					
	165		170		175
Glu Glu Ala Gly Val Gly Leu Leu Val Leu Glu Gly Ile Thr Thr Pro					
	180		185		190
Ile Ala Gln Lys Ile Thr Gln Lys Ile Lys Ile Pro Thr Ile Gly Ile					
	195		200		205
Gly Ser Gly Lys Asp Cys Asp Gly Gln Ile Leu Val Trp Ser Asp Met					
	210		215		220
Leu Gly Phe Phe Asp Ser Phe Lys Pro Lys Phe Val Arg Glu Tyr Leu					
225		230		235	240
Lys Gly Lys Glu Leu Ile Gln Asn Ala Ile Lys Gln Tyr Ala Asp Asp					
	245		250		255
Val Lys Lys Gly Asn Phe Pro Asn Glu Leu Glu Ser Tyr His					
	260		265		270

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 41...520
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

AATAACGATA AAATTTTAAA GGGTGTA AAA GTAGATTGTT	ATG TTT GGC ATG GGC	55
	Met Phe Gly Met Gly	
	1 5	
TTT TTT GAA ATC CTT GTG GTG TTG GTT GTA GCG ATT ATT TTT TTA GGG		103
Phe Phe Glu Ile Leu Val Val Leu Val Val Ala Ile Ile Phe Leu Gly		
	10 15 20	
CCA GAA AAA TTC CCC CAG GCT GTC GTG GAT GTG GTG AAG TTT TTT CGC		151
Pro Glu Lys Phe Pro Gln Ala Val Val Asp Val Val Lys Phe Phe Arg		
	25 30 35	
GCG GTT AAA AAA ACG CTC AAT GAC GCT AAG GAC ACT TTA GAT AAA GAA		199
Ala Val Lys Lys Thr Leu Asn Asp Ala Lys Asp Thr Leu Asp Lys Glu		
	40 45 50	
ATC AAT ATT GAA GAA ATC AAA AAA GAA ACC CTA GAG TAT CAA AAG CTC		247
Ile Asn Ile Glu Glu Ile Lys Lys Glu Thr Leu Glu Tyr Gln Lys Leu		
	55 60 65	
TTT GAA AAC AAA GTG GAG AGT CTT AAG GGC GTT AAG ATT GAA GAA TTA		295
Phe Glu Asn Lys Val Glu Ser Leu Lys Gly Val Lys Ile Glu Glu Leu		

70	75	80	85	
GAA GAC GCT AAA GTG ACT GCA GAA AAT GAG ATT AAA AGC ATT CAG GAT				343
Glu Asp Ala Lys Val Thr Ala Glu Asn Glu Ile Lys Ser Ile Gln Asp	90	95	100	
TTG ATG CAA GAT TAC CAA AAA AGC TTA GAA ACC AAC ACA ATC CCT AAC				391
Leu Met Gln Asp Tyr Gln Lys Ser Leu Glu Thr Asn Thr Ile Pro Asn	105	110	115	
CAT TTA AAC GAA GAA GTT TCC AAT GAA GAA GCC TTA AAC AAA GAA GTT				439
His Leu Asn Glu Glu Val Ser Asn Glu Glu Ala Leu Asn Lys Glu Val	120	125	130	
TCA AGC GAT GAA TCC CCT AAA GAA GTC CAA TTA GCA ACC GAT AAC AAC				487
Ser Ser Asp Glu Ser Pro Lys Glu Val Gln Leu Ala Thr Asp Asn Asn	135	140	145	
ACC AAA GAA CAC GAC AAA GAA AAA GAG AAT GTT TGAAGATTTA AAACCGCATT				540
Thr Lys Glu His Asp Lys Glu Lys Glu Asn Val	150	155	160	
TACAGGAATT AAGAAAGCGT TTGATGGT				568

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Met	Phe	Gly	Met	Gly	Phe	Phe	Glu	Ile	Leu	Val	Val	Leu	Val	Val	Ala
1				5					10					15	
Ile	Ile	Phe	Leu	Gly	Pro	Glu	Lys	Phe	Pro	Gln	Ala	Val	Val	Asp	Val
			20					25					30		
Val	Lys	Phe	Phe	Arg	Ala	Val	Lys	Lys	Thr	Leu	Asn	Asp	Ala	Lys	Asp
		35					40					45			
Thr	Leu	Asp	Lys	Glu	Ile	Asn	Ile	Glu	Glu	Ile	Lys	Lys	Glu	Thr	Leu
		50				55					60				
Glu	Tyr	Gln	Lys	Leu	Phe	Glu	Asn	Lys	Val	Glu	Ser	Leu	Lys	Gly	Val
					70					75				80	
Lys	Ile	Glu	Glu	Leu	Glu	Asp	Ala	Lys	Val	Thr	Ala	Glu	Asn	Glu	Ile
				85					90					95	
Lys	Ser	Ile	Gln	Asp	Leu	Met	Gln	Asp	Tyr	Gln	Lys	Ser	Leu	Glu	Thr
			100					105					110		
Asn	Thr	Ile	Pro	Asn	His	Leu	Asn	Glu	Glu	Val	Ser	Asn	Glu	Glu	Ala
			115				120					125			
Leu	Asn	Lys	Glu	Val	Ser	Ser	Asp	Glu	Ser	Pro	Lys	Glu	Val	Gln	Leu
		130				135					140				
Ala	Thr	Asp	Asn	Asn	Thr	Lys	Glu	His	Asp	Lys	Glu	Lys	Glu	Asn	Val
145					150					155					160

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...324
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

TAAAGGCGAG CAGTTAAAAG ATGAAATCGC TTGTAAAGAC ACTGA ATG CTT TAT GCA	57
Met Leu Tyr Ala	
1	
TCA AAA ACG AGT TTA TTT TTA CAA ATC AAA GGA AAG TTT ATG TTA AGA	105
Ser Lys Thr Ser Leu Phe Leu Gln Ile Lys Gly Lys Phe Met Leu Arg	
5 10 15 20	
ATT TTA ATC CCC TTG CTC ATT ATT GTG TGG GTT TTA TGG CGT TTG TTT	153
Ile Leu Ile Pro Leu Leu Ile Ile Val Trp Val Leu Trp Arg Leu Phe	
25 30 35	
TTG AGG CAA AAA CCC CCT AAA GAC AAC CAC TCT TAC ACG CAA CAA ACC	201
Leu Arg Gln Lys Pro Pro Lys Asp Asn His Ser Tyr Thr Gln Gln Thr	
40 45 50	
CCT AAA GAA TTA GAA GAT CAC ATG ATT GTA TGC TCT AAA TGC CAA ACC	249
Pro Lys Glu Leu Glu Asp His Met Ile Val Cys Ser Lys Cys Gln Thr	
55 60 65	
TAT GTC TCT AGC AAA GAC GCT ATT TAT AGC GGG GCG GTG GCG TAT TGC	297
Tyr Val Ser Ser Lys Asp Ala Ile Tyr Ser Gly Ala Val Ala Tyr Cys	
70 75 80	
AGT GAA ACC TGT TTG AAG GAT AAG AGG TAAATATGCT TATTTTAGGA CACCCTT	351
Ser Glu Thr Cys Leu Lys Asp Lys Arg	
85 90	
TAATCCCT	359

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

[illegible]

(2) INFORMATION FOR SEO ID NO:234:

(ii) MOLECULE TYPE: protein

Met	Lys	Pro	Thr	Asn	Glu	Pro	Lys	Lys	Pro	Phe	Phe	Gln	Ser	Pro	Ile
1				5					10					15	
Ile	Leu	Ala	Val	Leu	Gly	Gly	Ile	Leu	Leu	Ile	Phe	Phe	Leu	Arg	Ser
			20					25					30		
Phe	Asn	Ser	Asp	Gly	Ser	Phe	Ser	Asp	Asn	Phe	Leu	Ala	Ser	Ser	Thr
			35				40					45			
Lys	Asn	Val	Ser	Tyr	His	Glu	Ile	Lys	Gln	Leu	Ile	Ser	Asn	Asn	Glu
	50					55					60				

CGT TCA TTC TAA GAT AGA ATT ATT AGA GTT ATT GAG TTT AGC GCT CAG	252
Val His Ser Lys Ile Glu Leu Leu Glu Leu Leu Ser Leu Ala Leu Ser	
50 55 60 65	
TAT TGA AAA GAG TAG CGA ACA TGT CAT CGC TAA AGG GAT TGT AGA ATA	300
Ile Glu Lys Ser Ser Glu His Val Ile Ala Lys Gly Ile Val Glu Tyr	
70 75 80	
CGC AAA AGA GCA TAA CGC TCC CTT AAA AGA AAT GAG CGG GGT TAA AGT	348
Ala Lys Glu His Asn Ala Pro Leu Lys Glu Met Ser Gly Val Lys Val	
85 90 95	
GAA AAC GGG TTT TGG CAT TAG TGC TAA AAC AGA TTA TCA AGG CAC TAA	396
Lys Thr Gly Phe Gly Ile Ser Ala Lys Thr Asp Tyr Gln Gly Thr Lys	
100 105 110	
AGA GAT TAT TAA AGT AGG CAA CAG CGA GTT TTT TAA CCC TAT TAA CAC	444
Glu Ile Ile Lys Val Gly Asn Ser Glu Phe Phe Asn Pro Ile Asn Thr	
115 120 125	
GCT AGA AAT TAA AGA AAA CGG GAT TTT AGT GTT TGT TGG TAG AGC GAT	492
Leu Glu Ile Lys Glu Asn Gly Ile Leu Val Phe Val Gly Arg Ala Ile	
130 135 140 14	
CAG TGA AAA AGA AGA CGA GCT TTT AGG GGC GTT TGT TTT AGA AGA TTT	540
Ser Glu Lys Glu Asp Glu Leu Leu Gly Ala Phe Val Leu Glu Asp Leu	
5 150 155 160	
GCC CAA AAA AGG CGT GAA AGA GCA TAT CGC TCA AAT CAA AAA TTT AGG	588
Pro Lys Lys Gly Val Lys Glu His Ile Ala Gln Ile Lys Asn Leu Gly	
165 170 175	
CAT TAA CAC CTT TCT TTT AAG CGG AGA CAA TAG GGA GAA TGT CCA AAA	636
Ile Asn Thr Phe Leu Leu Ser Gly Asp Asn Arg Glu Asn Val Gln Lys	
180 185 190	
ATG CGC GTT TGA ATT AGG GAT TGA TGG TTA TAT CAG CAA CGC TAA ACC	684
Cys Ala Phe Glu Leu Gly Ile Asp Gly Tyr Ile Ser Asn Ala Lys Pro	
195 200 205	
ACA AGA CAA GCT CAA TAA GAT CAA AGA GCT TAA GGA AAA AGG GCA GAT	732
Gln Asp Lys Leu Asn Lys Ile Lys Glu Leu Lys Glu Lys Gly Gln Ile	
210 215 220 22	
CGT TAT GAT GGT GGG CGA TGG CTT GAA TGA CGC TCC TAG TCT TGC TAT	780
Val Met Met Val Gly Asp Gly Leu Asn Asp Ala Pro Ser Leu Ala Met	
5 230 235 240	
GAG CGA TGT GGC GGT GGT GAT GGC TAA AGG GAG CGA TGT GAG CGT GCA	828
Ser Asp Val Ala Val Val Met Ala Lys Gly Ser Asp Val Ser Val Gln	
245 250 255	
AGC AGC GGA CAT TGT GAG TTT TAA TAA CGA TAT TAA ATC GGT TTA TAG	876
Ala Ala Asp Ile Val Ser Phe Asn Asn Asp Ile Lys Ser Val Tyr Ser	
260 265 270	
CGC GAT TAA ATT AAG CCA GGC GAC AAT TAA AAA TAT CAA AGA AAA TTT	924
Ala Ile Lys Leu Ser Gln Ala Thr Ile Lys Asn Ile Lys Glu Asn Leu	

275	280	285	
GTT TTG GGC TTT TTG TTA TAA TAG CGT GTT CAT CCC TTT AGC TTG TGG			972
Phe Trp Ala Phe Cys Tyr Asn Ser Val Phe Ile Pro Leu Ala Cys Gly			
290	295	300	30
GGT TCT TTA TAA GGC TAA TCT CAT GTT AAG CCC GGC GAT TGC GGG TTT			1020
Val Leu Tyr Lys Ala Asn Leu Met Leu Ser Pro Ala Ile Ala Gly Leu			
5	310	315	320
AGC GAT GAG TTT AAG CTC TGT GAG TGT GGT CTT AAA CTC CCA AAG GCT			1068
Ala Met Ser Leu Ser Ser Val Ser Val Val Leu Asn Ser Gln Arg Leu			
	325	330	335
AAG GAA TTT TAA AAT TAA GGA TCA T TGAATGAAAG CAACTTTTCA AGTGCCAAG			1122
Arg Asn Phe Lys Ile Lys Asp His			
	340	345	
CATTACTTGC AACCA			1137

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Met	Ser	Ile	Leu	Val	Ala	Asn	Gln	Lys	Ala	Ser	Ser	Leu	Gly	Leu	Phe
1				5					10					15	
Phe	Lys	Asp	Ala	Lys	Ser	Leu	Glu	Lys	Ala	Arg	Leu	Val	Asn	Thr	Ile
			20					25					30		
Val	Phe	Asp	Lys	Thr	Gly	Thr	Leu	Thr	Asn	Gly	Lys	Pro	Val	Val	Lys
		35				40						45			
Ser	Val	His	Ser	Lys	Ile	Glu	Leu	Leu	Glu	Leu	Ser	Leu	Ala	Leu	
	50				55					60					
Ser	Ile	Glu	Lys	Ser	Ser	Glu	His	Val	Ile	Ala	Lys	Gly	Ile	Val	Glu
65				70						75				80	
Tyr	Ala	Lys	Glu	His	Asn	Ala	Pro	Leu	Lys	Glu	Met	Ser	Gly	Val	Lys
			85					90						95	
Val	Lys	Thr	Gly	Phe	Gly	Ile	Ser	Ala	Lys	Thr	Asp	Tyr	Gln	Gly	Thr
			100					105					110		
Lys	Glu	Ile	Ile	Lys	Val	Gly	Asn	Ser	Glu	Phe	Phe	Asn	Pro	Ile	Asn
		115				120						125			
Thr	Leu	Glu	Ile	Lys	Glu	Asn	Gly	Ile	Leu	Val	Phe	Val	Gly	Arg	Ala
	130					135					140				
Ile	Ser	Glu	Lys	Glu	Asp	Glu	Leu	Leu	Gly	Ala	Phe	Val	Leu	Glu	Asp
145				150						155				160	
Leu	Pro	Lys	Lys	Gly	Val	Lys	Glu	His	Ile	Ala	Gln	Ile	Lys	Asn	Leu
			165					170						175	
Gly	Ile	Asn	Thr	Phe	Leu	Leu	Ser	Gly	Asp	Asn	Arg	Glu	Asn	Val	Gln
		180						185					190		
Lys	Cys	Ala	Phe	Glu	Leu	Gly	Ile	Asp	Gly	Tyr	Ile	Ser	Asn	Ala	Lys
		195					200					205			

```

Pro Gln Asp Lys Leu Asn Lys Ile Lys Glu Leu Lys Glu Lys Gly Gln
  210                215                220
Ile Val Met Met Val Gly Asp Gly Leu Asn Asp Ala Pro Ser Leu Ala
225                230                235                240
Met Ser Asp Val Ala Val Val Met Ala Lys Gly Ser Asp Val Ser Val
                245                250                255
Gln Ala Ala Asp Ile Val Ser Phe Asn Asn Asp Ile Lys Ser Val Tyr
                260                265                270
Ser Ala Ile Lys Leu Ser Gln Ala Thr Ile Lys Asn Ile Lys Glu Asn
                275                280                285
Leu Phe Trp Ala Phe Cys Tyr Asn Ser Val Phe Ile Pro Leu Ala Cys
                290                295                300
Gly Val Leu Tyr Lys Ala Asn Leu Met Leu Ser Pro Ala Ile Ala Gly
305                310                315                320
Leu Ala Met Ser Leu Ser Ser Val Ser Val Val Leu Asn Ser Gln Arg
                325                330                335
Leu Arg Asn Phe Lys Ile Lys Asp His
                340                345

```

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs .
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...537
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

```

TCAATTCTAT TTAAAAGGTT TTTT ATG GAT ATT TTA AAA ACT CTT CAA AAA      51
                Met Asp Ile Leu Lys Thr Leu Gln Lys
                1                5

CAT TTG GGC GAT GTT GAA ACA AGC GAT TTT ACA ACC AAT GCG ATA GAA      99
His Leu Gly Asp Val Glu Thr Ser Asp Phe Thr Thr Asn Ala Ile Glu
10                15                20                25

AAA TCC CAA CAA ATC GCT AAA TTC AGT AGG GAC ATG AAA AAT ATA AAC      147
Lys Ser Gln Gln Ile Ala Lys Phe Ser Arg Asp Met Lys Asn Ile Asn
                30                35                40

GAG AGC GTT GGA GCG TTA CAA GTC TTG CAA ATC GCT TGC AAA AAG CTT      195
Glu Ser Val Gly Ala Leu Gln Val Leu Gln Ile Ala Cys Lys Lys Leu
                45                50                55

TTC AAT AAG AGC ATG GGT TTA GAA GAT AAA GAC GCT TTG CAA GCT TCT      243
Phe Asn Lys Ser Met Gly Leu Glu Asp Lys Asp Ala Leu Gln Ala Ser
                60                65                70

ATC ATC AAA CAG GAA TTG CGA GAA ATT GTA GAA AAT TGC CAG TTT TTA      291

```


Ser Leu Ser Asn Pro Lys Ala Phe Met Pro Ser Phe Ser Asn Gln Ser
 145 150 155 160
 Leu Lys Asp Leu Leu Ser Asp Asn Leu Arg Ala
 165 170

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1025 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...972
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TTTTTAGCGA TTGTGTTCTT GCATGCATTG GGTTTAGCGT TGCTCTTT ATG GCC AAT	57
Met Ala Asn	
1	
AAC GCT TCG TTT TAT GCG GCG GCG TCT ATG GCC TAC ATG CTA GGG GCA	105
Asn Ala Ser Phe Tyr Ala Ala Ala Ser Met Ala Tyr Met Leu Gly Ala	
5 10 15	
AAG CAT GCG TTT GAT GCG GAT CAC ATC GCT TGC ATA GAT AAC ACC ATT	153
Lys His Ala Phe Asp Ala Asp His Ile Ala Cys Ile Asp Asn Thr Ile	
20 25 30 35	
AGA AAG CTC ACC CAA CAA GGC AAA AAC GCC TAT GGT GTG GGG TTT TAC	201
Arg Lys Leu Thr Gln Gln Gly Lys Asn Ala Tyr Gly Val Gly Phe Tyr	
40 45 50	
TTT TCT ATG GGG CAT TCA AGC GTG GTG ATT TTA ATG ACC ATC ATC AGC	249
Phe Ser Met Gly His Ser Ser Val Val Ile Leu Met Thr Ile Ile Ser	
55 60 65	
GCG TTT GCG ATC GCT TGG GCT AAA GAA CAC ACG CCG ATG CTA GAA GAA	297
Ala Phe Ala Ile Ala Trp Ala Lys Glu His Thr Pro Met Leu Glu Glu	
70 75 80	
ATA GGG GGG GTA GTG GGG ACT TTA GTT TCT GGG CTT TTT TTG CTC ATT	345
Ile Gly Gly Val Val Gly Thr Leu Val Ser Gly Leu Phe Leu Leu Ile	
85 90 95	
ATA GGG CTA TTG AAT GCG ATT ATT CTC TTG GAT TTA TTA AAA ATA TTC	393
Ile Gly Leu Leu Asn Ala Ile Ile Leu Leu Asp Leu Leu Lys Ile Phe	
100 105 110 115	
AAA AAA TCG CAC TCT AAT GAA AGC CTA AGC CAG CAA CAA AAT GAA GAG	441
Lys Lys Ser His Ser Asn Glu Ser Leu Ser Gln Gln Gln Asn Glu Glu	
120 125 130	

ATC GAG CGG CTC TTA ACG AGT AGG GGC TTG CTC AAC CGC TTT TTT AAA Ile Glu Arg Leu Leu Thr Ser Arg Gly Leu Leu Asn Arg Phe Phe Lys 135 140 145	489
CCC TTG TTT AAT TTT GTC TCC AAG TCG TGG CAT ATT TAT CCT ATC GGT Pro Leu Phe Asn Phe Val Ser Lys Ser Trp His Ile Tyr Pro Ile Gly 150 155 160	537
TTT CTT TTT GGG CTG GGT TTT GAT ACC GCT AGT GAA ATC GCG CTT TTG Phe Leu Phe Gly Leu Gly Phe Asp Thr Ala Ser Glu Ile Ala Leu Leu 165 170 175	585
GCC CTC TCT AGC AGC GCG ATT AAA GTG AGT ATG GTG GGC ATG CTC TCT Ala Leu Ser Ser Ser Ala Ile Lys Val Ser Met Val Gly Met Leu Ser 180 185 190 195	633
TTA CCC ATT CTT TTT GCC GCT GGC ATG AGT TTG TTT GAC ACT TTA GAT Leu Pro Ile Leu Phe Ala Ala Gly Met Ser Leu Phe Asp Thr Leu Asp 200 205 210	681
GGG GCG TTC ATG CTC AAG GCG TAT GAC TGG GCG TTC AAA ACC CCT TTA Gly Ala Phe Met Leu Lys Ala Tyr Asp Trp Ala Phe Lys Thr Pro Leu 215 220 225	729
AGA AAA ATC TAT TAC AAT ATC TCT ATC ACG GCC TTA AGC GTG TTT ATC Arg Lys Ile Tyr Tyr Asn Ile Ser Ile Thr Ala Leu Ser Val Phe Ile 230 235 240	777
GCG CTC TTT ATT GGC TTG ATT GAG CTT TTT CAA GTC GTT AGC GAG AAA Ala Leu Phe Ile Gly Leu Ile Glu Leu Phe Gln Val Val Ser Glu Lys 245 250 255	825
CTC CAT TTA AAA TTT GAA AAC CGC CTT TTA AGA GCC TTA CAA AGC CTG Leu His Leu Lys Phe Glu Asn Arg Leu Leu Arg Ala Leu Gln Ser Leu 260 265 270 275	873
GAA TTT ACA GAC TTG GGC TAT TAC TTG GTG GGC TTA TTT GTA ATA GCG Glu Phe Thr Asp Leu Gly Tyr Tyr Leu Val Gly Leu Phe Val Ile Ala 280 285 290	921
TTT CTA GGA TCG TTC TTT TTA TGG AAA ATC AAA TTT TCT AAA CTA GAG Phe Leu Gly Ser Phe Phe Leu Trp Lys Ile Lys Phe Ser Lys Leu Glu 295 300 305	969
AGC TGAATTCTAA GCCCTCAAAT TATCGCTTAA TAAATCTTTA AGGCTTTGAT TTG Ser	1025

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Met	Ala	Asn	Asn	Ala	Ser	Phe	Tyr	Ala	Ala	Ala	Ser	Met	Ala	Tyr	Met
1				5				10						15	
Leu	Gly	Ala	Lys	His	Ala	Phe	Asp	Ala	Asp	His	Ile	Ala	Cys	Ile	Asp
			20					25					30		
Asn	Thr	Ile	Arg	Lys	Leu	Thr	Gln	Gln	Gly	Lys	Asn	Ala	Tyr	Gly	Val
			35					40					45		
Gly	Phe	Tyr	Phe	Ser	Met	Gly	His	Ser	Ser	Val	Val	Ile	Leu	Met	Thr
			50					55				60			
Ile	Ile	Ser	Ala	Phe	Ala	Ile	Ala	Trp	Ala	Lys	Glu	His	Thr	Pro	Met
65					70					75					80
Leu	Glu	Glu	Ile	Gly	Gly	Val	Val	Gly	Thr	Leu	Val	Ser	Gly	Leu	Phe
				85				90						95	
Leu	Leu	Ile	Ile	Gly	Leu	Leu	Asn	Ala	Ile	Ile	Leu	Leu	Asp	Leu	Leu
				100				105					110		
Lys	Ile	Phe	Lys	Lys	Ser	His	Ser	Asn	Glu	Ser	Leu	Ser	Gln	Gln	Gln
				115				120					125		
Asn	Glu	Glu	Ile	Glu	Arg	Leu	Leu	Thr	Ser	Arg	Gly	Leu	Leu	Asn	Arg
						135					140				
Phe	Phe	Lys	Pro	Leu	Phe	Asn	Phe	Val	Ser	Lys	Ser	Trp	His	Ile	Tyr
145						150					155				160
Pro	Ile	Gly	Phe	Leu	Phe	Gly	Leu	Gly	Phe	Asp	Thr	Ala	Ser	Glu	Ile
				165				170						175	
Ala	Leu	Leu	Ala	Leu	Ser	Ser	Ser	Ala	Ile	Lys	Val	Ser	Met	Val	Gly
				180				185					190		
Met	Leu	Ser	Leu	Pro	Ile	Leu	Phe	Ala	Ala	Gly	Met	Ser	Leu	Phe	Asp
				195				200				205			
Thr	Leu	Asp	Gly	Ala	Phe	Met	Leu	Lys	Ala	Tyr	Asp	Trp	Ala	Phe	Lys
						215					220				
Thr	Pro	Leu	Arg	Lys	Ile	Tyr	Tyr	Asn	Ile	Ser	Ile	Thr	Ala	Leu	Ser
225						230					235				240
Val	Phe	Ile	Ala	Leu	Phe	Ile	Gly	Leu	Ile	Glu	Leu	Phe	Gln	Val	Val
				245				250						255	
Ser	Glu	Lys	Leu	His	Leu	Lys	Phe	Glu	Asn	Arg	Leu	Leu	Arg	Ala	Leu
				260				265					270		
Gln	Ser	Leu	Glu	Phe	Thr	Asp	Leu	Gly	Tyr	Tyr	Leu	Val	Gly	Leu	Phe
				275				280				285			
Val	Ile	Ala	Phe	Leu	Gly	Ser	Phe	Phe	Leu	Trp	Lys	Ile	Lys	Phe	Ser
				290			295				300				
Lys	Leu	Glu	Ser												
305															

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 75...989
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

TTGTGAAAGA	AAATGAAGCG	TTTTTTAAAA	TCGGTATCAA	AAACATCGCC	GTGGCTGAAA	60
TTTCTTCGCC	TTTA	ATG	GAG	TTT	TTA	110
	Met	Glu	Phe	Leu	Gly	
	1			5		
					10	
ATT	TAT	TTA	GGG	GGG	AAT	158
Ile	Tyr	Leu	Gly	Gly	Asn	
	15				20	
						25
GCG	TTT	TTT	TCT	TTC	ATT	206
Ala	Phe	Phe	Ser	Phe	Ile	
	30				35	
						40
AAA	CGC	TTA	ACT	AGG	ATT	254
Lys	Arg	Leu	Thr	Arg	Ile	
	45				50	
						55
						60
AGC	GAC	AGG	ATC	CAT	GAG	302
Ser	Asp	Arg	Ile	His	Glu	
				65	Ile	
					70	
						75
GGG	GAA	TTG	ACG	CTA	AAT	350
Gly	Glu	Leu	Thr	Leu	Asn	
				80	Asn	
					85	
						90
GTA	TGG	CTG	GCT	TAT	ACG	398
Val	Trp	Leu	Ala	Tyr	Thr	
		95			100	
						105
GAT	ATT	AGT	TTG	AAG	TTC	446
Asp	Ile	Ser	Leu	Lys	Phe	
	110				115	
						120
GAA	AGC	GGG	AGC	GGT	AAA	494
Glu	Ser	Gly	Ser	Gly	Lys	
	125				130	
						135
						140
TAT	GAG	CCA	AGC	AAA	GGC	542
Tyr	Glu	Pro	Ser	Lys	Gly	
				145	Glu	
					150	
						155
AGC	ATC	ACT	CAA	AAA	TCC	590
Ser	Ile	Thr	Gln	Lys	Ser	
				160	Leu	
					165	
						170
AGG	GTG	TTT	ATT	TTT	AAC	638
Arg	Val	Phe	Ile	Phe	Asn	
		175			Gly	
					180	
						185
TTA	GAA	ATT	GAT	GAG	GTA	686
Leu	Glu	Ile	Asp	Glu	Val	
				190	Lys	
					195	
						200
GCC	TTA	GAT	TTT	GTT	GAA	734
					AAA	
					ATG	
					CCT	
					CAT	
					GGG	
					ATA	
					GAG	
					AGC	
					GTT	
					TTA	

Ala	Leu	Asp	Phe	Val	Glu	Lys	Met	Pro	His	Gly	Ile	Glu	Ser	Val	Leu		
205					210					215					220		
GAT	GAA	TTT	GGC	GCT	AAT	CTT	AGC	GGC	GGC	CAA	CGC	CAA	AGA	ATC	GCC	782	
Asp	Glu	Phe	Gly	Ala	Asn	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ala		
			225					230						235			
ATT	GCA	AGA	GCT	TTG	TAT	AAA	GAC	GTT	CAA	GTT	TTA	ATC	TTT	GAT	GAA	830	
Ile	Ala	Arg	Ala	Leu	Tyr	Lys	Asp	Val	Gln	Val	Leu	Ile	Phe	Asp	Glu		
			240					245						250			
GCC	ACT	TCC	GCT	TTA	GAC	AAT	AAC	ACA	GAA	GAG	AGC	GTT	AAA	CAA	AGC	878	
Ala	Thr	Ser	Ala	Leu	Asp	Asn	Asn	Thr	Glu	Glu	Ser	Val	Lys	Gln	Ser		
		255					260					265					
ATT	TTA	GAA	TTG	AAA	CAA	AAC	CGC	TTG	ATC	ATT	CTT	ATT	TCG	CAC	AAC	926	
Ile	Leu	Glu	Leu	Lys	Gln	Asn	Arg	Leu	Ile	Ile	Leu	Ile	Ser	His	Asn		
	270				275						280						
CCA	AGC	ACG	CTA	AAA	TTA	GCC	ACT	AAG	CAT	GTG	AAA	TTA	GAG	CAT	GGG	974	
Pro	Ser	Thr	Leu	Lys	Leu	Ala	Thr	Lys	His	Val	Lys	Leu	Glu	His	Gly		
285					290					295					300		
CGT	TTG	ACA	GAA	TGC	TAAGGGTTTT	AAGCGTTGGT	GTTGCTTTTA	TTTTACTAGG	G	1030							
Arg	Leu	Thr	Glu	Cys	305												
TGTC																1034	

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Met	Glu	Phe	Leu	Gly	Ser	Ile	Ala	Ile	Ala	Leu	Val	Ile	Tyr	Leu	Gly		
1				5					10					15			
Gly	Asn	Glu	Val	Ile	Arg	Gly	His	Ile	Ser	Val	Gly	Ala	Phe	Phe	Ser		
			20					25					30				
Phe	Ile	Thr	Ala	Leu	Phe	Met	Leu	Tyr	Thr	Pro	Ile	Lys	Arg	Leu	Thr		
		35				40						45					
Arg	Ile	Val	Ser	Asn	Phe	Gln	Glu	Ala	Leu	Val	Ala	Ser	Asp	Arg	Ile		
	50				55					60							
His	Glu	Ile	Leu	Glu	Arg	Glu	Pro	Ala	Ile	Val	Asp	Gly	Glu	Leu	Thr		
65				70						75				80			
Leu	Asn	Asn	Ala	Ile	His	Thr	Ile	Glu	Phe	Lys	Lys	Val	Trp	Leu	Ala		
			85					90					95				
Tyr	Thr	Leu	Asp	Asn	Gln	Glu	Arg	Tyr	Val	Leu	Asn	Asp	Ile	Ser	Leu		
		100				105						110					
Lys	Phe	Gln	Gln	Asn	Glu	Ile	Ile	Ala	Leu	Lys	Gly	Glu	Ser	Gly	Ser		
		115				120						125					
Gly	Lys	Ser	Ser	Leu	Val	Asn	Leu	Ile	Leu	Arg	Leu	Tyr	Glu	Pro	Ser		

Lys	Leu	Ala	Lys	Ser	His	Gln	Glu	Ser	Asn	Ala	Lys	Ile	Thr	Ala	Arg
130						135					140				
Leu	Ser	Glu	Val	Phe	Asn	Asn	Val	Gly	Ser	Asp					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...738
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

TTTCGCTTAT CAAGTCCCCC TACCTCAATT TTA ATG CGC TTA GAT TAC GCC TTA	54
Met Arg Leu Asp Tyr Ala Leu	
1 5	
TTC AGT CAG CAT TTA GTA AAT AGC AGA GAA AAA GCT AAA GCG TTG GTT	102
Phe Ser Gln His Leu Val Asn Ser Arg Glu Lys Ala Lys Ala Leu Val	
10 15 20	
TTA AAA AAT CAG GTT TTA GTC AAT AAA ATG GTG GTT TCC AAA CCC TCT	150
Leu Lys Asn Gln Val Leu Val Asn Lys Met Val Val Ser Lys Pro Ser	
25 30 35	
TTT ATA GTG AAA GAG AAC GAT AAA ATT GAA CTC ATC GCT GAA AAA CTT	198
Phe Ile Val Lys Glu Asn Asp Lys Ile Glu Leu Ile Ala Glu Lys Leu	
40 45 50 55	
TTC GTT AGC AGG GCT GGG GAA AAA TTA GGG GCT TTT TTA GAA ACC CAT	246
Phe Val Ser Arg Ala Gly Glu Lys Leu Gly Ala Phe Leu Glu Thr His	
60 65 70	
TTC GTG GAT TTT AAG GGA AAG GTG GTT TTA GAT GTG GGA GCG AGC AAA	294
Phe Val Asp Phe Lys Gly Lys Val Val Leu Asp Val Gly Ala Ser Lys	
75 80 85	
GGG GGC TTT AGT CAA GTG GCT CTT TTA AAA GGG GCT AAA AGA GTG CTT	342
Gly Gly Phe Ser Gln Val Ala Leu Leu Lys Gly Ala Lys Arg Val Leu	
90 95 100	
TGC GTG GAT GTG GGG AAA ATG CAA TTA GAT GAA AGT TTG AAA CAA GAC	390
Cys Val Asp Val Gly Lys Met Gln Leu Asp Glu Ser Leu Lys Gln Asp	
105 110 115	
AAG CGC ATA GAA TGT TAC GAA GAA TGC GAT ATT AGA GGG TTT AAA ACG	438
Lys Arg Ile Glu Cys Tyr Glu Glu Cys Asp Ile Arg Gly Phe Lys Thr	
120 125 130 135	

CCA GAA ACA ATT GAT TTA GCG CTT TGC GAT GTG AGC TTT ATT TCT TTA	486
Pro Glu Thr Ile Asp Leu Ala Leu Cys Asp Val Ser Phe Ile Ser Leu	
140 145 150	
TAT TAT ATT TTA GAA GCG ATT TTG CCT TTA AGC GAT GAA TTT TTA ACA	534
Tyr Tyr Ile Leu Glu Ala Ile Leu Pro Leu Ser Asp Glu Phe Leu Thr	
155 160 165	
CTT TTC AAA CCG CAA TTT GAA GTG GGC AGA GGA ATA AAA CGC AAT AAA	582
Leu Phe Lys Pro Gln Phe Glu Val Gly Arg Gly Ile Lys Arg Asn Lys	
170 175 180	
AAA GGG GTG GTG GTG GAT AAA GAA GCC ATT TTG AAC GCT TTA GAA AAC	630
Lys Gly Val Val Val Asp Lys Glu Ala Ile Leu Asn Ala Leu Glu Asn	
185 190 195	
TTT AAA AAC CAT TTA AAA ACA AAG GAT TTT CAA ATC TTA AAG ATC CAA	678
Phe Lys Asn His Leu Lys Thr Lys Asp Phe Gln Ile Leu Lys Ile Gln	
200 205 210 215	
GAA AGC TTA GTG AAA GGG AAA AAC GGG AAT GTT GAA TTT TTT ATC CAT	726
Glu Ser Leu Val Lys Gly Lys Asn Gly Asn Val Glu Phe Phe Ile His	
220 225 230	
TTC AAG CGA GCC TAAAATTAAA AGCCTAGCTA TCGGTAAATT TGACGGCTTG CATTT	783
Phe Lys Arg Ala	
235	
AGGGCA	789

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Met Arg Leu Asp Tyr Ala Leu Phe Ser Gln His Leu Val Asn Ser Arg	
1 5 10 15	
Glu Lys Ala Lys Ala Leu Val Leu Lys Asn Gln Val Leu Val Asn Lys	
20 25 30	
Met Val Val Ser Lys Pro Ser Phe Ile Val Lys Glu Asn Asp Lys Ile	
35 40 45	
Glu Leu Ile Ala Glu Lys Leu Phe Val Ser Arg Ala Gly Glu Lys Leu	
50 55 60	
Gly Ala Phe Leu Glu Thr His Phe Val Asp Phe Lys Gly Lys Val Val	
65 70 75 80	
Leu Asp Val Gly Ala Ser Lys Gly Gly Phe Ser Gln Val Ala Leu Leu	
85 90 95	
Lys Gly Ala Lys Arg Val Leu Cys Val Asp Val Gly Lys Met Gln Leu	
100 105 110	
Asp Glu Ser Leu Lys Gln Asp Lys Arg Ile Glu Cys Tyr Glu Glu Cys	
115 120 125	

Asp	Ile	Arg	Gly	Phe	Lys	Thr	Pro	Glu	Thr	Ile	Asp	Leu	Ala	Leu	Cys
130						135					140				
Asp	Val	Ser	Phe	Ile	Ser	Leu	Tyr	Tyr	Ile	Leu	Glu	Ala	Ile	Leu	Pro
145					150					155					160
Leu	Ser	Asp	Glu	Phe	Leu	Thr	Leu	Phe	Lys	Pro	Gln	Phe	Glu	Val	Gly
			165						170					175	
Arg	Gly	Ile	Lys	Arg	Asn	Lys	Lys	Gly	Val	Val	Val	Asp	Lys	Glu	Ala
			180					185					190		
Ile	Leu	Asn	Ala	Leu	Glu	Asn	Phe	Lys	Asn	His	Leu	Lys	Thr	Lys	Asp
		195					200					205			
Phe	Gln	Ile	Leu	Lys	Ile	Gln	Glu	Ser	Leu	Val	Lys	Gly	Lys	Asn	Gly
	210				215						220				
Asn	Val	Glu	Phe	Phe	Ile	His	Phe	Lys	Arg	Ala					
225					230					235					

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...858
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TGAAAGGGGAA	AAACGGGA	ATG	TTG	AAT	TTT	TTA	TCC	ATT	TCA	AGC	GAG	CCT			51
		Met	Leu	Asn	Phe	Leu	Ser	Ile	Ser	Ser	Glu	Pro			
		1				5					10				
AAA	ATT	AAA	AGC	CTA	GCT	ATC	GGT	AAA	TTT	GAC	GGC	TTG	CAT	TTA	GGG
Lys	Ile	Lys	Ser	Leu	Ala	Ile	Gly	Lys	Phe	Asp	Gly	Leu	His	Leu	Gly
		15					20					25			99
CAT	CAA	GCC	CTT	TTT	AAA	GAG	TTA	AAA	GAT	CCC	AAA	GCC	CTT	TTA	ATC
His	Gln	Ala	Leu	Phe	Lys	Glu	Leu	Lys	Asp	Pro	Lys	Ala	Leu	Leu	Ile
		30				35						40			147
ATA	GAA	AAA	AAA	CAT	TAC	ACT	AAA	GGC	TAT	TTA	ACC	CCC	CTA	AAA	TAC
Ile	Glu	Lys	Lys	His	Tyr	Thr	Lys	Gly	Tyr	Leu	Thr	Pro	Leu	Lys	Tyr
	45					50				55					195
CGC	GCT	AAA	CTC	GTG	GGC	ATG	CCT	TTA	TTT	TTT	GTG	TAT	TTA	GAA	GAG
Arg	Ala	Lys	Leu	Val	Gly	Met	Pro	Leu	Phe	Phe	Val	Tyr	Leu	Glu	Glu
60				65					70					75	243
ATT	TCA	CAA	TTA	AAC	GCC	CTA	GAT	TTT	TTA	GAT	CTT	TTA	AAA	AAG	AAA
Ile	Ser	Gln	Leu	Asn	Ala	Leu	Asp	Phe	Leu	Asp	Leu	Leu	Lys	Lys	Lys
			80					85					90		291
TTT	CCC	CAT	TTA	GAA	CGC	CTG	GTC	GTG	GGC	TAT	GAT	TTC	AGG	TTT	GGG
															339

Phe	Pro	His	Leu	Glu	Arg	Leu	Val	Val	Gly	Tyr	Asp	Phe	Arg	Phe	Gly		
			95					100					105				
CAT	GAG	AGG	CAA	AAT	GAC	GCT	TTA	TTT	TTA	AAA	GAG	CGT	TTT	GAA	AAA	387	
His	Glu	Arg	Gln	Asn	Asp	Ala	Leu	Phe	Leu	Lys	Glu	Arg	Phe	Glu	Lys		
		110					115					120					
ACC	ATT	ATT	GTG	CCT	GAA	GTG	AAA	GTC	CAA	GAG	ATT	AGC	GTG	CAT	TCT	435	
Thr	Ile	Ile	Val	Pro	Glu	Val	Lys	Val	Gln	Glu	Ile	Ser	Val	His	Ser		
	125					130					135						
AAG	ATG	ATC	AAA	CTA	GCC	CTA	AGT	CAT	GGC	GAC	TTA	TCT	TTA	GCT	AAC	483	
Lys	Met	Ile	Lys	Leu	Ala	Leu	Ser	His	Gly	Asp	Leu	Ser	Leu	Ala	Asn		
140					145					150					155		
AAG	CTC	TTA	GGC	AGA	CCT	TAT	GAA	GTG	TGT	GGG	GAA	GTC	ATT	AGT	GAT	531	
Lys	Leu	Leu	Gly	Arg	Pro	Tyr	Glu	Val	Cys	Gly	Glu	Val	Ile	Ser	Asp		
				160					165					170			
CAA	GGT	TTG	GGG	CAT	AAA	GAA	TTA	GCA	CCC	ACT	TTA	AAT	ATA	AAA	ACT	579	
Gln	Gly	Leu	Gly	His	Lys	Glu	Leu	Ala	Pro	Thr	Leu	Asn	Ile	Lys	Thr		
			175					180						185			
AAA	GAT	TTT	ATC	CTC	CCT	AGT	TTT	GGG	GTG	TAT	GCG	AGT	TTA	GTG	AAA	627	
Lys	Asp	Phe	Ile	Leu	Pro	Ser	Phe	Gly	Val	Tyr	Ala	Ser	Leu	Val	Lys		
		190					195					200					
ATA	AAA	GAT	CCA	ATT	TAT	CAA	AAA	AGC	GTG	AGT	TTT	ATA	GGC	AAT	CGC	675	
Ile	Lys	Asp	Pro	Ile	Tyr	Gln	Lys	Ser	Val	Ser	Phe	Ile	Gly	Asn	Arg		
	205					210					215						
TTA	AGC	ACG	GAT	CAA	AAT	TTC	GCC	ATA	GAA	TGC	CAT	GTC	CTT	GAT	ACC	723	
Leu	Ser	Thr	Asp	Gln	Asn	Phe	Ala	Ile	Glu	Cys	His	Val	Leu	Asp	Thr		
220					225					230					235		
ATC	ATA	GAA	AAC	CCG	CCC	CAA	GAA	ATC	GCT	TTG	CGT	TGG	GTT	CAA	AAA	771	
Ile	Ile	Glu	Asn	Pro	Pro	Gln	Glu	Ile	Ala	Leu	Arg	Trp	Val	Gln	Lys		
				240					245					250			
ATA	CGA	GAC	AAC	ATG	CGT	TTT	TCT	TCT	TTA	AAA	GAG	CTT	AAA	AAT	CAG	819	
Ile	Arg	Asp	Asn	Met	Arg	Phe	Ser	Ser	Leu	Lys	Glu	Leu	Lys	Asn	Gln		
			255					260					265				
ATC	CAA	CAA	GAC	ATC	TTA	AGA	GCC	AAA	GAG	ATT	TTG	AGA	TAATTTGTGT	TA		870	
Ile	Gln	Gln	Asp	Ile	Leu	Arg	Ala	Lys	Glu	Ile	Leu	Arg					
		270					275					280					
AAATGACTCT	CAAAAACCTT	AAAAATGGAA	AAATTT													906	

(2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Met	Leu	Asn	Phe	Leu	Ser	Ile	Ser	Ser	Glu	Pro	Lys	Ile	Lys	Ser	Leu
1				5					10					15	
Ala	Ile	Gly	Lys	Phe	Asp	Gly	Leu	His	Leu	Gly	His	Gln	Ala	Leu	Phe
			20					25					30		
Lys	Glu	Leu	Lys	Asp	Pro	Lys	Ala	Leu	Leu	Ile	Ile	Glu	Lys	Lys	His
			35				40					45			
Tyr	Thr	Lys	Gly	Tyr	Leu	Thr	Pro	Leu	Lys	Tyr	Arg	Ala	Lys	Leu	Val
	50					55					60				
Gly	Met	Pro	Leu	Phe	Phe	Val	Tyr	Leu	Glu	Glu	Ile	Ser	Gln	Leu	Asn
65					70					75				80	
Ala	Leu	Asp	Phe	Leu	Asp	Leu	Leu	Lys	Lys	Lys	Phe	Pro	His	Leu	Glu
			85					90						95	
Arg	Leu	Val	Val	Gly	Tyr	Asp	Phe	Arg	Phe	Gly	His	Glu	Arg	Gln	Asn
			100					105						110	
Asp	Ala	Leu	Phe	Leu	Lys	Glu	Arg	Phe	Glu	Lys	Thr	Ile	Ile	Val	Pro
			115				120							125	
Glu	Val	Lys	Val	Gln	Glu	Ile	Ser	Val	His	Ser	Lys	Met	Ile	Lys	Leu
	130					135						140			
Ala	Leu	Ser	His	Gly	Asp	Leu	Ser	Leu	Ala	Asn	Lys	Leu	Leu	Gly	Arg
145					150					155					160
Pro	Tyr	Glu	Val	Cys	Gly	Glu	Val	Ile	Ser	Asp	Gln	Gly	Leu	Gly	His
				165					170					175	
Lys	Glu	Leu	Ala	Pro	Thr	Leu	Asn	Ile	Lys	Thr	Lys	Asp	Phe	Ile	Leu
			180					185					190		
Pro	Ser	Phe	Gly	Val	Tyr	Ala	Ser	Leu	Val	Lys	Ile	Lys	Asp	Pro	Ile
		195					200						205		
Tyr	Gln	Lys	Ser	Val	Ser	Phe	Ile	Gly	Asn	Arg	Leu	Ser	Thr	Asp	Gln
	210					215					220				
Asn	Phe	Ala	Ile	Glu	Cys	His	Val	Leu	Asp	Thr	Ile	Ile	Glu	Asn	Pro
225					230					235					240
Pro	Gln	Glu	Ile	Ala	Leu	Arg	Trp	Val	Gln	Lys	Ile	Arg	Asp	Asn	Met
				245					250					255	
Arg	Phe	Ser	Ser	Leu	Lys	Glu	Leu	Lys	Asn	Gln	Ile	Gln	Gln	Asp	Ile
			260					265						270	
Leu	Arg	Ala	Lys	Glu	Ile	Leu	Arg								
		275					280								

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 18...2582
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

AAAGACATGT	GCAACCG	ATG	AAA	TCT	AAA	AAA	CTT	TAT	TTG	GCT	TTA	ATC					50
		Met	Lys	Ser	Lys	Lys	Leu	Tyr	Leu	Ala	Leu	Ile					
		1				5					10						
ATA	GGG	GTT	TTA	TTA	GCG	TTT	TTA	ACC	CTA	TCT	TCA	TGG	CTG	GGT	AAT	98	
Ile	Gly	Val	Leu	Leu	Ala	Phe	Leu	Thr	Leu	Ser	Ser	Trp	Leu	Gly	Asn		
			15					20					25				
AGC	GGT	TTA	GTG	GGG	CGT	TTT	GGG	GTG	TGG	TTT	GCC	GCA	CTC	AAT	AAA	146	
Ser	Gly	Leu	Val	Gly	Arg	Phe	Gly	Val	Trp	Phe	Ala	Ala	Leu	Asn	Lys		
		30					35				40						
AAA	TAT	TTT	GGG	CAT	CTT	TCA	TTC	ATT	AAT	TTA	CCC	TAT	TTA	GCA	TGG	194	
Lys	Tyr	Phe	Gly	His	Leu	Ser	Phe	Ile	Asn	Leu	Pro	Tyr	Leu	Ala	Trp		
	45					50					55						
GTT	TTA	TTC	CTT	TTA	TAC	AAG	ACT	AAA	AAC	CCT	TTT	ACA	GAA	ATC	GTT	242	
Val	Leu	Phe	Leu	Leu	Tyr	Lys	Thr	Lys	Asn	Pro	Phe	Thr	Glu	Ile	Val		
60					65					70					75		
TTA	GAA	AAA	ACT	TTA	GGG	CAT	CTA	TTA	GGC	ATT	TTA	TCT	TTG	CTC	TTT	290	
Leu	Glu	Lys	Thr	Leu	Gly	His	Leu	Leu	Gly	Ile	Leu	Ser	Leu	Leu	Phe		
				80					85					90			
TTA	CAA	TCT	AGC	CTA	TTA	AAT	CAA	GGG	GAA	ATC	GGC	AAC	AGC	GCG	CGT	338	
Leu	Gln	Ser	Ser	Leu	Leu	Asn	Gln	Gly	Glu	Ile	Gly	Asn	Ser	Ala	Arg		
			95				100					105					
TTG	TTT	TTA	CGC	CCT	TTT	ATA	GGG	GAT	TTT	GGG	CTT	TAT	GCG	CTG	ATA	386	
Leu	Phe	Leu	Arg	Pro	Phe	Ile	Gly	Asp	Phe	Gly	Leu	Tyr	Ala	Leu	Ile		
		110					115					120					
ACG	CTT	ATG	GTA	GTT	ATT	TCT	TAT	TTG	ATT	CTA	TTC	AAA	CTA	CCC	CCT	434	
Thr	Leu	Met	Val	Val	Ile	Ser	Tyr	Leu	Ile	Leu	Phe	Lys	Leu	Pro	Pro		
		125				130					135						
AAA	AGC	GTT	TTT	TAT	CCT	TAT	ATG	AAC	AAA	ACA	CAA	AAC	CTT	TTA	AAA	482	
Lys	Ser	Val	Phe	Tyr	Pro	Tyr	Met	Asn	Lys	Thr	Gln	Asn	Leu	Leu	Lys		
140					145					150					155		
GAG	ATT	TAC	AAA	CAA	TGC	TTA	CAA	GCC	TTT	AGC	CCT	AAT	TTT	AGC	CCA	530	
Glu	Ile	Tyr	Lys	Gln	Cys	Leu	Gln	Ala	Phe	Ser	Pro	Asn	Phe	Ser	Pro		
				160				165						170			
AAA	AAA	GAG	GGT	TTT	GAA	AAC	ACC	CCA	TCA	GAT	ATT	CAA	AAA	AAA	GAA	578	
Lys	Lys	Glu	Gly	Phe	Glu	Asn	Thr	Pro	Ser	Asp	Ile	Gln	Lys	Lys	Glu		
			175					180					185				
ACC	AAA	AAC	GAC	AAA	GAA	AAA	GAA	AAC	CGC	AAA	GAA	AAC	CCT	ATT	AAT	626	
Thr	Lys	Asn	Asp	Lys	Glu	Lys	Glu	Asn	Arg	Lys	Glu	Asn	Pro	Ile	Asn		
		190					195					200					
GAA	AAC	CAC	AAA	ACC	CCT	AAC	GAA	GAA	CCG	TTT	TTA	GCG	ATC	CCT	ACC	674	
Glu	Asn	His	Lys	Thr	Pro	Asn	Glu	Glu	Pro	Phe	Leu	Ala	Ile	Pro	Thr		
	205					210					215						
CCC	TAT	AAC	ACG	ACT	TTA	AAT	GAT	TCA	GAG	CCG	CAA	GAA	GGC	TTA	GTC	722	
Pro	Tyr	Asn	Thr	Thr	Leu	Asn	Asp	Ser	Glu	Pro	Gln	Glu	Gly	Leu	Val		

220				225				230				235				
CAA Gln	ATT Ile	TCC Ser	TCC Ser	CAC His 240	CCC Pro	CCT Pro	ACC Thr	CAT His	TAC Tyr 245	ACC Thr	ATT Ile	TAC Tyr	CCT Pro	AAA Lys 250	AGA Arg	770
AAC Asn	CGA Arg	TTT Phe	GAT Asp 255	GAT Asp	TTG Leu	ACT Thr	AAC Asn	CCC Pro 260	ACT Thr	AAC Asn	CCC Pro	CCT Pro	TTA Leu 265	AAA Lys	GAA Glu	818
ATT Ile	AAA Lys	CAA Gln 270	GAA Glu	ACT Thr	AAA Lys	GAA Glu	AGA Arg 275	GAA Glu	CCC Pro	ACG Thr	CCT Pro	ACA Thr 280	AAA Lys	GAA Glu	ACT Thr	866
CTT Leu	ACG Thr 285	CCC Pro	ACC Thr	ACG Thr	CCC Pro	AAA Lys 290	CCT Pro	ATC Ile	ATG Met	CCC Pro	ACA Thr 295	CTT Leu	GCA Ala	CCC Pro	ATA Ile	914
ATA Ile 300	GAA Glu	AAT Asn	GAC Asp	AAC Asn	AAA Lys 305	ACA Thr	GAA Glu	AAC Asn	CAA Gln 310	AAA Lys	ACC Thr	CCC Pro	AAC Asn	CAC His	CCT Pro 315	962
AAA Lys	AAA Lys	GAA Glu	GAA Glu	AAC Asn 320	CCA Pro	CAA Gln	GAA Glu	AAC Asn	ACG Thr 325	CAA Gln	GAA Glu	GAA Glu	ATG Met	ATA Ile 330	GAA Glu	1010
GGA Gly	AGG Arg	ATA Ile	GAA Glu 335	GAA Glu	ATG Met	ATA Ile	AAG Lys	GAA Glu 340	AAT Asn	CTA Leu	AAA Lys	AAA Lys	GAA Glu 345	GAA Glu	AAA Lys	1058
GAA Glu	GTG Val 350	CAA Gln	AAC Asn	GCT Ala	CCA Pro	AAC Asn	TTT Phe 355	AGC Ser	CCA Pro	GTA Val	ACC Thr	CCC Pro 360	ACA Thr	AGC Ser	GCT Ala	1106
AAA Lys	AAA Lys 365	CCC Pro	GTT Val	ATG Met	GTT Val	AAA Lys 370	GAA Glu	TTG Leu	AGC Ser	GAA Glu	AAT Asn 375	AAA Lys	GAG Glu	ATA Ile	TTA Leu	1154
GAC Asp 380	GGA Gly	TTG Leu	GAT Asp	TAT Tyr 385	GGC Gly	GAA Glu	GTG Val	CAA Gln	AAA Lys	CCC Pro 390	AAA Lys	GAT Asp	TAT Tyr	GAG Glu	CTT Leu 395	1202
CCC Pro	ACC Thr	ACG Thr	CAA Gln	TTA Leu 400	TTG Leu	AAT Asn	GCG Ala	GTT Val	TGT Cys 405	TTG Leu	AAA Lys	GAC Asp	ACT Thr	TCT Ser 410	TTA Leu	1250
GAC Asp	GAA Glu	AAC Asn	GAG Glu 415	ATT Ile	GAC Asp	CAA Gln	AAA Lys	ATC Ile 420	CAG Gln	GAT Asp	CTA Leu	TTG Leu	AGC Ser 425	AAA Lys	CTG Leu	1298
CGC Arg	ACC Thr	TTT Phe 430	AAA Lys	ATT Ile	GAT Asp	GGC Gly	GAT Asp 435	ATT Ile	ATC Ile	CGC Arg	ACT Thr 440	TAT Tyr	TCA Ser	GGC Gly	CCT Pro	1346
ATT Ile	GTA Val 445	ACC Thr	ACT Thr	TTT Phe	GAA Glu	TTC Phe 450	CGC Arg	CCA Pro	GCC Ala	CCT Pro	AAC Asn 455	GTT Val	AAG Lys	GTG Val	AGT Ser	1394

CGT Arg 460	ATT Ile	TTA Leu	GGC Gly	TTG Leu 480	AGC Ser 465	GAT Asp	GAT Asp	TTA Leu	GCG Ala 485	ATG Met 470	ACT Thr	TTA Leu	TGC Cys	GCT Ala 475	GAA Glu	1442
TCC Ser	ATC Ile	CGC Arg	ATT Ile	CAA Gln 480	GCC Ala	CCT Pro	ATT Ile	AAG Lys	GGT Gly 485	AAA Lys	GAT Asp	GTC Val	GTT Val	GGC Gly 490	ATT Ile	1490
GAA Glu	ATC Ile	CCT Pro	AAC Asn 495	AGC Ser	CAA Gln	AGC Ser	CAA Gln 500	ATT Ile	ATT Ile	TAT Tyr	TTA Leu	AGA Arg	GAA Glu 505	ATT Ile	CTA Leu	1538
GAG Glu	AGC Ser	GAA Glu 510	TTG Leu	TTT Phe	CAA Gln	AAA Lys 515	TCC Ser 515	AGC Ser	TCG Ser	CCC Pro	TTA Leu 520	ACT Thr	CTA Leu	GCT Ala	TTA Leu	1586
GGC Gly 525	AAA Lys	GAC Asp	ATT Ile	GTG Val	GGT Gly 530	AAC Asn 530	CCT Pro	TTC Phe	ATC Ile	ACG Thr 535	GAT Asp 535	TTA Leu	AAA Lys	AAG Lys	CTC Leu	1634
CCC Pro 540	CAT His	TTG Leu	CTC Leu	ATC Ile 545	GCT Ala 545	GGC Gly	ACG Thr	ACA Thr	GGA Gly 550	AGC Ser 550	GGT Gly	AAG Lys	AGC Ser	GTG Val	GGC Gly 555	1682
GTG Val	AAT Asn	GCG Ala	ATG Met 560	ATT Ile 560	TTA Leu	TCC Ser	TTA Leu	CTT Leu	TAT Tyr 565	AAA Lys	AAC Asn	CCT Pro	CCC Pro	GAT Asp 570	CAA Gln	1730
CTC Leu	AAA Lys	TTA Leu	GTG Val 575	ATG Met	ATC Ile	GAT Asp	CCC Pro	AAA Lys 580	ATG Met	GTA Val	GAA Glu	TTT Phe	AGT Ser 585	ATT Ile	TAT Tyr	1778
GCG Ala	GAT Asp 590	ATC Ile	CCT Pro	CAT His	TTG Leu	CTC Leu	ACG Thr 595	CCC Pro	ATT Ile	ATC Ile	ACC Thr 600	GAC Asp	CCT Pro	AAA Lys	AAA Lys	1826
GCT Ala 605	ATT Ile	GGG Gly	GCT Ala	TTG Leu	CAA Gln 610	AGC Ser 610	GTG Val	GCT Ala	AAA Lys	GAA Glu 615	ATG Met 615	GAA Glu	CGC Arg	CGG Arg	TAT Tyr	1874
TCT Ser 620	TTA Leu	ATG Met	AGC Ser	GAA Glu 625	TAC Tyr 625	AAG Lys	GTT Val	AAA Lys	ACC Thr 630	ATT Ile 630	GAT Asp	TCT Ser	TAT Tyr	AAT Asn	GAA Glu 635	1922
CAA Gln 640	GCC Ala	CCA Pro	AGT Ser	AAC Asn 640	GGC Gly	GTT Val	GAA Glu	GCG Ala 645	TTC Phe 645	CCC Pro	TAT Tyr	TTG Leu	ATT Ile	GTG Val 650	GTG Val	1970
ATT Ile	GAT Asp	GAA Glu 655	TTA Leu	GCG Ala	GAT Asp	TTA Leu	ATG Met 660	ATG Met	ACA Thr	GGG Gly	GGC Gly	AAA Lys	GAA Glu 665	GCG Ala	GAG Glu	2018
TTT Phe	CCT Pro	ATC Ile 670	GCT Ala	AGA Arg	ATC Ile	GCT Ala	CAA Gln 675	ATG Met	GGG Gly	CGC Arg	GCG Ala 680	AGC Ser	GGC Gly	TTA Leu	CAC His	2066
CTC Leu	ATT Ile	GTA Val	GCG Ala	ACC Thr	CAA Gln	CGC Arg	CCA Pro	AGC Ser	GTG Val	GAT Asp	GTC Val	GTA Val	ACC Thr	GGC Gly	TTG Leu	2114

685	690	695	
ATT AAA ACC AAC TTG CCT TCA AGG GTG AGT TTT AGG GTA GGC ACT AAG Ile Lys Thr Asn Leu Pro Ser Arg Val Ser Phe Arg Val Gly Thr Lys 700 705 710 715			2162
ATT GAT TCT AAA GTG ATT TTA GAC ACT GAT GGG GCG CAA AGC TTG TTA Ile Asp Ser Lys Val Ile Leu Asp Thr Asp Gly Ala Gln Ser Leu Leu 720 725 730			2210
GGA AGA GGC GAT ATG CTC TTT ACC CCC CCA GGA GCG AAC GGG TTA GTG Gly Arg Gly Asp Met Leu Phe Thr Pro Pro Gly Ala Asn Gly Leu Val 735 740 745			2258
CGC TTG CAT GCC CCC TTT GCC ACT GAA GAT GAA ATC AAA AAA ATC GTG Arg Leu His Ala Pro Phe Ala Thr Glu Asp Glu Ile Lys Lys Ile Val 750 755 760			2306
GAT TTT ATT AAA GCC CAA AAA GAA GTA CAA TAC GAT AAA GAT TTC TTG Asp Phe Ile Lys Ala Gln Lys Glu Val Gln Tyr Asp Lys Asp Phe Leu 765 770 775			2354
CTA GAA GAA TCA CGC ATG CCT TTA GAC ACC CCT AAT TAT CAA GGC GAT Leu Glu Glu Ser Arg Met Pro Leu Asp Thr Pro Asn Tyr Gln Gly Asp 780 785 790 795			2402
GAC ATT TTA GAA AGG GCT AAA GCG GTG ATT TTA GAA AAA AAG ATC ACT Asp Ile Leu Glu Arg Ala Lys Ala Val Ile Leu Glu Lys Lys Ile Thr 800 805 810			2450
TCT ACG AGT TTT TTA CAA CGC CAA TTA AAA ATC GGC TAC AAC CAA GCC Ser Thr Ser Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala 815 820 825			2498
GCT ACC ATT ACT GAC GAA TTA GAA GCT CAA GGC TTT TTA TCC CCA AGA Ala Thr Ile Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg 830 835 840			2546
AAC GCT AAA GGC AAC AGA GAG ATT TTG CAA AAC TTT TAGGCTTTGT TTTCAT Asn Ala Lys Gly Asn Arg Glu Ile Leu Gln Asn Phe 845 850 855			2598
TGGATATTGG CAAACATTAT TTTTGATT			2627

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Met	Lys	Ser	Lys	Lys	Leu	Tyr	Leu	Ala	Leu	Ile	Ile	Gly	Val	Leu	Leu
1				5				10					15		

Ala	Phe	Leu	Thr	Leu	Ser	Ser	Trp	Leu	Gly	Asn	Ser	Gly	Leu	Val	Gly
			20					25					30		
Arg	Phe	Gly	Val	Trp	Phe	Ala	Ala	Leu	Asn	Lys	Lys	Tyr	Phe	Gly	His
		35					40					45			
Leu	Ser	Phe	Ile	Asn	Leu	Pro	Tyr	Leu	Ala	Trp	Val	Leu	Phe	Leu	Leu
	50					55					60				
Tyr	Lys	Thr	Lys	Asn	Pro	Phe	Thr	Glu	Ile	Val	Leu	Glu	Lys	Thr	Leu
65				70						75				80	
Gly	His	Leu	Leu	Gly	Ile	Leu	Ser	Leu	Leu	Phe	Leu	Gln	Ser	Ser	Leu
				85					90					95	
Leu	Asn	Gln	Gly	Glu	Ile	Gly	Asn	Ser	Ala	Arg	Leu	Phe	Leu	Arg	Pro
			100					105					110		
Phe	Ile	Gly	Asp	Phe	Gly	Leu	Tyr	Ala	Leu	Ile	Thr	Leu	Met	Val	Val
		115					120					125			
Ile	Ser	Tyr	Leu	Ile	Leu	Phe	Lys	Leu	Pro	Pro	Lys	Ser	Val	Phe	Tyr
	130					135					140				
Pro	Tyr	Met	Asn	Lys	Thr	Gln	Asn	Leu	Leu	Lys	Glu	Ile	Tyr	Lys	Gln
145				150						155				160	
Cys	Leu	Gln	Ala	Phe	Ser	Pro	Asn	Phe	Ser	Pro	Lys	Lys	Glu	Gly	Phe
				165					170					175	
Glu	Asn	Thr	Pro	Ser	Asp	Ile	Gln	Lys	Lys	Glu	Thr	Lys	Asn	Asp	Lys
			180					185					190		
Glu	Lys	Glu	Asn	Arg	Lys	Glu	Asn	Pro	Ile	Asn	Glu	Asn	His	Lys	Thr
		195					200					205			
Pro	Asn	Glu	Glu	Pro	Phe	Leu	Ala	Ile	Pro	Thr	Pro	Tyr	Asn	Thr	Thr
	210					215					220				
Leu	Asn	Asp	Ser	Glu	Pro	Gln	Glu	Gly	Leu	Val	Gln	Ile	Ser	Ser	His
225				230						235				240	
Pro	Pro	Thr	His	Tyr	Thr	Ile	Tyr	Pro	Lys	Arg	Asn	Arg	Phe	Asp	Asp
				245					250					255	
Leu	Thr	Asn	Pro	Thr	Asn	Pro	Pro	Leu	Lys	Glu	Ile	Lys	Gln	Glu	Thr
			260					265					270		
Lys	Glu	Arg	Glu	Pro	Thr	Pro	Thr	Lys	Glu	Thr	Leu	Thr	Pro	Thr	Thr
	275						280					285			
Pro	Lys	Pro	Ile	Met	Pro	Thr	Leu	Ala	Pro	Ile	Ile	Glu	Asn	Asp	Asn
	290					295					300				
Lys	Thr	Glu	Asn	Gln	Lys	Thr	Pro	Asn	His	Pro	Lys	Lys	Glu	Glu	Asn
305				310						315				320	
Pro	Gln	Glu	Asn	Thr	Gln	Glu	Glu	Met	Ile	Glu	Gly	Arg	Ile	Glu	Glu
				325					330					335	
Met	Ile	Lys	Glu	Asn	Leu	Lys	Lys	Glu	Glu	Lys	Glu	Val	Gln	Asn	Ala
			340					345					350		
Pro	Asn	Phe	Ser	Pro	Val	Thr	Pro	Thr	Ser	Ala	Lys	Lys	Pro	Val	Met
	355						360					365			
Val	Lys	Glu	Leu	Ser	Glu	Asn									

Ala	Pro	Ile	Lys	Gly	Lys	Asp	Val	Val	Gly	Ile	Glu	Ile	Pro	Asn	Ser	485	490	495
Gln	Ser	Gln	Ile	Ile	Tyr	Leu	Arg	Glu	Ile	Leu	Glu	Ser	Glu	Leu	Phe	500	505	510
Gln	Lys	Ser	Ser	Ser	Pro	Leu	Thr	Leu	Ala	Leu	Gly	Lys	Asp	Ile	Val	515	520	525
Gly	Asn	Pro	Phe	Ile	Thr	Asp	Leu	Lys	Lys	Leu	Pro	His	Leu	Leu	Ile	530	535	540
Ala	Gly	Thr	Thr	Gly	Ser	Gly	Lys	Ser	Val	Gly	Val	Asn	Ala	Met	Ile	545	550	555
Leu	Ser	Leu	Leu	Tyr	Lys	Asn	Pro	Pro	Asp	Gln	Leu	Lys	Leu	Val	Met	565	570	575
Ile	Asp	Pro	Lys	Met	Val	Glu	Phe	Ser	Ile	Tyr	Ala	Asp	Ile	Pro	His	580	585	590
Leu	Leu	Thr	Pro	Ile	Ile	Thr	Asp	Pro	Lys	Lys	Ala	Ile	Gly	Ala	Leu	595	600	605
Gln	Ser	Val	Ala	Lys	Glu	Met	Glu	Arg	Arg	Tyr	Ser	Leu	Met	Ser	Glu	610	615	620
Tyr	Lys	Val	Lys	Thr	Ile	Asp	Ser	Tyr	Asn	Glu	Gln	Ala	Pro	Ser	Asn	625	630	635
Gly	Val	Glu	Ala	Phe	Pro	Tyr	Leu	Ile	Val	Val	Ile	Asp	Glu	Leu	Ala	645	650	655
Asp	Leu	Met	Met	Thr	Gly	Gly	Lys	Glu	Ala	Glu	Phe	Pro	Ile	Ala	Arg	660	665	670
Ile	Ala	Gln	Met	Gly	Arg	Ala	Ser	Gly	Leu	His	Leu	Ile	Val	Ala	Thr	675	680	685
Gln	Arg	Pro	Ser	Val	Asp	Val	Val	Thr	Gly	Leu	Ile	Lys	Thr	Asn	Leu	690	695	700
Pro	Ser	Arg	Val	Ser	Phe	Arg	Val	Gly	Thr	Lys	Ile	Asp	Ser	Lys	Val	705	710	715
Ile	Leu	Asp	Thr	Asp	Gly	Ala	Gln	Ser	Leu	Leu	Gly	Arg	Gly	Asp	Met	725	730	735
Leu	Phe	Thr	Pro	Gly	Ala	Asn	Gly	Leu	Val	Arg	Leu	His	Ala	Pro		740	745	750
Phe	Ala	Thr	Glu	Asp	Glu	Ile	Lys	Lys	Ile	Val	Asp	Phe	Ile	Lys	Ala	755	760	765
Gln	Lys	Glu	Val	Gln	Tyr	Asp	Lys	Asp	Phe	Leu	Leu	Glu	Glu	Ser	Arg	770	775	780
Met	Pro	Leu	Asp	Thr	Pro	Asn	Tyr	Gln	Gly	Asp	Asp	Ile	Leu	Glu	Arg	785	790	795
Ala	Lys	Ala	Val	Ile	Leu	Glu	Lys	Lys	Ile	Thr	Ser	Thr	Ser	Phe	Leu	805	810	815
Gln	Arg	Gln	Leu	Lys	Ile	Gly	Tyr	Asn	Gln	Ala	Ala	Thr	Ile	Thr	Asp	820	825	830
Glu	Leu	Glu	Ala	Gln	Gly	Phe	Leu	Ser	Pro	Arg	Asn	Ala	Lys	Gly	Asn	835	840	845
Arg	Glu	Ile	Leu	Gln	Asn	Phe										850	855	

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1094
- (D) OTHER INFORMATION:

1094...51

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

AACCATAAAA	ACGATACAAT	AGCGGTATTT	TAATAAAACA	AGGAGTTTTA	ATG	AGA	56
					Met	Arg	
					1		
GTT CAA TCT AAA GGT TTT GCT ATT TTT TCT AAA GAC GGG CAT TTC AAA	104						
Val Gln Ser Lys Gly Phe Ala Ile Phe Ser Lys Asp Gly His Phe Lys							
5 10 15							
CCC CAT GAT TTT AGC CGC CAT GCT GTA GGC CCT AAA GAT GTG TTG ATT	152						
Pro His Asp Phe Ser Arg His Ala Val Gly Pro Lys Asp Val Leu Ile							
20 25 30							
GAC ATT CTT TAT GCA GGG ATT TGT CAT AGC GAT ATT CAT AGC GCT TAT	200						
Asp Ile Leu Tyr Ala Gly Ile Cys His Ser Asp Ile His Ser Ala Tyr							
35 40 45 50							
AGC GAA TGG AAA GAA GGC ATT TAC CCT ATG GTT CCT GGG CAT GAA ATT	248						
Ser Glu Trp Lys Glu Gly Ile Tyr Pro Met Val Pro Gly His Glu Ile							
55 60 65							
GCT GGG GCC ATC AAA GAA GTG GGT AAG GAA GTT AAG AAA TTT AAG GTT	296						
Ala Gly Ala Ile Lys Glu Val Gly Lys Glu Val Lys Lys Phe Lys Val							
70 75 80							
GGC GAT GTG GTG GGC GTG GGC TGT TTT GTC AAT TCA TGC AAA GCG TGT	344						
Gly Asp Val Val Gly Val Gly Cys Phe Val Asn Ser Cys Lys Ala Cys							
85 90 95							
AAG CCC TGT AAA GAA CAC CAA GAG CAA TTT TGC GCC AAA GTG GTA TTC	392						
Lys Pro Cys Lys Glu His Gln Glu Gln Phe Cys Ala Lys Val Val Phe							
100 105 110							
ACT TAC GAT TGT TTG GAT TAT TTC CAT GAC AAC GAA CCC CAC ATG GGC	440						
Thr Tyr Asp Cys Leu Asp Tyr Phe His Asp Asn Glu Pro His Met Gly							
115 120 125 130							
GGA TAC TCT AAT AAT ATT GTA GTG GAT GAA AAC TAT GTG ATT AGC GTG	488						
Gly Tyr Ser Asn Asn Ile Val Val Asp Glu Asn Tyr Val Ile Ser Val							
135 140 145							
GAT AAA AAC GCT CCT TTA GAA AAA GTA GCC CCC TTG CTT TGT GCG GGC	536						
Asp Lys Asn Ala Pro Leu Glu Lys Val Ala Pro Leu Leu Cys Ala Gly							
150 155 160							
ATC ACC ACT TAT TCG CCC TTA AAA TTT TCT AAG GTT ACT AAA GGC ACA	584						
Ile Thr Thr Tyr Ser Pro Leu Lys Phe Ser Lys Val Thr Lys Gly Thr							
165 170 175							
AAA GTT GGC GTC GCT GGG TTT GGC GGG CTA GGA AGC ATG GCG GTT AAA	632						
Lys Val Gly Val Ala Gly Phe Gly Gly Leu Gly Ser Met Ala Val Lys							
180 185 190							
TAC GCT GTG GCT ATG GGG GCT GAA GTG AGC GTT TTT GCA AGA AAC GAA	680						
Tyr Ala Val Ala Met Gly Ala Glu Val Ser Val Phe Ala Arg Asn Glu							
195 200 205 210							

CAC AAA AAG CAA GAC GCT TTG AGC ATG GGG GTT AAA CAT TTC TAC ACT	728
His Lys Lys Gln Asp Ala Leu Ser Met Gly Val Lys His Phe Tyr Thr	
215 220 225	
GAC CCC AAA CAA TGC AAA GAG GAA TTG GAC TTT ATC ATT TCA ACC ATT	776
Asp Pro Lys Gln Cys Lys Glu Glu Leu Asp Phe Ile Ile Ser Thr Ile	
230 235 240	
CCT ACC CAT TAT GAT TTA AAA GAC TAC CTC AAG CTC TTA ACT TAT AAT	824
Pro Thr His Tyr Asp Leu Lys Asp Tyr Leu Lys Leu Leu Thr Tyr Asn	
245 250 255	
GGC GAT CTA GCC CTT GTG GGA CTC CCC CCT GTA GAA ATC GCT CCA GCG	872
Gly Asp Leu Ala Leu Val Gly Leu Pro Pro Val Glu Ile Ala Pro Ala	
260 265 270	
CTT AGC GTT TTT GAT TTT ATC CAT TTA GGC AAT CGC AAG GTT TAT GGC	920
Leu Ser Val Phe Asp Phe Ile His Leu Gly Asn Arg Lys Val Tyr Gly	
275 280 285 290	
TCA TTG ATT GGG GGC ATT AAA GAA ACC CAA GAA ATG ATG GAT TTT TCT	968
Ser Leu Ile Gly Gly Ile Lys Glu Thr Gln Glu Met Met Asp Phe Ser	
295 300 305	
ATC AAA CAC AAT ATT TAC CCT GAA ATA GAT TTG ATC TTA GGC AAG GAT	1016
Ile Lys His Asn Ile Tyr Pro Glu Ile Asp Leu Ile Leu Gly Lys Asp	
310 315 320	
ATT GAC ACC GCT TAT CAT AAT CTA ACC CAT GGG AAA GCG AAA TTC CGC	1064
Ile Asp Thr Ala Tyr His Asn Leu Thr His Gly Lys Ala Lys Phe Arg	
325 330 335	
TAT GTG ATT GAT ATG AAA AAA TCG TTT GAT TAAAAGTTTT GGCTCTAGCT CTT	1117
Tyr Val Ile Asp Met Lys Lys Ser Phe Asp	
340 345	
TTTTAAGAGC TTGAGTTGG	1136

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Met Arg Val Gln Ser Lys Gly Phe Ala Ile Phe Ser Lys Asp Gly His	
1 5 10 15	
Phe Lys Pro His Asp Phe Ser Arg His Ala Val Gly Pro Lys Asp Val	
20 25 30	
Leu Ile Asp Ile Leu Tyr Ala Gly Ile Cys His Ser Asp Ile His Ser	
35 40 45	
Ala Tyr Ser Glu Trp Lys Glu Gly Ile Tyr Pro Met Val Pro Gly His	
50 55 60	

AAA Lys 10	GAA Glu	CAA Gln	GAT Asp	TTT Phe 30	CAT His 15	ATT Ile	CCT Pro	ATC Ile	GCT Ala	TTT Phe 20	GCT Ala	TTT Phe	GAT Asp	AAG Lys	AAT Asn 25	99
TAC Tyr	CTC Leu	ATT Ile	CCT Pro	GCG Ala 30	GGC Gly	GCG Ala	TGT Cys	CTT Leu	TAT Tyr 35	TCC Ser	TTG Leu	CTA Leu	GAA Glu 40	AGC Ser	ATC Ile	147
GCT Ala	AAA Lys	GCC Ala	AAT Asn 45	AAA Lys	AAA Lys	ATC Ile	CGT Arg	TAC Tyr 50	ACC Thr	CTA Leu	CAC His	GCT Ala	TTA Leu 55	GTG Val	GTA Val	195
GGC Gly	TTG Leu	AAT Asn 60	GAA Glu	GAA Glu	GAT Asp	AAA Lys	GCA Ala 65	AAG Lys	CTT Leu	AAT Asn	CAA Gln	ATC Ile 70	ACA Thr	GAG Glu	CCT Pro	243
TTT Phe 75	AAA Lys	GAA Glu	TTT Phe	GCC Ala	GCT Ala	TTG Leu 80	GAA Glu	GTG Val	AGA Arg	GAT Asp 85	ATT Ile	GAG Glu	TCT Ser	TTT Phe	TTA Leu	291
GAC Asp 90	ACT Thr	ATC Ile	CCT Pro	AAC Asn	CCT Pro 95	TTT Phe	GAT Asp	GAG Glu	GAT Asp 100	TTC Phe	ACT Thr	AAG Lys	CGT Arg	TTT Phe 105	TCT Ser	339
AAA Lys	ATG Met	GTG Val	TTA Leu	GTG Val 110	AAG Lys	TAT Tyr	TTT Phe	TTG Leu	GCG Ala 115	GAT Asp	TTG Leu	TTC Phe	CCC Pro 120	AAA Lys	TAT Tyr	387
TCC Ser	AAA Lys	ATG Met	GTG Val 125	TGG Trp	AGC Ser	GAT Asp	GTG Val	GAT Asp 130	GTC Val	ATC Ile	TTT Phe	TGC Cys	AAT Asn 135	GAA Glu	TTT Phe	435
AGC Ser	GCT Ala	GAT Asp 140	TTC Phe	TTA Leu	AAC Asn	CTT Leu	GAA Glu 145	GAA Glu	AAT Asn	GAT Asp	GAG Glu	AAT Asn 150	TAT Tyr	TTT Phe	TAT Tyr	483
GGA Gly	GTT Val 155	TTA Leu	GAA Glu	GTT Val	GAA Glu 160	AAG Lys	CAC His	CAC His	ATG Met	ATG Met	GAA Glu 165	GGG Gly	TTT Phe	TTG Leu	TTT Phe	531
TGC Cys 170	AAT Asn	TTA Leu	GAT Asp	TAC Tyr	CAG Gln 175	CGC Arg	AAG Lys	AAA Lys	AAT Asn	TTC Phe 180	ACC Thr	TTA Leu	AGA Arg	ATG Met	CAT His 185	579
GAG Glu	CTT Leu	TTA Leu	AGG Arg	GGG Gly 190	AAT Asn	GAG Glu	GCT Ala	AAA Lys	GGG Gly 195	GAG Glu	TTG Leu	GAT Asp	TTC Phe	ACG Thr 200	AAA Lys	627
TGG Trp	TGT Cys	TGG Trp	CCT Pro 205	AAC Asn	ATG Met	AAA Lys	GCT Ala	TTA Leu 210	GGG Gly	ATT Ile	GAA Glu	TAT Tyr	TGC Cys 215	GTT Val	TTC Phe	675
CCT Pro	TAT Tyr	TAT Tyr 220	TAC Tyr	ACC Thr	ATT Ile	AAA Lys	GAT Asp 225	TTT Phe	TCT Ser	AAC Asn	GCG Ala	TAT Tyr 230	TTA Leu	AAC Asn	GAG Glu	723
AAT Asn	TAC Tyr	AAG Lys	AAA Lys	ACC Thr	ATT Ile	TTA Leu	GAG Glu	GCA Ala	CGA Arg	GAA Glu	AAC Asn	CCT Pro	ACC Thr	ATT Ile	ATC Ile	771

235	240	245	
CAC TAT GAC GCT TGG TGG GGA GCG GTG AAG CCT TGG GAC TAT CCT TTT			819
His Tyr Asp Ala Trp Trp Gly Ala Val Lys Pro Trp Asp Tyr Pro Phe			
250	255	260	265
GGT TTA AAA GCG GAT TTA TGG CTG AAC GCT TTG GCT AAA ACC CCT TTT			867
Gly Leu Lys Ala Asp Leu Trp Leu Asn Ala Leu Ala Lys Thr Pro Phe			
	270	275	280
ATG AGC GAT TGG ATT GAT TCG ATC GCT AGG GTG GAA ATA GGC AGC GAA			915
Met Ser Asp Trp Ile Asp Ser Ile Ala Arg Val Glu Ile Gly Ser Glu			
	285	290	295
AAA TGG CAT CGT TAC CAC AGC ATC GTT GCC TAT CAC TAC TAC TTT CCC			963
Lys Trp His Arg Tyr His Ser Ile Val Ala Tyr His Tyr Tyr Phe Pro			
	300	305	310
CTA TGG AAG ACT GAA GAG CAG ATC GCC CAT GAC GCA CTC AAG ACC TTT			1011
Leu Trp Lys Thr Glu Glu Gln Ile Ala His Asp Ala Leu Lys Thr Phe			
	315	320	325
TTA GAC CAT TAT TTT TCG TGC ATC CAT GCC GCA ATC AAG CAA GAA AAT			1059
Leu Asp His Tyr Phe Ser Cys Ile His Ala Ala Ile Lys Gln Glu Asn			
	330	335	340
CTC GGA ATG TTC TTG AAC CAC TAC TTC TCG CAT GCC CAT GCA GAG ATC			1107
Leu Gly Met Phe Leu Asn His Tyr Phe Ser His Ala His Ala Glu Ile			
	350	355	360
AAA GAA AAC TCC CTT GAA ATG TTC TTG AAC CAC TAC TTC TCG CAT GTT			1155
Lys Glu Asn Ser Leu Glu Met Phe Leu Asn His Tyr Phe Ser His Val			
	365	370	375
TAT AGG CTC CCT AAA AAA GCA CGG AAG AGA CTC TTT AGG GTG TTT GTC			1203
Tyr Arg Leu Pro Lys Lys Ala Arg Lys Arg Leu Phe Arg Val Phe Val			
	380	385	390
AAA CAC TGC ATC CTC ATA CCA CTC AAG AGC CTT GTG GGT AAG ACT CTA			1251
Lys His Cys Ile Leu Ile Pro Leu Lys Ser Leu Val Gly Lys Thr Leu			
	395	400	405
CGA CTC TTA AAA CTC CAT GCG CTA GCT AAA AAA ATC CTA ATC CAA CTC			1299
Arg Leu Leu Lys Leu His Ala Leu Ala Lys Lys Ile Leu Ile Gln Leu			
	410	415	420
AAG CTC TTA AAA AAG AGC TAGAGCCAAA ACTTTTAATC AAACGATTTT TTCATATC			1355
Lys Leu Leu Lys Lys Ser			
	430		
AATCACATAG CGGAATTTTCG CTT			1378

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Met	Thr	Ser	Ala	Ser	Ser	His	Ser	Phe	Lys	Glu	Gln	Asp	Phe	His	Ile	
1				5					10					15		
Pro	Ile	Ala	Phe	Ala	Phe	Asp	Lys	Asn	Tyr	Leu	Ile	Pro	Ala	Gly	Ala	
			20					25					30			
Cys	Leu	Tyr	Ser	Leu	Leu	Glu	Ser	Ile	Ala	Lys	Ala	Asn	Lys	Lys	Ile	
		35					40					45				
Arg	Tyr	Thr	Leu	His	Ala	Leu	Val	Val	Gly	Leu	Asn	Glu	Glu	Asp	Lys	
	50					55					60					
Ala	Lys	Leu	Asn	Gln	Ile	Thr	Glu	Pro	Phe	Lys	Glu	Phe	Ala	Ala	Leu	
65					70					75					80	
Glu	Val	Arg	Asp	Ile	Glu	Ser	Phe	Leu	Asp	Thr	Ile	Pro	Asn	Pro	Phe	
			85						90					95		
Asp	Glu	Asp	Phe	Thr	Lys	Arg	Phe	Ser	Lys	Met	Val	Leu	Val	Lys	Tyr	
			100					105					110			
Phe	Leu	Ala	Asp	Leu	Phe	Pro	Lys	Tyr	Ser	Lys	Met	Val	Trp	Ser	Asp	
		115					120					125				
Val	Asp	Val	Ile	Phe	Cys	Asn	Glu	Phe	Ser	Ala	Asp	Phe	Leu	Asn	Leu	
	130					135					140					
Glu	Glu	Asn	Asp	Glu	Asn	Tyr	Phe	Tyr	Gly	Val	Leu	Glu	Val	Glu	Lys	
145					150					155					160	
His	His	Met	Met	Glu	Gly	Phe	Leu	Phe	Cys	Asn	Leu	Asp	Tyr	Gln	Arg	
			165						170					175		
Lys	Lys	Asn	Phe	Thr	Leu	Arg	Met	His	Glu	Leu	Leu	Arg	Gly	Asn	Glu	
			180					185					190			
Ala	Lys	Gly	Glu	Leu	Asp	Phe	Thr	Lys	Trp	Cys	Trp	Pro	Asn	Met	Lys	
		195					200					205				
Ala	Leu	Gly	Ile	Glu	Tyr	Cys	Val	Phe	Pro	Tyr	Tyr	Tyr	Thr	Ile	Lys	
	210					215					220					
Asp	Phe	Ser	Asn	Ala	Tyr	Leu	Asn	Glu	Asn	Tyr	Lys	Lys	Thr	Ile	Leu	
225					230					235					240	
Glu	Ala	Arg	Glu	Asn	Pro	Thr	Ile	Ile	His	Tyr	Asp	Ala	Trp	Trp	Gly	
			245						250					255		
Ala	Val	Lys	Pro	Trp	Asp	Tyr	Pro	Phe	Gly	Leu	Lys	Ala	Asp	Leu	Trp	
		260						265					270			
Leu	Asn	Ala	Leu	Ala	Lys	Thr	Pro	Phe	Met	Ser	Asp	Trp	Ile	Asp	Ser	
	275						280					285				
Ile	Ala	Arg	Val	Glu	Ile	Gly	Ser	Glu	Lys	Trp	His	Arg	Tyr	His	Ser	
	290					295					300					
Ile	Val	Ala	Tyr	His	Tyr	Tyr	Phe	Pro	Leu	Trp	Lys	Thr	Glu	Glu	Gln	
305					310					315					320	
Ile	Ala	His	Asp	Ala	Leu	Lys	Thr	Phe	Leu	Asp	His	Tyr	Phe	Ser	Cys	
			325						330					335		
Ile	His	Ala	Ala	Ile	Lys	Gln	Glu	Asn	Leu	Gly	Met	Phe	Leu	Asn	His	
		340						345					350			
Tyr	Phe	Ser	His	Ala	His	Ala	Glu	Ile	Lys	Glu	Asn	Ser	Leu	Glu	Met	
		355					360					365				
Phe	Leu	Asn	His	Tyr	Phe	Ser	His	Val	Tyr	Arg	Leu	Pro	Lys	Lys	Ala	
	370					375					380					
Arg	Lys	Arg	Leu	Phe	Arg	Val	Phe	Val	Lys	His	Cys	Ile	Leu	Ile	Pro	
385					390					395					400	
Leu	Lys	Ser	Leu	Val	Gly	Lys	Thr	Leu	Arg	Leu	Leu	Lys	Leu	His	Ala	
			405						410					415		

Leu Ala Lys Lys Ile Leu Ile Gln Leu Lys Leu Leu Lys Lys Ser
420 425 430

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...603
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GCTGAATTCA ATTTATTTTA TACGATATTA AGGAGACATA TTACC ATG TTT CAA ATT	57
Met Phe Gln Ile	
1	
AGA TGG CAT GCA CGA GCG GGT CAA GGT GCA ATC ACT GGC GCT AAA GGG	105
Arg Trp His Ala Arg Ala Gly Gln Gly Ala Ile Thr Gly Ala Lys Gly	
5 10 15 20	
TTG GCT GAT GTG ATT TCA AAA ACA GGC AAA GAA GTG CAA GCG TTC GCT	153
Leu Ala Asp Val Ile Ser Lys Thr Gly Lys Glu Val Gln Ala Phe Ala	
25 30 35	
TCT TAT GGT TCA GCT AAA AGG GGG GCT GCT ATG ATG GCT TAT AAC CGC	201
Ser Tyr Gly Ser Ala Lys Arg Gly Ala Ala Met Met Ala Tyr Asn Arg	
40 45 50	
GTT GAT GAT GAA CCT ATC TTA AAC CAT GAA CGC TTC ATG CAG CCT GAT	249
Val Asp Asp Glu Pro Ile Leu Asn His Glu Arg Phe Met Gln Pro Asp	
55 60 65	
TAT GTG CTG GTG ATT GAC CCT GGT TTG GTT TTC ATT GAA AAC ATC TTC	297
Tyr Val Leu Val Ile Asp Pro Gly Leu Val Phe Ile Glu Asn Ile Phe	
70 75 80	
GCC AAT GAA AAA GAA GAC ACG ACT TAT ATT ATC ACT AGC TAC CTT AAC	345
Ala Asn Glu Lys Glu Asp Thr Thr Tyr Ile Ile Thr Ser Tyr Leu Asn	
85 90 95 100	
AAA GAA GAA TTG TTT GAA AAA AAA CCT GAA TTA AAA ACC CGT AAG GTG	393
Lys Glu Glu Leu Phe Glu Lys Lys Pro Glu Leu Lys Thr Arg Lys Val	
105 110 115	
TTT TTA GTG GAT TGT TTA AAA ATC TCT ATG GAA ACC TTA AAA CGC CCC	441
Phe Leu Val Asp Cys Leu Lys Ile Ser Met Glu Thr Leu Lys Arg Pro	
120 125 130	
ATC CCT AAC ACG CCC ATG TTA GGG GCG TTA ATG AAA GTG TCT GGC ATG	489

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 19...954
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

TTGGGGATTT TAACTTTT ATG GAT TTT TGC TCT GGC ATT GGT GGA GGC CGT	51
Met Asp Phe Cys Ser Gly Ile Gly Gly Gly Arg	
1 5 10	
TTG GGC TTG GAG CAA TGC CAT TTA AAA TGC GTA GGG CAT GCA GAA ATC	99
Leu Gly Leu Glu Gln Cys His Leu Lys Cys Val Gly His Ala Glu Ile	
15 20 25	
AAT CAT GAA GCC CTT AGG ACT TAT GAA TTA TTT TTT AAA GAT ACC CAT	147
Asn His Glu Ala Leu Arg Thr Tyr Glu Leu Phe Phe Lys Asp Thr His	
30 35 40	
AAT TTT GGG GAT TTG ATG CGA ATC AAC CCT AAT GAT TTA CCC GAT TTT	195
Asn Phe Gly Asp Leu Met Arg Ile Asn Pro Asn Asp Leu Pro Asp Phe	
45 50 55	
GAT GCA CTC ATT AGC GGG TTT CCT TGT CAA GCT TTT TCT ATC AAT GGC	243
Asp Ala Leu Ile Ser Gly Phe Pro Cys Gln Ala Phe Ser Ile Asn Gly	
60 65 70 75	
AAA AGG AAG GGG CTT GAA GAT GAA AGA GGG ACG ATT ATT TAC GGG CTT	291
Lys Arg Lys Gly Leu Glu Asp Glu Arg Gly Thr Ile Ile Tyr Gly Leu	
80 85 90	
ATT CGC ATT TTA AAA GTT AAA CAG CCT GAA TGT TTC TTG CTT GAA AAT	339
Ile Arg Ile Leu Lys Val Lys Gln Pro Glu Cys Phe Leu Leu Glu Asn	
95 100 105	
GTT AAG GGC TTG ATC AAT CAT AAT AAA AAG GCA ACT TTT AAT ATT ATT	387
Val Lys Gly Leu Ile Asn His Asn Lys Lys Ala Thr Phe Asn Ile Ile	
110 115 120	
ATC AAA GCC CTA CAA GAA GTG GGT TAT ACA ACT TAT TAT AAA ATT TTA	435
Ile Lys Ala Leu Gln Glu Val Gly Tyr Thr Thr Tyr Tyr Lys Ile Leu	
125 130 135	
AAC AGC GCT GAT TTT CAA TTA GCC CAA AAT AGA GAA CGC CTT TAT ATC	483
Asn Ser Ala Asp Phe Gln Leu Ala Gln Asn Arg Glu Arg Leu Tyr Ile	
140 145 150 155	
GTA GGG TTT AGG AAG GAT TTA AAA CAC CCA TTT AAT TTC CCT TTA GGT	531
Val Gly Phe Arg Lys Asp Leu Lys His Pro Phe Asn Phe Pro Leu Gly	
160 165 170	

TTA GCC AAT GAT TAT TAT TTC AAG GAT TTT TTA GAC GCT GAT AAT GAA	579
Leu Ala Asn Asp Tyr Tyr Phe Lys Asp Phe Leu Asp Ala Asp Asn Glu	
175 180 185	
TGT TAT TTG GAT GTG AGT AAC GCT GCA TTT CAA AGA TAC TTG CAC AAC	627
Cys Tyr Leu Asp Val Ser Asn Ala Ala Phe Gln Arg Tyr Leu His Asn	
190 195 200	
CGA TAC AAC CAT AAC CGG GTT TCT TTA GAG GAT CTC TTA ACT TTA GAA	675
Arg Tyr Asn His Asn Arg Val Ser Leu Glu Asp Leu Leu Thr Leu Glu	
205 210 215	
AAC GCT GTT TTA GAC ACA AGA CAA TCT GAT TTA AGG TTG TAT TCT AAT	723
Asn Ala Val Leu Asp Thr Arg Gln Ser Asp Leu Arg Leu Tyr Ser Asn	
220 225 230 235	
GTT TTT CCT ACT TTA AGG ACT TCT CGG CAT GGC CTG TTT TAT ACC CAA	771
Val Phe Pro Thr Leu Arg Thr Ser Arg His Gly Leu Phe Tyr Thr Gln	
240 245 250	
AAA GGC AAA ATC AAA AGA TTA AAC GCT ATT GAA AGC TTG CTT TTG CAA	819
Lys Gly Lys Ile Lys Arg Leu Asn Ala Ile Glu Ser Leu Leu Leu Gln	
255 260 265	
GGA TTT CCT AGG GAT TTG ATC GCT AAG ATT AAA GAT AAT CCT AAC TTT	867
Gly Phe Pro Arg Asp Leu Ile Ala Lys Ile Lys Asp Asn Pro Asn Phe	
270 275 280	
AAA GCA AGC CAT TTG CTA TCC CAA GCG GGG AAT GCG ATG AGC GTG AAT	915
Lys Ala Ser His Leu Leu Ser Gln Ala Gly Asn Ala Met Ser Val Asn	
285 290 295	
GTG ATT GCT GCA ATC GCT AAA CAA ATG TTA AAG GCG ATT TAATAAGGGA GC	966
Val Ile Ala Ala Ile Ala Lys Gln Met Leu Lys Ala Ile	
300 305 310	
TTTAAGGGGA GAATGATTTTC AAAATACCCC CTATCCCCTT AA	1008

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Met Asp Phe Cys Ser Gly Ile Gly Gly Gly Arg Leu Gly Leu Glu Gln	
1 5 10 15	
Cys His Leu Lys Cys Val Gly His Ala Glu Ile Asn His Glu Ala Leu	
20 25 30	
Arg Thr Tyr Glu Leu Phe Phe Lys Asp Thr His Asn Phe Gly Asp Leu	
35 40 45	
Met Arg Ile Asn Pro Asn Asp Leu Pro Asp Phe Asp Ala Leu Ile Ser	
50 55 60	

Gly	Phe	Pro	Cys	Gln	Ala	Phe	Ser	Ile	Asn	Gly	Lys	Arg	Lys	Gly	Leu
65					70					75					80
Glu	Asp	Glu	Arg	Gly	Thr	Ile	Ile	Tyr	Gly	Leu	Ile	Arg	Ile	Leu	Lys
				85					90					95	
Val	Lys	Gln	Pro	Glu	Cys	Phe	Leu	Leu	Glu	Asn	Val	Lys	Gly	Leu	Ile
			100					105					110		
Asn	His	Asn	Lys	Lys	Ala	Thr	Phe	Asn	Ile	Ile	Ile	Lys	Ala	Leu	Gln
		115					120					125			
Glu	Val	Gly	Tyr	Thr	Thr	Tyr	Tyr	Lys	Ile	Leu	Asn	Ser	Ala	Asp	Phe
	130					135					140				
Gln	Leu	Ala	Gln	Asn	Arg	Glu	Arg	Leu	Tyr	Ile	Val	Gly	Phe	Arg	Lys
145				150					155						160
Asp	Leu	Lys	His	Pro	Phe	Asn	Phe	Pro	Leu	Gly	Leu	Ala	Asn	Asp	Tyr
			165					170						175	
Tyr	Phe	Lys	Asp	Phe	Leu	Asp	Ala	Asp	Asn	Glu	Cys	Tyr	Leu	Asp	Val
			180				185						190		
Ser	Asn	Ala	Ala	Phe	Gln	Arg	Tyr	Leu	His	Asn	Arg	Tyr	Asn	His	Asn
		195				200						205			
Arg	Val	Ser	Leu	Glu	Asp	Leu	Leu	Thr	Leu	Glu	Asn	Ala	Val	Leu	Asp
	210					215					220				
Thr	Arg	Gln	Ser	Asp	Leu	Arg	Leu	Tyr	Ser	Asn	Val	Phe	Pro	Thr	Leu
225				230					235						240
Arg	Thr	Ser	Arg	His	Gly	Leu	Phe	Tyr	Thr	Gln	Lys	Gly	Lys	Ile	Lys
			245					250						255	
Arg	Leu	Asn	Ala	Ile	Glu	Ser	Leu	Leu	Leu	Gln	Gly	Phe	Pro	Arg	Asp
			260				265					270			
Leu	Ile	Ala	Lys	Ile	Lys	Asp	Asn	Pro	Asn	Phe	Lys	Ala	Ser	His	Leu
	275					280					285				
Leu	Ser	Gln	Ala	Gly	Asn	Ala	Met	Ser	Val	Asn	Val	Ile	Ala	Ala	Ile
	290				295					300					
Ala	Lys	Gln	Met	Leu	Lys	Ala	Ile								
305					310										

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...1436
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

AAAATAAAAA	TTATATTAAT	CAAGGAGCG	ATG	AAA	GCG	ATG	GAA	GGT	AAA	ATC	53					
			Met	Lys	Ala	Met	Glu	Gly	Lys	Ile						
			1				5									
ATT	CAG	GTT	TTA	GGC	CCT	GTG	GTA	GAT	GTG	GAG	TTT	GAA	TCC	TAT	CTG	101
Ile	Gln	Val	Leu	Gly	Pro	Val	Val	Asp	Val	Glu	Phe	Glu	Ser	Tyr	Leu	
	10				15				20							

CCG Pro 25	GCG Ala	ATT Ile	TTT Phe	GAA Glu	GCG Ala 30	TTA Leu	GAC Asp	ATT Ile	AAT Asn	TTT Phe 35	GAA Glu	GTC Val	AAT Asn	GGT Gly	GTT Val 40	149
CAA Gln	AAG Lys	TCT Ser	TTA Leu	GTT Val 45	TTA Leu	GAG Glu	GTG Val	GCA Ala	GCC Ala 50	CAT His	TTG Leu	GGC Gly	GGT Gly	AAT Asn 55	CGG Arg	197
GTG Val	CGA Arg	GCG Ala	ATT Ile 60	GCT Ala	ATG Met	GAT Asp	ATG Met	ACA Thr 65	GAA Glu	GGC Gly	TTA Leu	GTG Val	CGT Arg 70	AAC Asn	CAA Gln	245
GTG Val	ATC Ile	AAG Lys 75	GCT Ala	CGC Arg	GGC Gly	AAA Lys	ATG Met 80	ATT Ile	GAA Glu	GTG Val	CCT Pro	GTG Val	GGC Gly	GAA Glu	GAA Glu	293
GTA Val 90	TTA Leu	GGG Gly	CGT Arg	ATT Ile	TTT Phe	AAT Asn 95	GTT Val	GTG Val	GGC Gly	GAG Glu	AGC Ser 100	ATT Ile	GAC Asp	AAT Asn	TTA Leu	341
GAG Glu 105	CCG Pro	CTT Leu	AAG Lys	CCG Pro	TCC Ser 110	TTA Leu	ACT Thr	TGG Trp	CCC Pro	ATT Ile 115	CAC His	AGA Arg	AAA Lys	GCC Ala	CCT Pro 120	389
AGT Ser	TTT Phe	GAG Glu	CAG Gln	CAA Gln 125	AGC Ser	ACT Thr	AAA Lys	ACA Thr	GAA Glu 130	ATG Met	TTT Phe	GAA Glu	ACT Thr	GGT Gly 135	ATT Ile	437
AAA Lys	GTC Val	ATT Ile	GAC Asp 140	TTA Leu	CTC Leu	GCG Ala	CCT Pro	TAT Tyr 145	TCT Ser	AAG Lys	GGC Gly	GGT Gly	AAA Lys 150	GTA Val	GGC Gly	485
TTG Leu	TTT Phe	GGT Gly 155	GGG Gly	GCT Ala	GGC Gly	GTA Val	GGC Gly 160	AAA Lys	ACG Thr	GTG Val	ATC Ile	ATT Ile 165	ATG Met	GAG Glu	CTT Leu	533
ATC Ile 170	CAT His	AAT Asn	GTG Val	GCT Ala	TAT Tyr	AAG Lys 175	CAT His	AAC Asn	GGG Gly	TAT Tyr	TCG Ser 180	GTG Val	TTT Phe	GCA Ala	GGT Gly	581
GTG Val 185	GGG Gly	GAG Glu	CGC Arg	ACC Thr	AGA Arg 190	GAG Glu	GGG Gly	AAT Asn	GAT Asp	CTG Leu 195	TAT Tyr	TTT Phe	GAA Glu	ATG Met	AAA Lys 200	629
GAA Glu	GGG Gly	GGC Gly	GTT Val	TTA Leu 205	GAC Asp	AAA Lys	GTC Val	GCA Ala	CTG Leu 210	TGT Cys	TAT Tyr	GGG Gly	CAA Gln	ATG Met 215	AAT Asn	677
GAG Glu	CCA Pro	CCA Pro	GGC Gly 220	GCG Ala	AGG Arg	AAC Asn	CGC Arg	ATC Ile 225	GCA Ala	TTC Phe	ACC Thr	GGC Gly	TTG Leu 230	ACG Thr	ATG Met	725
GCG Ala	GAG Glu	TAT Tyr 235	TTT Phe	CGT Arg	GAT Asp	GAA Glu	AAG Lys 240	GGC Gly	TTA Leu	GAT Asp	GTG Val	TTG Leu 245	ATG Met	TTT Phe	ATT Ile	773
GAC Asp	AAC Asn	ATC Ile	TTT Phe	AGA Arg	TAC Tyr	GCT Ala	CAA Gln	AGC Ser	GGT Gly	GCG Ala	GAA Glu	ATG Met	AGC Ser	GCG Ala	CTA Leu	821

250				255				260								
TTA Leu 265	GGC Gly	CGT Arg	ATC Ile	CCT Pro	TCA Ser 270	GCG Ala	GTG Val	GGG Gly	TAT Tyr 275	CAG Gln	CCC Pro	ACG Thr	CTA Leu	GCC Ala	GGG Gly 280	869
GAA Glu	ATG Met	GGG Gly	AAA Lys	CTT Leu 285	CAA Gln	GAG Glu	CGT Arg	ATC Ile	GCT Ala 290	TCC Ser	ACT Thr	AAA Lys	AAT Asn	GGC Gly 295	TCT Ser	917
ATC Ile	ACT Thr	TCC Ser	GTT Val 300	CAA Gln	GCG Ala	GTG Val	TAT Tyr	GTG Val 305	CCA Pro	GCA Ala	GAT Asp	GAC Asp	TTG Leu 310	ACT Thr	GAC Asp	965
CCA Pro	GCC Ala	CCT Pro 315	GCT Ala	TCG Ser	GTG Val	TTT Phe	GCG Ala 320	CAT His	TTG Leu	GAT Asp	GCG Ala 325	ACT Thr	ACG Thr	GTG Val	TTG Leu	1013
AAT Asn 330	AGA Arg	AAG Lys	ATC Ile	GCT Ala	GAA Glu	AAA Lys 335	GGG Gly	ATT Ile	TAT Tyr	CCG Pro	GCG Ala 340	GTG Val	GAT Asp	CCT Pro	TTG Leu	1061
GAT Asp 345	TCC Ser	ACT Thr	TCA Ser	AGG Arg	ATT Ile 350	TTA Leu	AGC Ser	CCT Pro	CAA Gln	ATG Met 355	ATC Ile	GGT Gly	GAG Glu	AAA Lys	CAC His 360	1109
TAT Tyr	GAA Glu	GTC Val	GCT Ala	ACC Thr 365	GGT Gly	ATC Ile	CAG Gln	CAG Gln	GTT Val 370	TTA Leu	CAA Gln	AAA Lys	TAC Tyr	AAG Lys 375	GAT Asp	1157
TTG Leu	CAA Gln	GAC Asp	ATT Ile 380	ATT Ile	GCG Ala	ATT Ile	TTG Leu	GGA Gly 385	TTA Leu	GAC Asp	GAA Glu	TTG Leu	AGC Ser 390	GAA Glu	GAG Glu	1205
GAT Asp	AAA Lys	AAA Lys 395	ACG Thr	GTT Val	GAA Glu	AGG Arg	GCC Ala 400	AGA Arg	AAA Lys	ATT Ile	GAG Glu	AAG Lys 405	TTT Phe	TTA Leu	TCC Ser	1253
CAG Gln 410	CCG Pro	TTC Phe	TTT Phe	GTG Val	GCT Ala	GAA Glu 415	GTG Val	TTT Phe	ACA Thr	GGA Gly	AGT Ser 420	CCT Pro	GGT Gly	AAA Lys	TAT Tyr	1301
GTA Val 425	ACC Thr	CTT Leu	CAA Gln	GAG Glu	ACT Thr 430	TTA Leu	GAG Glu	GGC Gly	TTT Phe	GGA Gly 435	GGG Gly	ATT Ile	TTA Leu	GAG Glu	GGC Gly 440	1349
AAA Lys	TAC Tyr	GAT Asp	CAT His	ATT Ile 445	CCC Pro	GAG Glu	AAC Asn	GCG Ala	TTT Phe 450	TAT Tyr	ATG Met	GTG Val	GGT Gly	AGC Ser 455	ATT Ile	1397
CAA Gln	GAG Glu	GTT Val	TTA Leu 460	GAA Glu	AAA Lys	GCT Ala	AAA Lys 465	AAC Asn	ATG Met	AAA Lys	AAT Asn	TCC Ser	TAAGGGT	TTTT	GT	1448
GATGGCTTTG TTGAAAATTA																1468

-349-

Gly Leu Asp Glu Leu Ser Glu Glu Asp Lys Lys Thr Val Glu Arg Ala
 385 390 395 400
 Arg Lys Ile Glu Lys Phe Leu Ser Gln Pro Phe Phe Val Ala Glu Val
 405 410 415
 Phe Thr Gly Ser Pro Gly Lys Tyr Val Thr Leu Gln Glu Thr Leu Glu
 420 425 430
 Gly Phe Gly Gly Ile Leu Glu Gly Lys Tyr Asp His Ile Pro Glu Asn
 435 440 445
 Ala Phe Tyr Met Val Gly Ser Ile Gln Glu Val Leu Glu Lys Ala Lys
 450 455 460
 Asn Met Lys Asn Ser
 465

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...2649
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

TAAGGAACGC TCTATTTTAG GATAATA ATG ATA ATG AAA CAA GAA CCC ACC ACC	54
Met Ile Met Lys Gln Glu Pro Thr Thr	
1 5	
TAC CAA CCA GAA GAG ATA GAA AAA AAG ATT TAT GAA ATT TGC TCT CAT	102
Tyr Gln Pro Glu Glu Ile Glu Lys Lys Ile Tyr Glu Ile Cys Ser His	
10 15 20 25	
AGG GGG TAT TTT GAA ATT GAT GGC AAT GAA GCG ATC CAA GAA AAA AAC	150
Arg Gly Tyr Phe Glu Ile Asp Gly Asn Glu Ala Ile Gln Glu Lys Asn	
30 35 40	
AAA CGA TTT TGC TTG ATG ATG CCC CCT CCT AAT GTG ACC GGT GTG TTG	198
Lys Arg Phe Cys Leu Met Met Pro Pro Pro Asn Val Thr Gly Val Leu	
45 50 55	
CAC ATA GGG CAT GCC CTG ACT TTA AGC TTG CAA GAT ATT TTA GCG CGT	246
His Ile Gly His Ala Leu Thr Leu Ser Leu Gln Asp Ile Leu Ala Arg	
60 65 70	
TAC AAA CGC ATG GAT GGG TAT AAG ACT TTG TAT CAG CCC GGG TTG GAT	294
Tyr Lys Arg Met Asp Gly Tyr Lys Thr Leu Tyr Gln Pro Gly Leu Asp	
75 80 85	
CAC GCT GGC ATT GCA ACG CAA AAT GTC GTG GAA AAG CAG CTT TTA AGT	342
His Ala Gly Ile Ala Thr Gln Asn Val Val Glu Lys Gln Leu Leu Ser	
90 95 100 105	

CAA Gln	GGG Gly	ATT Ile	AAA Lys	AAA Lys 110	GAA Glu	GAT Asp	TTA Leu	GGG Gly	CGT Arg 115	GAA Glu	GAG Glu	TTC Phe	ATT Ile	AAA Lys 120	AAA Lys	390
GTG Val	TGG Trp	GAA Glu	TGG Trp 125	AAA Lys	GAA Glu	AAG Lys	AGC Ser	GGG Gly 130	GGA Gly	GCG Ala	ATT Ile	TTA Leu	GAG Glu 135	CAA Gln	ATG Met	438
AAG Lys	CGT Arg	TTA Leu 140	GGC Gly	GTG Val	AGC Ser	GCG Ala	GCC Ala 145	TTT Phe	TCT Ser	AGG Arg	ACT Thr	CGT Arg 150	TTC Phe	ACG Thr	ATG Met	486
GAT Asp	AAG Lys 155	GGC Gly	TTG Leu	CAA Gln	AGA Arg	GCG Ala 160	GTC Val	AAA Lys	TTG Leu	GCG Ala	TTT Phe 165	TTG Leu	AAA Lys	TGG Trp	TAT Tyr	534
GAA Glu 170	AAA Lys	GGT Gly	CTC Leu	ATT Ile 175	ATT Ile	CAA Gln	GAT Asp	AAT Asn	TAC Tyr	ATG Met 180	GTG Val	AAT Asn	TGG Trp	TGC Cys	ACT Thr 185	582
AAA Lys	GAT Asp	GGG Gly	GCG Ala 190	TTG Leu	AGC Ser	GAT Asp	ATT Ile	GAA Glu 195	GTG Val	GAG Glu	TAT Tyr	GAA Glu	GAG Glu	CGT Arg 200	AAG Lys	630
GGG Gly	GCG Ala	TTG Leu	TAT Tyr 205	TAT Tyr	ATT Ile	AGA Arg	TAT Tyr	TAT Tyr 210	TTA Leu	GAA Glu	AAT Asn	CAA Gln	AAA Lys 215	GAT Asp	TAT Tyr	678
TTA Leu	GTG Val 220	GTG Val	GCT Ala	ACC Thr	ACA Thr	CGC Arg	CCT Pro 225	GAA Glu	ACC Thr	TTG Leu	TTT Phe	GGC Gly 230	GAT Asp	AGC Ser	GCG Ala	726
CTT Leu	ATG Met 235	GTC Val	AAT Asn	CCT Pro	AAC Asn	GAT Asp 240	GAG Glu	AGA Arg	TAC Tyr	AAG Lys	CAT His 245	TTG Leu	GTG Val	GGG Gly	CAA Gln	774
AAA Lys 250	GCG Ala	ATC Ile	TTG Leu	CCT Pro	TTA Leu 255	ATC Ile	CAT His	CGC Arg	ACA Thr	ATC Ile 260	CCT Pro	ATT Ile	ATC Ile	GCT Ala	GAT Asp 265	822
GAA Glu	CAT His	GTT Val	GAA Glu	ATG Met 270	GAG Glu	TTT Phe	GGC Gly	ACA Thr	GGG Gly 275	TGT Cys	GTG Val	AAA Lys	GTA Val	ACC Thr 280	CCT Pro	870
GGG Gly	CAT His	GAT Asp	TTT Phe 285	AAC Asn	GAT Asp	TAT Tyr	GAA Glu	GTG Val 290	GGC Gly	AAA Lys	CGC Arg	CAC His 295	CAT His	TTG Leu	GAA Glu	918
ACG Thr	ATT Ile	AAA Lys 300	ATC Ile	TTT Phe	GAT Asp	GAA Glu	AAG Lys 305	GGG Gly	ATT Ile	TTA Leu	AAC Asn	GCG Ala 310	CAT His	TGC Cys	GGG Gly	966
GAG Glu	TTT Phe 315	GAA Glu	AAT Asn	TTA Leu	GAA Glu	CGA Arg 320	TTA Leu	GAA Glu	GCT Ala	AGA Arg	GAT Asp 325	AAG Lys	GTC Val	GTA Val	GAA Glu	1014
AGA Arg	TTA Leu	AAA Lys	GAA Glu	AAC Asn	GCC Ala	CTA Leu	TTG Leu	GAA Glu	AAA Lys	ATA Ile	GAA Glu	GAA Glu	CAC His	ACG Thr	CAT His	1062

330				335				340				345				
CAA Gln	GTG Val	GGG Gly	CAT His	TGC Cys 350	TAT Tyr	CGT Arg	TGT Cys	CAT His	AAT Asn 355	GTG Val	GTA Val	GAA Glu	CCT Pro	TAT Tyr 360	GTG Val	1110
TCT Ser	AAG Lys	CAA Gln	TGG Trp 365	TTT Phe	GTC Val	AAG Lys	CCT Pro	GAA Glu	ATC Ile	GCT Ala	CAA Gln	AGT Ser	TCT Ser 375	ATT Ile	GAA Glu	1158
AAA Lys	ATC Ile	CAA Gln 380	CAA Gln	GGT Gly	TTG Leu	GCG Ala	CGA Arg 385	TTC Phe	TAC Tyr	CCT Pro	TCT Ser	AAT Asn 390	TGG Trp	ATC Ile	AAT Asn	1206
AAT Asn	TAC Tyr 395	AAC Asn	GCT Ala	TGG Trp	ATG Met	AGG Arg 400	GAA Glu	TTA Leu	CGC Arg	CCT Pro	TGG Trp 405	TGT Cys	ATC Ile	AGC Ser	AGG Arg	1254
CAA Gln 410	TTG Leu	TTT Phe	TGG Trp	GGG Gly 415	CAT His 415	CAA Gln	ATA Ile	CCG Pro	GTA Val 420	TTC Phe	ACT Thr	TGC Cys	GAG Glu	AAT Asn 425	AAC Asn 425	1302
CAC His	CAG Gln	TTC Phe	GTA Val 430	AGC Ser 430	TTA Leu	GAC Asp	ACC Thr	CCC Pro	TTA Leu 435	AGT Ser	TGC Cys	CCT Pro	ACT Thr 440	TGT Cys 440	AAG Lys 440	1350
AGC Ser	GAA Glu	ACA Thr	CTA Leu 445	GAG Glu	CAA Gln	GAT Asp	AAG Lys 450	GAT Asp 450	GTG Val	CTA Leu	GAC Asp	ACA Thr	TGG Trp 455	TTT Phe	AGT Ser 455	1398
TCA Ser	GGG Gly 460	CTA Leu 460	TGG Trp	GCG Ala	TTT Phe	TCC Ser	ACT Thr 465	CTA Leu	GGG Gly	TGG Trp	GGG Gly	CAA Gln 470	GAA Glu	AAA Lys	AGC Ser 470	1446
GGT Gly 475	TTG Leu	TTT Phe	AAT Asn 480	GAA Glu	AGC Ser	GAT Asp 480	TTG Leu	AAA Lys	GAT Asp	TTC Phe	TAC Tyr 485	CCT Pro	AAC Asn	ACA Thr	ACG Thr 485	1494
CTC Leu 490	ATT Ile	ACT Thr	GGG Gly	TTT Phe	GAC Asp 495	ATC Ile	CTC Leu	TTT Phe	TTT Phe	TGG Trp 500	GTG Val	GCT Ala	AGG Arg	ATG Met	CTT Leu 505	1542
TTT Phe	TGC Cys	AGC Ser	GAA Glu 510	TCG Ser	CTT Leu	TTA Leu	GGC Gly	GAA Glu 515	TTG Leu	CCC Pro	TTT Phe	AAA Lys	GAT Asp 520	ATT Ile	TAC Tyr 520	1590
TTG Leu	CAC His	GCC Ala 525	TTA Leu 525	GTG Val	AGA Arg	GAT Asp	GAA Glu 530	AAG Lys 530	GGT Gly	GAA Glu	AAA Lys	ATG Met	AGC Ser 535	AAA Lys	TCT Ser 535	1638
AAG Lys	GGT Gly	AAT Asn 540	GTG Val	ATC Ile	GAT Asp	CCT Pro	TTA Leu 545	GAG Glu	ATG Met	ATA Ile	GAA Glu	AAA Lys 550	TAC Tyr	GGC Gly	GCG Ala	1686
GAT Asp	AGC Ser 555	TTG Leu	CGT Arg	TTC Phe	ACT Thr	TTA Leu 560	GCC Ala	AAT Asn	TTG Leu	TGC Cys	GCT Ala 565	ACG Thr	GGT Gly	AGG Arg	GAC Asp	1734

ATT Ile 570	AAG Lys	CTT Leu	TCC Ser	ACT Thr	ACG Thr 575	CAT His	TTA Leu	GAA Glu	AAT Asn	AAC Asn 580	AAG Lys	AAT Asn	TTC Phe	GCC Ala	AAC Asn 585	1782
AAG Lys	CTT Leu	TTT Phe	AAT Asn 590	GCG Ala	GCG Ala	AGT Ser	TAC Tyr	TTG Leu	AAG Lys 595	CTC Leu	AAA Lys	CAA Gln	GAA Glu	TCT Ser 600	TTC Phe	1830
AAA Lys	GAT Asp	AAA Lys	GAG Glu 605	CGT Arg	TTG Leu	AAT Asn	GAA Glu	TAC Tyr 610	CAA Gln	ACG Thr	CCT Pro	TTG Leu	GGG Gly 615	CGT Arg	TAT Tyr	1878
GCG Ala	AAA Lys	TCG Ser 620	CGC Arg	TTG Leu	AAT Asn	TCA Ser	GCG Ala 625	ACT Thr	AAA Lys	GAG Glu	GCG Ala	CGT Arg 630	AAC Asn	GCT Ala	TTA Leu	1926
GAT Asp 635	AAT Asn	TAT Tyr	CGT Arg	TTT Phe	AAT Asn	GAC Asp 640	GCC Ala	ACG Thr	ACT Thr	TTG Leu	TTA Leu 645	TAC Tyr	CGC Arg	TTT Phe	TTG Leu	1974
TGG Trp 650	GGG Gly	GAA Glu	TTT Phe	TGC Cys	GAC Asp 655	TGG Trp	TTC Phe	ATT Ile	GAA Glu	TTT Phe 660	TCT Ser	AAA Lys	GTG Val	GAA Glu	AAT Asn 665	2022
GAA Glu	GCG Ala	ATA Ile	GAC Asp	GAA Glu 670	TTA Leu	GGG Gly	AGC Ser	GTG Val	TTA Leu 675	AAA Lys	GAG Glu	GCT Ala	TTA Leu	AAA Lys 680	CTC Leu	2070
TTG Leu	CAC His	CCT Pro	TTC Phe 685	ATG Met	CCC Pro	TTT Phe	ATC Ile	AGC Ser 690	GAG Glu	TCT Ser	TTA Leu	TAC Tyr	CAC His 695	AAG Lys	CTC Leu	2118
AGC Ser	AAT Asn 700	ACG Thr	GAA Glu	CTA Leu	GAA Glu	AAC Asn	ACT Thr 705	GAA Glu	TCT Ser	ATC Ile	ATG Met 710	GTC Val	ATG Met	CCT Pro	TAC Tyr	2166
CCT Pro 715	AAA Lys	GAT Asp	TTG Leu	GCG Ala	CAA Gln 720	GAT Asp	GAA Glu	AAA Lys	TTA Leu	GAG Glu 725	CAT His	GAA Glu	TTT Phe	GAA Glu	GTG Val	2214
ATT Ile 730	AAA Lys	GAT Asp	TGC Cys	ATT Ile	GTG Val 735	TCT Ser	TTA Leu	AGG Arg	CGT Arg	TTA Leu 740	AAA Lys	ATC Ile	ATG Met	CTA Leu	GAA Glu 745	2262
ACC Thr	CCA Pro	CCG Pro	ATT Ile 750	GTT Val	CTA Leu	AAA Lys	GAA Glu	GCG Ala	AGC Ser 755	GTG Val	GGA Gly	TTA Leu	AGA Arg	GAA Glu 760	GCC Ala	2310
ATA Ile	GAA Glu	AAC Asn 765	ACA Thr	GAG Glu	CGT Arg	TTG Leu	CAA Gln 770	ACT Thr	TAC Tyr	GCC Ala	CAA Gln	AAA Lys	TTA Leu 775	GCG Ala	AGG Arg	2358
TTG Leu	GAA Glu	AAA Lys 780	GTC Val	AGC Ser	GTG Val	ATT Ile	AGT Ser 785	TCT Ser	AAG Lys	CCT Pro	TTA Leu 790	AAA Lys	AGC Ser	GTG Val	AGC Ser	2406
GAT Asp	GTG Val	GGG Gly	GAA Glu	TTT Phe	TGC Cys	CAG Gln	ACT Thr	TAT Tyr	GCG Ala	AAT Asn	TTA Leu	GAA Glu	AAT Asn	CTT Leu	GAT Asp	2454

795	800	805	
TTA AGC CCG CTT GTT GCG CGT TTG AAA AAG CAG TTG GAA AAA TTG GAA			2502
Leu Ser Pro Leu Val Ala Arg Leu Lys Lys Gln Leu Glu Lys Leu Glu			
810	815	820	825
AAA GAA AAA TTA AAA CTC AAT TTG CAC AAT GAA AAT TTT GTC AAA AAC			2550
Lys Glu Lys Leu Lys Leu Asn Leu His Asn Glu Asn Phe Val Lys Asn			
	830	835	840
GCG CCT AAA AGC GTG CTA GAA AAA GCT AAA GAG AGT TTA AAA ACG CTT			2598
Ala Pro Lys Ser Val Leu Glu Lys Ala Lys Glu Ser Leu Lys Thr Leu			
	845	850	855
TTA GAA AAA GAA AGT AAA ATT AAG CAA GAA TTG GAC TTG TTA GAA CAA			2646
Leu Glu Lys Glu Ser Lys Ile Lys Gln Glu Leu Asp Leu Leu Glu Gln			
	860	865	870
CCA TAATAAAAGG ATAGAAAATG TTTCAAGCGT TAAGCGATGG GTTTAAAAAC GCGCTC			2705
Pro			
AATAAAATCC G			2716

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met	Ile	Met	Lys	Gln	Glu	Pro	Thr	Thr	Tyr	Gln	Pro	Glu	Glu	Ile	Glu
1				5					10					15	
Lys	Lys	Ile	Tyr	Glu	Ile	Cys	Ser	His	Arg	Gly	Tyr	Phe	Glu	Ile	Asp
		20						25					30		
Gly	Asn	Glu	Ala	Ile	Gln	Glu	Lys	Asn	Lys	Arg	Phe	Cys	Leu	Met	Met
		35					40					45			
Pro	Pro	Pro	Asn	Val	Thr	Gly	Val	Leu	His	Ile	Gly	His	Ala	Leu	Thr
		50				55					60				
Leu	Ser	Leu	Gln	Asp	Ile	Leu	Ala	Arg	Tyr	Lys	Arg	Met	Asp	Gly	Tyr
65				70					75					80	
Lys	Thr	Leu	Tyr	Gln	Pro	Gly	Leu	Asp	His	Ala	Gly	Ile	Ala	Thr	Gln
			85					90						95	
Asn	Val	Val	Glu	Lys	Gln	Leu	Leu	Ser	Gln	Gly	Ile	Lys	Lys	Glu	Asp
		100						105					110		
Leu	Gly	Arg	Glu	Glu	Phe	Ile	Lys	Lys	Val	Trp	Glu	Trp	Lys	Glu	Lys
		115					120					125			
Ser	Gly	Gly	Ala	Ile	Leu	Glu	Gln	Met	Lys	Arg	Leu	Gly	Val	Ser	Ala
		130				135					140				
Ala	Phe	Ser	Arg	Thr	Arg	Phe	Thr	Met	Asp	Lys	Gly	Leu	Gln	Arg	Ala
145				150					155					160	
Val	Lys	Leu	Ala	Phe	Leu	Lys	Trp	Tyr	Glu	Lys	Gly	Leu	Ile	Ile	Gln
			165					170						175	

Asp	Asn	Tyr	Met	Val	Asn	Trp	Cys	Thr	Lys	Asp	Gly	Ala	Leu	Ser	Asp
			180					185					190		
Ile	Glu	Val	Glu	Tyr	Glu	Glu	Arg	Lys	Gly	Ala	Leu	Tyr	Tyr	Ile	Arg
		195					200					205			
Tyr	Tyr	Leu	Glu	Asn	Gln	Lys	Asp	Tyr	Leu	Val	Val	Ala	Thr	Thr	Arg
	210					215					220				
Pro	Glu	Thr	Leu	Phe	Gly	Asp	Ser	Ala	Leu	Met	Val	Asn	Pro	Asn	Asp
225					230					235					240
Glu	Arg	Tyr	Lys	His	Leu	Val	Gly	Gln	Lys	Ala	Ile	Leu	Pro	Leu	Ile
				245					250					255	
His	Arg	Thr	Ile	Pro	Ile	Ile	Ala	Asp	Glu	His	Val	Glu	Met	Glu	Phe
			260					265					270		
Gly	Thr	Gly	Cys	Val	Lys	Val	Thr	Pro	Gly	His	Asp	Phe	Asn	Asp	Tyr
		275					280					285			
Glu	Val	Gly	Lys	Arg	His	His	Leu	Glu	Thr	Ile	Lys	Ile	Phe	Asp	Glu
	290					295					300				
Lys	Gly	Ile	Leu	Asn	Ala	His	Cys	Gly	Glu	Phe	Glu	Asn	Leu	Glu	Arg
305				310						315					320
Leu	Glu	Ala	Arg	Asp	Lys	Val	Val	Glu	Arg	Leu	Lys	Glu	Asn	Ala	Leu
				325					330					335	
Leu	Glu	Lys	Ile	Glu	Glu	His	Thr	His	Gln	Val	Gly	His	Cys	Tyr	Arg
			340					345					350		
Cys	His	Asn	Val	Val	Glu	Pro	Tyr	Val	Ser	Lys	Gln	Trp	Phe	Val	Lys
		355					360					365			
Pro	Glu	Ile	Ala	Gln	Ser	Ser	Ile	Glu	Lys	Ile	Gln	Gln	Gly	Leu	Ala
	370					375					380				
Arg	Phe	Tyr	Pro	Ser	Asn	Trp	Ile	Asn	Asn	Tyr	Asn	Ala	Trp	Met	Arg
385					390					395					400
Glu	Leu	Arg	Pro	Trp	Cys	Ile	Ser	Arg	Gln	Leu	Phe	Trp	Gly	His	Gln
				405					410					415	
Ile	Pro	Val	Phe	Thr	Cys	Glu	Asn	Asn	His	Gln	Phe	Val	Ser	Leu	Asp
			420					425					430		
Thr	Pro	Leu	Ser	Cys	Pro	Thr	Cys	Lys	Ser	Glu	Thr	Leu	Glu	Gln	Asp
		435					440					445			
Lys	Asp	Val	Leu	Asp	Thr	Trp	Phe	Ser	Ser	Gly	Leu	Trp	Ala	Phe	Ser
	450				455						460				
Thr	Leu	Gly	Trp	Gly	Gln	Glu	Lys	Ser	Gly	Leu	Phe	Asn	Glu	Ser	Asp
465					470					475					480
Leu	Lys	Asp	Phe	Tyr	Pro	Asn	Thr	Thr	Leu	Ile	Thr	Gly	Phe	Asp	Ile
				485					490					495	
Leu	Phe	Phe	Trp	Val	Ala	Arg	Met	Leu	Phe	Cys	Ser	Glu	Ser	Leu	Leu
			500					505					510		
Gly	Glu	Leu	Pro	Phe	Lys	Asp	Ile	Tyr	Leu	His	Ala	Leu	Val	Arg	Asp
		515					520					525			
Glu	Lys	Gly													

125	130	135	
CGC CCT ACT GCT TAT AAA ATC CCT GTT GCG CTC TCT AAA CAA GTG GTT Arg Pro Thr Ala Tyr Lys Ile Pro Val Ala Leu Ser Lys Gln Val Val 140 145 150			483
TTT AGC ATC AAT GAT TGT AAG GAA AAT GAA AAA ACC CTT GTG ATC GGC Phe Ser Ile Asn Asp Cys Lys Glu Asn Glu Lys Thr Leu Val Ile Gly 155 160 165			531
GGA GGC AAC TCA GCG GTG GAA TAC GCC ATT GCT TTG TGC AAA ACC ACC Gly Gly Asn Ser Ala Val Glu Tyr Ala Ile Ala Leu Cys Lys Thr Thr 170 175 180 185			579
CCT ACC ACC CTC AAT TAC CGC AAA AAA GAA TTC AGC CGC ATC AAT GAA Pro Thr Thr Leu Asn Tyr Arg Lys Lys Glu Phe Ser Arg Ile Asn Glu 190 195 200			627
GAC AAC GCT AAA AAC TTG CAA GAA GTC CTA AAC AAT AAC ACG CTT AAA Asp Asn Ala Lys Asn Leu Gln Glu Val Leu Asn Asn Asn Thr Leu Lys 205 210 215			675
AGC AAG CTT GGA GTG GAT ATT GAA AGC CTA GAA GAA GAT AAC ACT CAG Ser Lys Leu Gly Val Asp Ile Glu Ser Leu Glu Glu Asp Asn Thr Gln 220 225 230			723
ATT AAG GTT AAC TTC ACC GAT AAC ACG AGC GAA AGT TTT GAT CGT TTG Ile Lys Val Asn Phe Thr Asp Asn Thr Ser Glu Ser Phe Asp Arg Leu 235 240 245			771
CTG TAT GCG ATC GGC GGC TCT ACC CCT TTA GAG TTT TTT AAA CGC TGT Leu Tyr Ala Ile Gly Ser Thr Pro Leu Glu Phe Phe Lys Arg Cys 250 255 260 265			819
TCT TTA GAG CTG GAT CCT AGC ACC AAT ATC CCT GTG GTG AAA GAA AAT Ser Leu Glu Leu Asp Pro Ser Thr Asn Ile Pro Val Val Lys Glu Asn 270 275 280			867
TTA GAG AGC AAC AAT ATC CCT AAT TTG TTC ATC GTG GGC GAT ATT TTA Leu Glu Ser Asn Asn Ile Pro Asn Leu Phe Ile Val Gly Asp Ile Leu 285 290 295			915
TTC AAA TCA GGG GCG AGC ATC GCT ACC GCT TTA AAC CAT GGC TAT GAT Phe Lys Ser Gly Ala Ser Ile Ala Thr Ala Leu Asn His Gly Tyr Asp 300 305 310			963
GTT GCT ATA GAA ATC GCT AAA AGG TTG CAC TCT TAAAGCCGCT CACTCATCAA Val Ala Ile Glu Ile Ala Lys Arg Leu His Ser 315 320			1016
ACGGCTTAGC CTTATACAAA AA			1038

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met Asn Gln Glu Ile Leu Asp Val Leu Ile Val Gly Ala Gly Pro Gly
1 5 10 15
Gly Ile Ala Thr Ala Val Glu Cys Glu Ile Ala Gly Val Lys Lys Val
20 25 30
Leu Leu Cys Glu Lys Thr Glu Ser His Ser Gly Met Leu Glu Lys Phe
35 40 45
Tyr Lys Ala Gly Lys Arg Ile Asp Lys Asp Tyr Lys Lys Gln Val Val
50 55 60
Glu Leu Lys Gly His Ile Pro Phe Lys Asp Ser Phe Lys Glu Glu Thr
65 70 75 80
Leu Glu Asn Phe Thr Asn Leu Leu Lys Glu His His Ile Thr Pro Ser
85 90 95
Tyr Lys Thr Asp Ile Glu Ser Val Lys Lys Glu Gly Glu Tyr Phe Lys
100 105 110
Ile Thr Thr Thr Ser Asn Thr Thr Tyr His Ala Lys Phe Val Val Val
115 120 125
Ala Ile Gly Lys Met Gly Gln Pro Asn Arg Pro Thr Ala Tyr Lys Ile
130 135 140
Pro Val Ala Leu Ser Lys Gln Val Val Phe Ser Ile Asn Asp Cys Lys
145 150 155 160
Glu Asn Glu Lys Thr Leu Val Ile Gly Gly Gly Asn Ser Ala Val Glu
165 170 175
Tyr Ala Ile Ala Leu Cys Lys Thr Thr Pro Thr Thr Leu Asn Tyr Arg
180 185 190
Lys Lys Glu Phe Ser Arg Ile Asn Glu Asp Asn Ala Lys Asn Leu Gln
195 200 205
Glu Val Leu Asn Asn Asn Thr Leu Lys Ser Lys Leu Gly Val Asp Ile
210 215 220
Glu Ser Leu Glu Glu Asp Asn Thr Gln Ile Lys Val Asn Phe Thr Asp
225 230 235 240
Asn Thr Ser Glu Ser Phe Asp Arg Leu Leu Tyr Ala Ile Gly Gly Ser
245 250 255
Thr Pro Leu Glu Phe Phe Lys Arg Cys Ser Leu Glu Leu Asp Pro Ser
260 265 270
Thr Asn Ile Pro Val Val Lys Glu Asn Leu Glu Ser Asn Asn Ile Pro
275 280 285
Asn Leu Phe Ile Val Gly Asp Ile Leu Phe Lys Ser Gly Ala Ser Ile
290 295 300
Ala Thr Ala Leu Asn His Gly Tyr Asp Val Ala Ile Glu Ile Ala Lys
305 310 315 320
Arg Leu His Ser

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 20...670
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

ATTTTTAAGG TATAGCGTT ATG GCA TTA GAT TGG GAT TTT ATG TTT CAC TCC	52
Met Ala Leu Asp Trp Asp Phe Met Phe His Ser	
1 5 10	
ATC CCT GCG TTT TTT AAG GGG TTA GAA CTC ACG CTT TAT ATT TCT TTC	100
Ile Pro Ala Phe Phe Lys Gly Leu Glu Leu Thr Leu Tyr Ile Ser Phe	
15 20 25	
TTT GGG ATT TTG CTC TCT CTT TTG GTG GGG TTT TTG TGC GCG ATC GTT	148
Phe Gly Ile Leu Leu Ser Leu Leu Val Gly Phe Leu Cys Ala Ile Val	
30 35 40	
TTG TAT TTT AAA ACG CGC TTT CTC TCT CCT GTT GTC TAT ATC TAT GGC	196
Leu Tyr Phe Lys Thr Arg Phe Leu Ser Pro Val Tyr Ile Tyr Gly	
45 50 55	
GAA ATC GCT AGG AAC ACG CCC CTG CTC ATC CAG CTT TTC TTT TTG TAT	244
Glu Ile Ala Arg Asn Thr Pro Leu Leu Ile Gln Leu Phe Phe Leu Tyr	
60 65 70 75	
TAC GGG TTG AAT GAA ATC GGT TTG AGC GCT TTA GAG TGC GCG ATT TTA	292
Tyr Gly Leu Asn Glu Ile Gly Leu Ser Ala Leu Glu Cys Ala Ile Leu	
80 85 90	
GCG TTA GGG TTT TTG GGT GGG GGG TAT ATG AGT CAA AGT TTT TTG CTT	340
Ala Leu Gly Phe Leu Gly Gly Gly Tyr Met Ser Gln Ser Phe Leu Leu	
95 100 105	
GGG TTT AAG AGC CTA GCT TCC ATT CAA AGA GAA AGC GCT TTG AGT TTG	388
Gly Phe Lys Ser Leu Ala Ser Ile Gln Arg Glu Ser Ala Leu Ser Leu	
110 115 120	
GGG TTT AGC CCT TTG AAA ATG ATG TAT TAT ATT ATT CTG CCT CAA AGT	436
Gly Phe Ser Pro Leu Lys Met Met Tyr Tyr Ile Ile Leu Pro Gln Ser	
125 130 135	
TTA AGC GTT TCT ATG CCT TCC ATA GGG GCG AAT GTG ATT TTT TTA CTC	484
Leu Ser Val Ser Met Pro Ser Ile Gly Ala Asn Val Ile Phe Leu Leu	
140 145 150 155	
AAA GAA ACT TCG GTG GTG GGC GCG ATA GCC CTA ACC GAT ATT ATG TTT	532
Lys Glu Thr Ser Val Val Gly Ala Ile Ala Leu Thr Asp Ile Met Phe	
160 165 170	
GTG GCG AAA GAT TTT ATT GGC ATT TAT TAT AAA ACG ACT GAA AGC CTT	580
Val Ala Lys Asp Phe Ile Gly Ile Tyr Tyr Lys Thr Thr Glu Ser Leu	
175 180 185	
TTG ATG TTA AGC CTC ACT TAT TTG ATC GCT TTA CTC CCT TTA AGC GTT	628

Leu Met Leu Ser Leu Thr Tyr Leu Ile Ala Leu Leu Pro Leu Ser Val
 190 195 200

TTG TTT GTG ATC TTA GAG CGT TTC TTT AAA AAG AAA GTG GCT TAAAATGGG 679
 Leu Phe Val Ile Leu Glu Arg Phe Phe Lys Lys Lys Val Ala
 205 210 215

AGTTTTACTA GAATTAGACA ACCTT 704

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Met Ala Leu Asp Trp Asp Phe Met Phe His Ser Ile Pro Ala Phe Phe
 1 5 10 15
 Lys Gly Leu Glu Leu Thr Leu Tyr Ile Ser Phe Phe Gly Ile Leu Leu
 20 25 30
 Ser Leu Leu Val Gly Phe Leu Cys Ala Ile Val Leu Tyr Phe Lys Thr
 35 40 45
 Arg Phe Leu Ser Pro Val Val Tyr Ile Tyr Gly Glu Ile Ala Arg Asn
 50 55 60
 Thr Pro Leu Leu Ile Gln Leu Phe Phe Leu Tyr Tyr Gly Leu Asn Glu
 65 70 75 80
 Ile Gly Leu Ser Ala Leu Glu Cys Ala Ile Leu Ala Leu Gly Phe Leu
 85 90 95
 Gly Gly Gly Tyr Met Ser Gln Ser Phe Leu Leu Gly Phe Lys Ser Leu
 100 105 110
 Ala Ser Ile Gln Arg Glu Ser Ala Leu Ser Leu Gly Phe Ser Pro Leu
 115 120 125
 Lys Met Met Tyr Tyr Ile Ile Leu Pro Gln Ser Leu Ser Val Ser Met
 130 135 140
 Pro Ser Ile Gly Ala Asn Val Ile Phe Leu Leu Lys Glu Thr Ser Val
 145 150 155 160
 Val Gly Ala Ile Ala Leu Thr Asp Ile Met Phe Val Ala Lys Asp Phe
 165 170 175
 Ile Gly Ile Tyr Tyr Lys Thr Thr Glu Ser Leu Leu Met Leu Ser Leu
 180 185 190
 Thr Tyr Leu Ile Ala Leu Leu Pro Leu Ser Val Leu Phe Val Ile Leu
 195 200 205
 Glu Arg Phe Phe Lys Lys Lys Val Ala
 210 215

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 31...699
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

AGCGTTTCTT TAAAAAGAAA GTGGCTTAAA	ATG GGA GTT TTA CTA GAA TTA GAC	54
	Met Gly Val Leu Leu Glu Leu Asp	
	1 5	
AAC CTT AAG CGT TTG TTA GAA GGG TTT GAA ACC ACT CTT TTG ATC GCT	102	
Asn Leu Lys Arg Leu Leu Glu Gly Phe Glu Thr Thr Leu Leu Ile Ala		
10 15 20		
CTT AGC TCT GCA ATG ATT TCA ATC ATT GTT GGA ATG CTT TTG GGG AGC	150	
Leu Ser Ser Ala Met Ile Ser Ile Ile Val Gly Met Leu Leu Gly Ser		
25 30 35 40		
TTG ATG GCG TTT GGT TCT CAA ATA GTG GTT TTG GCG TGT CGT GTG TAT	198	
Leu Met Ala Phe Gly Ser Gln Ile Val Val Leu Ala Cys Arg Val Tyr		
45 50 55		
TTA GAA AGC ATT CGC ATC ATC CCG CTT TTA GCA TGG CTT TTT ATT GTG	246	
Leu Glu Ser Ile Arg Ile Ile Pro Leu Leu Ala Trp Leu Phe Ile Val		
60 65 70		
TAT TTC GGG TTA GCG AGC TGG TTT GAT TTG CAT ATT AGC GCG GTT TTG	294	
Tyr Phe Gly Leu Ala Ser Trp Phe Asp Leu His Ile Ser Ala Val Leu		
75 80 85		
GCA AGC GTT ATT GTT TTT AGC TTG TGG GGT GGC GCT GAA ATG ATG GAT	342	
Ala Ser Val Ile Val Phe Ser Leu Trp Gly Gly Ala Glu Met Met Asp		
90 95 100		
TTA ACT AGG GGG GTT TTA ACT TCC GTG AGC AAA CAC CAA ATA GAA AGC	390	
Leu Thr Arg Gly Val Leu Thr Ser Val Ser Lys His Gln Ile Glu Ser		
105 110 115 120		
GCT CTG GCT TTA GGC TTA GAT TCA AAA AAG GTG ATT TTT AAT ATT ATT	438	
Ala Leu Ala Leu Gly Leu Asp Ser Lys Lys Val Ile Phe Asn Ile Ile		
125 130 135		
TTC CCT CAA AGC TTT TTG TCT TTA TTG CCC TCA AGC CTT AAT TTG TTC	486	
Phe Pro Gln Ser Phe Leu Ser Leu Leu Pro Ser Ser Leu Asn Leu Phe		
140 145 150		
ACG CGC ATG ATC AAA ACC ACG GCT TTA GTT TCT CTC ATT GGA GCG ATT	534	
Thr Arg Met Ile Lys Thr Thr Ala Leu Val Ser Leu Ile Gly Ala Ile		
155 160 165		
GAT TTG CTA AAA GTG GGC CAG CAA ATC ATA GAG CTT AAC CTC TTA CGC	582	
Asp Leu Leu Lys Val Gly Gln Gln Ile Ile Glu Leu Asn Leu Leu Arg		
170 175 180		

ATG CCT AAT GCG AGC TTT GTG GTT TAT GGC GTT ATC TTA ATG TTT TAT	630
Met Pro Asn Ala Ser Phe Val Val Tyr Gly Val Ile Leu Met Phe Tyr	
185 190 195 200	
TTT AGT TTA TGC TAT AGT TTG AGC CTG TAT AGT TCC TAT TTA GAA AAA	678
Phe Ser Leu Cys Tyr Ser Leu Ser Leu Tyr Ser Ser Tyr Leu Glu Lys	
205 210 215	
AAA TTC CAA CAC ATT AGA GGG TAAAATGAGC GTGATTTTAG AAACCAAAGG GTTA	733
Lys Phe Gln His Ile Arg Gly	
220	
AAAA	737

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Met Gly Val Leu Leu Glu Leu Asp Asn Leu Lys Arg Leu Leu Glu Gly	
1 5 10 15	
Phe Glu Thr Thr Leu Leu Ile Ala Leu Ser Ser Ala Met Ile Ser Ile	
20 25 30	
Ile Val Gly Met Leu Leu Gly Ser Leu Met Ala Phe Gly Ser Gln Ile	
35 40 45	
Val Val Leu Ala Cys Arg Val Tyr Leu Glu Ser Ile Arg Ile Ile Pro	
50 55 60	
Leu Leu Ala Trp Leu Phe Ile Val Tyr Phe Gly Leu Ala Ser Trp Phe	
65 70 75 80	
Asp Leu His Ile Ser Ala Val Leu Ala Ser Val Ile Val Phe Ser Leu	
85 90 95	
Trp Gly Gly Ala Glu Met Met Asp Leu Thr Arg Gly Val Leu Thr Ser	
100 105 110	
Val Ser Lys His Gln Ile Glu Ser Ala Leu Ala Leu Gly Leu Asp Ser	
115 120 125	
Lys Lys Val Ile Phe Asn Ile Ile Phe Pro Gln Ser Phe Leu Ser Leu	
130 135 140	
Leu Pro Ser Ser Leu Asn Leu Phe Thr Arg Met Ile Lys Thr Thr Ala	
145 150 155 160	
Leu Val Ser Leu Ile Gly Ala Ile Asp Leu Leu Lys Val Gly Gln Gln	
165 170 175	
Ile Ile Glu Leu Asn Leu Leu Arg Met Pro Asn Ala Ser Phe Val Val	
180 185 190	
Tyr Gly Val Ile Leu Met Phe Tyr Phe Ser Leu Cys Tyr Ser Leu Ser	
195 200 205	
Leu Tyr Ser Ser Tyr Leu Glu Lys Lys Phe Gln His Ile Arg Gly	
210 215 220	

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 807 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 31...774
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

AAAAAAAATT CCAACACATT AGAGGGTAAA	ATG AGC GTG ATT TTA GAA ACC AAA	54
	Met Ser Val Ile Leu Glu Thr Lys	
	1 5	
GGG TTA AAA AAA ACC TAT CAA AAC CAT TTG GTT TTA GAC GGC ATC AAT		102
Gly Leu Lys Lys Thr Tyr Gln Asn His Leu Val Leu Asp Gly Ile Asn		
10 15 20		
TTC ACT TTA AAT AAG GGT GAA GTG GCA GTG ATT TTA GGG CCT AGC GGG		150
Phe Thr Leu Asn Lys Gly Glu Val Ala Val Ile Leu Gly Pro Ser Gly		
25 30 35 40		
TGC GGG AAA AGC ACT TTT TTA AAA TGC CTA AAC GGG CTT GAA AAG ATT		198
Cys Gly Lys Ser Thr Phe Leu Lys Cys Leu Asn Gly Leu Glu Lys Ile		
45 50 55		
AAT GAA GGT GAA ATC CTT TTT GAA AAC ACT AAC CTT AAC AAT AAG GCC		246
Asn Glu Gly Glu Ile Leu Phe Glu Asn Thr Asn Leu Asn Asn Lys Ala		
60 65 70		
ACT AAC TGG AAT CAA ATG CGC CAA AAA ATA GGC ATG GTG TTT CAA AAT		294
Thr Asn Trp Asn Gln Met Arg Gln Lys Ile Gly Met Val Phe Gln Asn		
75 80 85		
TAT GAA TTG TTC CCG CAT TTA AAT GTG TTA GAT AAT ATC TTA CTC GCT		342
Tyr Glu Leu Phe Pro His Leu Asn Val Leu Asp Asn Ile Leu Leu Ala		
90 95 100		
CCT ATG AAA GTG CAA AAA CGA TCC AAA GAT GAG GTT ATT TCT CAA GCC		390
Pro Met Lys Val Gln Lys Arg Ser Lys Asp Glu Val Ile Ser Gln Ala		
105 110 115 120		
ATA GAG CTT TTA AAG CGA GTG GGT TTG GAG CAT AAA CAA CAA GCT TAC		438
Ile Glu Leu Leu Lys Arg Val Gly Leu Glu His Lys Gln Gln Ala Tyr		
125 130 135		
CCT AAA GAA TTG AGC GGC GGA CAA AAA CAA CGA GTA GCG ATC GTG CGC		486
Pro Lys Glu Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Val Arg		
140 145 150		
TCT TTA TGC ATG CGA CCA AAA ATC ATG CTT TTT GAT GAA GTA ACC GCC		534
Ser Leu Cys Met Arg Pro Lys Ile Met Leu Phe Asp Glu Val Thr Ala		
155 160 165		

Val	Ile	Val	Thr	His	Glu	Met	Lys	Phe	Ala	Gln	Lys	Ile	Ala	His	Lys
		195					200					205			
Ile	Val	Phe	Phe	Asp	Ser	Gly	Lys	Ile	Ala	Glu	Glu	Asn	Asn	Ala	Lys
	210					215					220				
Glu	Phe	Phe	Asn	His	Pro	Lys	Ser	Gln	Arg	Ala	Gln	Lys	Phe	Leu	Glu
225					230					235					240
Thr	Phe	His	Phe	Leu	Gly	Ser	Cys								
					245										

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...561
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

AAGGATTTGT	TG	ATG	AGT	TAT	TTT	TAT	AAG	CAC	TGT	TTG	AAA	TTT	TCG	TTG	51
	Met	Ser	Tyr	Phe	Tyr	Lys	His	Cys	Leu	Lys	Phe	Ser	Leu		
	1					5					10				
GTT GGG TTG CTA GGG CTT TTG AGC GTT CAG CTT GAC GCT AGG AGT TTT															99
Val Gly Leu Leu Gly Leu Leu Ser Val Gln Leu Asp Ala Arg Ser Phe															
15					20					25					
GTT GAT GGG GAT TTA GAC ATT CAG AAA TTC AGC TAT GAA GAT TCT CTA															147
Val Asp Gly Asp Leu Asp Ile Gln Lys Phe Ser Tyr Glu Asp Ser Leu															
30				35				40					45		
CTT AAA AAG GGA GAC CCT AAT GGC GTG CAT AAA GTG CAG GTG CGA GAT															195
Leu Lys Lys Gly Asp Pro Asn Gly Val His Lys Val Gln Val Arg Asp															
			50				55						60		
TAT AAA GGC AAA ATG CAA GAA GCT GAG ATC CAC TCA GAA ATA CGC ATT															243
Tyr Lys Gly Lys Met Gln Glu Ala Glu Ile His Ser Glu Ile Arg Ile															
			65				70						75		
GCG CTT AAA CCG GGG GTT AAA AAA GAA GTT AAA AAA GGC AAG ATT TAT															291
Ala Leu Lys Pro Gly Val Lys Lys Glu Val Lys Lys Gly Lys Ile Tyr															
			80				85					90			
AGC GCT CAA ATC AAT GAT GGC ATG TGC TAT GCT TTT AGA ATG CTC CAA															339
Ser Ala Gln Ile Asn Asp Gly Met Cys Tyr Ala Phe Arg Met Leu Gln															
			95				100					105			
ACC GGC GAT AAT ACC ACA GGC CTT GAT TCT AAA GAG TTC CCC AAG CAA															387
Thr Gly Asp Asn Thr Thr Gly Leu Asp Ser Lys Glu Phe Pro Lys Gln															
110						115						120			125

AGT CGT GAG AAA AAG GGC CGA GTG ATC ACT TTA ATC GGT AAA GGT GAA	435
Ser Arg Glu Lys Lys Gly Arg Val Ile Thr Leu Ile Gly Lys Gly Glu	
130 135 140	
GTG CCT TAT CTT ATT TTA GAA ACC GAT TGC CAA GTG GGT GAT ATT GCA	483
Val Pro Tyr Leu Ile Leu Glu Thr Asp Cys Gln Val Gly Asp Ile Ala	
145 150 155	
AAG ATC TCT TTG GTG GGT AAT TTT GAT GGC ACT GGG TTT CTT ACG GAA	531
Lys Ile Ser Leu Val Gly Asn Phe Asp Gly Thr Gly Phe Leu Thr Glu	
160 165 170	
TAT AAA TTC AAA GAC GCT AAA CCC ATT TAC TAGTCTTTAT TCTTCGCTTC ATT	584
Tyr Lys Phe Lys Asp Ala Lys Pro Ile Tyr	
175 180	
CTTAA	589

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met	Ser	Tyr	Phe	Tyr	Lys	His	Cys	Leu	Lys	Phe	Ser	Leu	Val	Gly	Leu
1				5					10					15	
Leu	Gly	Leu	Leu	Ser	Val	Gln	Leu	Asp	Ala	Arg	Ser	Phe	Val	Asp	Gly
			20					25					30		
Asp	Leu	Asp	Ile	Gln	Lys	Phe	Ser	Tyr	Glu	Asp	Ser	Leu	Leu	Lys	Lys
		35				40					45				
Gly	Asp	Pro	Asn	Gly	Val	His	Lys	Val	Gln	Val	Arg	Asp	Tyr	Lys	Gly
	50				55					60					
Lys	Met	Gln	Glu	Ala	Glu	Ile	His	Ser	Glu	Ile	Arg	Ile	Ala	Leu	Lys
65					70				75					80	
Pro	Gly	Val	Lys	Lys	Glu	Val	Lys	Lys	Gly	Lys	Ile	Tyr	Ser	Ala	Gln
			85					90					95		
Ile	Asn	Asp	Gly	Met	Cys	Tyr	Ala	Phe	Arg	Met	Leu	Gln	Thr	Gly	Asp
			100					105					110		
Asn	Thr	Thr	Gly	Leu	Asp	Ser	Lys	Glu	Phe	Pro	Lys	Gln	Ser	Arg	Glu
		115				120						125			
Lys	Lys	Gly	Arg	Val	Ile	Thr	Leu	Ile	Gly	Lys	Gly	Glu	Val	Pro	Tyr
	130					135					140				
Leu	Ile	Leu	Glu	Thr	Asp	Cys	Gln	Val	Gly	Asp	Ile	Ala	Lys	Ile	Ser
145					150					155					160
Leu	Val	Gly	Asn	Phe	Asp	Gly	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	Lys	Phe
			165					170						175	
Lys	Asp	Ala	Lys	Pro	Ile	Tyr									
			180												

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...875
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GGAATTTT	GGT	GCT	ACTC	CTTTCT	CGT	ATG	GGT	ATC	GCT	TTT	GCC	CAC	TCT		53	
						Met	Gly	Ile	Ala	Phe	Ala	His	Ser			
						1				5						
ATT	TTT	TGG	TCC	ATC	ACG	GCT	TCT	TTA	GTC	ATT	CGT	GTC	GCG	CCA	AGA	101
Ile	Phe	Trp	Ser	Ile	Thr	Ala	Ser	Leu	Val	Ile	Arg	Val	Ala	Pro	Arg	
10						15				20						
AAT	AAA	AAA	CAA	CAG	GCC	TTA	GGG	CTG	TTA	GCG	TTA	GGG	AGT	TCG	TTA	149
Asn	Lys	Lys	Gln	Gln	Ala	Leu	Gly	Leu	Leu	Ala	Leu	Gly	Ser	Ser	Leu	
25					30					35					40	
GCG	ATG	ATT	TTA	GGG	TTG	CCG	CTT	GGG	AGG	ATC	ATT	GGG	CAA	ATT	CTA	197
Ala	Met	Ile	Leu	Gly	Leu	Pro	Leu	Gly	Arg	Ile	Ile	Gly	Gln	Ile	Leu	
				45				50						55		
GAT	TGG	CGT	TCC	ACT	TTT	GGC	GTG	ATC	GGG	GGC	GTT	GCG	ACC	CTT	ATA	245
Asp	Trp	Arg	Ser	Thr	Phe	Gly	Val	Ile	Gly	Gly	Val	Ala	Thr	Leu	Ile	
			60					65					70			
GCG	TTG	CTT	ATG	TGG	AAA	TTG	CTC	CCG	CAT	CTA	CCC	AGT	AGA	AAC	GCA	293
Ala	Leu	Leu	Met	Trp	Lys	Leu	Leu	Pro	His	Leu	Pro	Ser	Arg	Asn	Ala	
	75					80						85				
GGC	ACG	CTC	GCA	AGT	GTC	CCT	GTA	TTA	ATG	AAA	CGG	CCG	CTT	TTA	ATG	341
Gly	Thr	Leu	Ala	Ser	Val	Pro	Val	Leu	Met	Lys	Arg	Pro	Leu	Leu	Met	
	90					95				100						
GGG	ATT	TAT	TTG	CTT	GTG	ATC	ATG	GTC	ATC	TCT	GGG	CAT	TTC	ACC	ACT	389
Gly	Ile	Tyr	Leu	Leu	Val	Ile	Met	Val	Ile	Ser	Gly	His	Phe	Thr	Thr	
105					110					115					120	
TAT	AGT	TAT	ATT	GAG	CCT	TTT	ATC	ATT	CAA	ATC	AGC	CAA	TTT	TCT	CCT	437
Tyr	Ser	Tyr	Ile	Glu	Pro	Phe	Ile	Ile	Gln	Ile	Ser	Gln	Phe	Ser	Pro	
				125					130					135		
GAC	ATT	ACA	ACG	CTA	ATG	TTG	TTT	GTG	TTT	GGG	TTA	GCG	GGC	GTG	GTG	485
Asp	Ile	Thr	Thr	Leu	Met	Leu	Phe	Val	Phe	Gly	Leu	Ala	Gly	Val	Val	
			140					145					150			
GGG	AGT	TTT	TTG	TTC	GGC	CGT	TTG	TAT	GCA	AAA	AAT	TCA	AGA	AAA	TTT	533
Gly	Ser	Phe	Leu	Phe	Gly	Arg	Leu	Tyr	Ala	Lys	Asn	Ser	Arg	Lys	Phe	
	155						160					165				

ATC GCT TTT GCG ATG GTT TTA GTC ATT TGC CCG CAA CTC TTG CTT TTT Ile Ala Phe Ala Met Val Leu Val Ile Cys Pro Gln Leu Leu Leu Phe 170 175 180	581
GTG TTT AAA AAC TTA GAG TGG GTG GTT TTC TTG CAA ATT TTC TTA TGG Val Phe Lys Asn Leu Glu Trp Val Val Phe Leu Gln Ile Phe Leu Trp 185 190 195 200	629
GGG ATT GGG ATC ACT TCG CTT GGG ATT TCC TTG CAA ATG AGG GTG TTG Gly Ile Gly Ile Thr Ser Leu Gly Ile Ser Leu Gln Met Arg Val Leu 205 210 215	677
CAG CTT GCG CCG GAT GCC ACG GAT GTT GCG AGT GCG ATT TAC TCA GGG Gln Leu Ala Pro Asp Ala Thr Asp Val Ala Ser Ala Ile Tyr Ser Gly 220 225 230	725
AGC TAT AAT GTG GGG ATT GGA TCA GGA GCG CTG TTT GGC AGT ATT GTG Ser Tyr Asn Val Gly Ile Gly Ser Gly Ala Leu Phe Gly Ser Ile Val 235 240 245	773
ATC CAC CAA CTA GGG CTA GGA TAT ATT GGC TTT GTG GGT GGG GCT TTA Ile His Gln Leu Gly Leu Gly Tyr Ile Gly Phe Val Gly Gly Ala Leu 250 255 260	821
GGT TTG TTG GCG CTC TTT TGG CTT AGA TTC ATT ACG ATA AAG TTT AAA Gly Leu Leu Ala Leu Phe Trp Leu Arg Phe Ile Thr Ile Lys Phe Lys 265 270 275 280	869
AAA ACA TAAAGAGCGT TAAAAGGATT AGCCCAATAA AGGAGAATCC CTTTCGCACT Lys Thr	925

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Met Gly Ile Ala Phe Ala His Ser Ile Phe Trp Ser Ile Thr Ala Ser 1 5 10 15
Leu Val Ile Arg Val Ala Pro Arg Asn Lys Lys Gln Gln Ala Leu Gly 20 25 30
Leu Leu Ala Leu Gly Ser Ser Leu Ala Met Ile Leu Gly Leu Pro Leu 35 40 45
Gly Arg Ile Ile Gly Gln Ile Leu Asp Trp Arg Ser Thr Phe Gly Val 50 55 60
Ile Gly Gly Val Ala Thr Leu Ile Ala Leu Leu Met Trp Lys Leu Leu 65 70 75 80
Pro His Leu Pro Ser Arg Asn Ala Gly Thr Leu Ala Ser Val Pro Val 85 90 95
Leu Met Lys Arg Pro Leu Leu Met Gly Ile Tyr Leu Leu Val Ile Met

ACC Thr	ACG Thr	CAT His 60	GAA Glu	GTT Val	TTT Phe	GAA Glu 65	AGA Arg 65	GAA Glu	AAA Lys	ATA Ile	GAC Asp 70	ATC Ile	GCC Ala	TTT Phe	TTT Phe	246
AGC Ser	GCT Ala 75	GGG Gly	GGG Gly	AGC Ser	GTG Val	AGC Ser 80	GMA Xaa	GAA Glu	TTT Phe	GCT Ala	ACA Thr 85	AGC Ser	GCT Ala	TCA Ser	AAA Lys	294
ACG Thr 90	GCC Ala	TTA Leu	GTG Val	GTT Val	GAT Asp 95	AAC Asn	ACG Thr	AGC Ser	TTT Phe	TTT Phe 100	AGA Arg	TTG Leu	AAT Asn	AAA Lys	GAT Asp 105	342
GTG Val	CCT Pro	TTA Leu	GTC Val	GTT Val 110	CCT Pro	GAA Glu	ATC Ile	AAC Asn	GCT Ala 115	AAA Lys	GAA Glu	ATT Ile	TTT Phe	AAC Asn 120	GCT Ala	390
CCC Pro	TTG Leu	AAT Asn	ATC Ile 125	ATC Ile	GCT Ala	AAC Asn	CCT Pro	AAT Asn 130	TGC Cys	TCC Ser	ACC Thr	ATT Ile	CAA Gln 135	ATG Met	ACG Thr	438
CAA Gln	ATC Ile 140	TTA Leu	AAC Asn	CCC Pro	TTA Leu	CAT His 145	CTC Leu	CAT His	TTT Phe	AAG Lys	ATA Ile 150	AAA Lys	AGC Ser	GTG Val	ATT Ile	486
GTT Val 155	AGC Ser	ACC Thr	TAT Tyr	CAA Gln	GCC Ala	GTG Val 160	AGT Ser	GGG Gly	GCA Ala	GGG Gly	AAC Asn 165	AAG Lys	GGC Gly	ATA Ile	GAG Glu	534
AGT Ser 170	TTA Leu	AAA Lys	AAT Asn	GAG Glu	TTA Leu 175	AAA Lys	ACC Thr	GCT Ala	TTA Leu	GAG Glu 180	TGT Cys	TTG Leu	GAA Glu	AAA Lys	GAC Asp 185	582
CCC Pro	ACT Thr	ATT Ile	GAT Asp	TTA Leu 190	AAC Asn	CAA Gln	GTC Val	TTG Leu 195	CAA Gln	GCT Ala	GGG Gly	GCT Ala	TTC Phe	GCT Ala 200	TAT Tyr	630
CCG Pro	ATC Ile	GCT Ala	TTC Phe 205	AAT Asn	GCG Ala	ATC Ile	GCT Ala	CAT His 210	ATT Ile	GAT Asp	ACT Thr	TTT Phe 215	AAG Lys	GAG Glu	AAT Asn	678
GGT Gly	TAC Tyr 220	ACG Thr	AAA Lys	GAA Glu	GAG Glu	CTA Leu	AAA Lys 225	ATG Met	CTG Leu	CAT His	GAA Glu	ACC Thr 230	CAT His	AAA Lys	ATC Ile	726
ATG Met	GGC Gly 235	GTG Val	GAT Asp	TTC Phe	CCT Pro	ATC Ile 240	AGC Ser	GCG Ala	ACT Thr	TGC Cys	GTG Val 245	CGC Arg	GTG Val	CCG Pro	GTA Val	774
TTG Leu 250	AGG Arg	AGC Ser	CAT His	AGC Ser	GAG Glu 255	AGT Ser	TTG Leu	AGT Ser	ATC Ile	GCT Ala 260	TTT Phe	GAA Glu	AAA Lys	GAA Glu 265	TTC Phe	822
GAT Asp	CTC Leu	AAA Lys	GAA Glu	GTC Val 270	TAT Tyr	GAA Glu	GTT Val	TTA Leu	AAA Lys 275	AAC Asn	GCC Ala	CCT Pro	AGC Ser	GTG Val 280	GCT Ala	870
GTT Val	TGC Cys	GAT Asp	GAT Asp	CCC Pro	AGT Ser	CAT His	AAT Asn	CTT Leu	TAC Tyr	CCC Pro	ACG Thr	CCC Pro	CTA Leu	AAA Lys	GCG Ala	918

210		215		220
Lys Met Leu His Glu Thr	His Lys Ile Met Gly	Val Asp Phe Pro Ile		
225	230	235	240	
Ser Ala Thr Cys Val Arg Val	Pro Val Leu Arg Ser	His Ser Glu Ser		
	245	250	255	
Leu Ser Ile Ala Phe Glu Lys	Glu Phe Asp Leu Lys	Glu Val Tyr Glu		
	260	265	270	
Val Leu Lys Asn Ala Pro Ser	Val Ala Val Cys Asp	Asp Pro Ser His		
	275	280	285	
Asn Leu Tyr Pro Thr Pro Leu	Lys Ala Ser His Thr	Asp Ser Val Phe		
	290	295	300	
Ile Gly Arg Leu Arg Lys Asp	Leu Phe Asp Lys Lys	Thr Leu His Gly		
305	310	315	320	
Phe Cys Val Ala Asp Gln Leu	Arg Val Gly Ala Ala	Thr Asn Ala Leu		
	325	330	335	
Lys Ile Ala Leu His Tyr Ile	Lys Asn Ala			
	340	345		

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1359
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

TAAAATTTTA GCATACAAAT ACAAGGAAAT GGA ATG ATT ACC CCT AAA GTG TTG	54
Met Ile Thr Pro Lys Val Leu	
1 5	
AGC GGG TTT AAA GAC CGC TTG CCT AAA GAT GCG ATA CAA AAA GCC CAG	102
Ser Gly Phe Lys Asp Arg Leu Pro Lys Asp Ala Ile Gln Lys Ala Gln	
10 15 20	
TTG CTT GCG AAA GTT TCA GTC GTG TTT CAA AGT TTT GGT TTT GTG CCG	150
Leu Leu Ala Lys Val Ser Val Val Phe Gln Ser Phe Gly Phe Val Pro	
25 30 35	
ATT GAA ACC CCT CAT TTG GAA TAC GCT CAA ACG TTA TTG CCT GAT GCG	198
Ile Glu Thr Pro His Leu Glu Tyr Ala Gln Thr Leu Leu Pro Asp Ala	
40 45 50 55	
AGC AGT GAT ATT CAA AAA GAA ATT TAT CGT TTT AAA GAC CAT GGG GAT	246
Ser Ser Asp Ile Gln Lys Glu Ile Tyr Arg Phe Lys Asp His Gly Asp	
60 65 70	
AGA GAT GTG GCT TTA AGG TTT GAT TTG ACT GTG CCA TTA GCC CGC TTT	294
Arg Asp Val Ala Leu Arg Phe Asp Leu Thr Val Pro Leu Ala Arg Phe	

75						80						85						
GTC	TCT	TTG	CAC	CAC	CAA	ACG	CTA	GGC	ATG	CCC	TTT	AAA	CGC	TAC	GCT	342		
Val	Ser	Leu	His	His	Gln	Thr	Leu	Gly	Met	Pro	Phe	Lys	Arg	Tyr	Ala			
		90					95					100						
ATA	GGC	AAT	GTC	TTT	AGG	GGC	GAA	AGG	GCG	CAA	AAA	GGG	CGT	TAT	AGG	390		
Ile	Gly	Asn	Val	Phe	Arg	Gly	Glu	Arg	Ala	Gln	Lys	Gly	Arg	Tyr	Arg			
	105					110					115							
GAA	TTT	ACG	CAA	TGC	GAT	TTT	GAT	TTT	ATA	GGG	AGC	GAG	AGT	TTG	GTG	438		
Glu	Phe	Thr	Gln	Cys	Asp	Phe	Asp	Phe	Ile	Gly	Ser	Glu	Ser	Leu	Val			
120					125					130					135			
TGC	GAT	GCT	GAG	ATC	ATT	CAA	GTG	ATT	GTC	GCT	TCT	TTA	AAA	GCC	CTA	486		
Cys	Asp	Ala	Glu	Ile	Ile	Gln	Val	Ile	Val	Ala	Ser	Leu	Lys	Ala	Leu			
				140					145					150				
GAT	TTA	GAA	GAT	TTT	TGC	GTC	TCT	ATC	AAC	CAC	AGA	AAA	ATT	TTG	AAC	534		
Asp	Leu	Glu	Asp	Phe	Cys	Val	Ser	Ile	Asn	His	Arg	Lys	Ile	Leu	Asn			
			155					160					165					
GGG	ATA	TGC	GAA	TAT	TTT	GGG	ATC	TCT	CAA	GTG	AAT	GAA	GCG	TTG	CGC	582		
Gly	Ile	Cys	Glu	Tyr	Phe	Gly	Ile	Ser	Gln	Val	Asn	Glu	Ala	Leu	Arg			
		170				175						180						
ATT	GTG	GAT	AAA	TTG	GAA	AAA	ATT	GGC	TTG	AAT	GGG	GTT	GAA	GAA	GAA	630		
Ile	Val	Asp	Lys	Leu	Glu	Lys	Ile	Gly	Leu	Asn	Gly	Val	Glu	Glu	Glu			
	185					190					195							
TTA	AAA	AAA	GAG	TGC	GGT	TTA	AAT	TCA	AAC	ACC	ATT	AAA	GAG	CTT	TTA	678		
Leu	Lys	Lys	Glu	Cys	Gly	Leu	Asn	Ser	Asn	Thr	Ile	Lys	Glu	Leu	Leu			
200					205					210					215			
GAA	TTA	ATT	CAA	ATC	AAA	CAA	AAC	GAT	TTA	AGC	CAT	GCG	GAA	TTT	TTT	726		
Glu	Leu	Ile	Gln	Ile	Lys	Gln	Asn	Asp	Leu	Ser	His	Ala	Glu	Phe	Phe			
				220					225					230				
GAA	AAA	ATT	GCT	TAT	TTG	AAA	GAC	TAT	AAT	GAA	AAT	CTA	AAA	AAA	GGC	774		
Glu	Lys	Ile	Ala	Tyr	Leu	Lys	Asp	Tyr	Asn	Glu	Asn	Leu	Lys	Lys	Gly			
			235					240					245					
ATA	CAG	GAT	TTA	GAA	AGG	CTA	TAC	CAG	TTG	CTA	GGG	GAT	TTG	CAA	ATT	822		
Ile	Gln	Asp	Leu	Glu	Arg	Leu	Tyr	Gln	Leu	Leu	Gly	Asp	Leu	Gln	Ile			
		250					255					260						
TCT	CAA	AAC	CTG	TAT	AAA	ATT	GAT	TTT	TCT	ATC	GCT	AGG	GGA	TTA	GGG	870		
Ser	Gln	Asn	Leu	Tyr	Lys	Ile	Asp	Phe	Ser	Ile	Ala	Arg	Gly	Leu	Gly			
	265					270					275							
TAT	TAT	ACA	GGG	ATT	GTG	TAT	GAA	ACC	ACG	CTT	AAT	GAA	ATG	AAG	TCT	918		
Tyr	Tyr	Thr	Gly	Ile	Val	Tyr	Glu	Thr	Thr	Leu	Asn	Glu	Met	Lys	Ser			
280					285					290					295			
TTA	GGG	AGC	GTG	TGT	TCA	GGG	GGG	CGT	TAT	GAT	CAT	TTG	ACT	AAA	AAT	966		
Leu	Gly	Ser	Val	Cys	Ser	Gly	Gly	Arg	Tyr	Asp	His	Leu	Thr	Lys	Asn			
			300						305					310				

TTT TCT AAA GAG AAT TTA CAA GGG GTA GGG GCT TCT ATT GGG ATT GAT	1014
Phe Ser Lys Glu Asn Leu Gln Gly Val Gly Ala Ser Ile Gly Ile Asp	
315 320 325	
CGA TTG ATT GTG GCT TTG AGT GAA ATG CAA TTA TTA GAC GAG CGC TCC	1062
Arg Leu Ile Val Ala Leu Ser Glu Met Gln Leu Leu Asp Glu Arg Ser	
330 335 340	
ACC CAA GCC AAA GTT TTA ATC GCT TGC ATG CAT GAA GAG TAT TTT TCT	1110
Thr Gln Ala Lys Val Leu Ile Ala Cys Met His Glu Glu Tyr Phe Ser	
345 350 355	
TAC GCC AAC CGC TTA GCG GAG TCT TTA AGG CAA AGC GGG ATT TTT AGT	1158
Tyr Ala Asn Arg Leu Ala Glu Ser Leu Arg Gln Ser Gly Ile Phe Ser	
360 365 370 375	
GAA GTC TAT CCA GAA GCT CAA AAA ATC AAA AAA CCC TTT TCT TAT GCC	1206
Glu Val Tyr Pro Glu Ala Gln Lys Ile Lys Lys Pro Phe Ser Tyr Ala	
380 385 390	
AAC CAT AAA GGG CAT GAG TTT GTG GCT GTC ATT GGC GAA GAA GAA TTT	1254
Asn His Lys Gly His Glu Phe Val Ala Val Ile Gly Glu Glu Glu Phe	
395 400 405	
AAA AGC GAA ACT TTA AGC TTG AAA AAC ATG CAT TCA GGC ATG CAG TTG	1302
Lys Ser Glu Thr Leu Ser Leu Lys Asn Met His Ser Gly Met Gln Leu	
410 415 420	
AAT TGC TTG AGT TTT TTA AAA GCC CTT GAA ATC ATT GGA GAA AAC GAT	1350
Asn Cys Leu Ser Phe Leu Lys Ala Leu Glu Ile Ile Gly Glu Asn Asp	
425 430 435	
GAA GAC TTA TAATGTCGCT ATTGTTGGGG CCAGTGGGGC GGTAGG	1395
Glu Asp Leu	
440	

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Met	Ile	Thr	Pro	Lys	Val	Leu	Ser	Gly	Phe	Lys	Asp	Arg	Leu	Pro	Lys
1				5					10				15		
Asp	Ala	Ile	Gln	Lys	Ala	Gln	Leu	Leu	Ala	Lys	Val	Ser	Val	Val	Phe
			20					25					30		
Gln	Ser	Phe	Gly	Phe	Val	Pro	Ile	Glu	Thr	Pro	His	Leu	Glu	Tyr	Ala
			35				40				45				
Gln	Thr	Leu	Leu	Pro	Asp	Ala	Ser	Ser	Asp	Ile	Gln	Lys	Glu	Ile	Tyr
	50				55				60						
Arg	Phe	Lys	Asp	His	Gly	Asp	Arg	Asp	Val	Ala	Leu	Arg	Phe	Asp	Leu

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 70...597
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

CACGCCCCATA GGAGAAGTGG CAGAAGTTAT GCAGCTCTTA TTAAAGAAGG AAAAATTAAA	60
GCTTGGGGG ATG AGT GAG GCA GGG TTA TCT AGC ATC CAA AAA GCC CAT CAA	111
Met Ser Glu Ala Gly Leu Ser Ser Ile Gln Lys Ala His Gln	
1 5 10	
ATT TGC CCT TTA AGC GCG TTG CAG AGC GAA TAT TCC TTG TGG TGG CGC	159
Ile Cys Pro Leu Ser Ala Leu Gln Ser Glu Tyr Ser Leu Trp Trp Arg	
15 20 25 30	
GAA CCT GAA AAA GAG ATT TTA GGT TTT TTA GAA AAA GAA AAA ATT GGA	207
Glu Pro Glu Lys Glu Ile Leu Gly Phe Leu Glu Lys Glu Lys Ile Gly	
35 40 45	
TTT GTC GCT TTT TCG CCT TTG GGT AAG GGG TTT TTA GGC GCG AAA TTT	255
Phe Val Ala Phe Ser Pro Leu Gly Lys Gly Phe Leu Gly Ala Lys Phe	
50 55 60	
GAA AAA AAT GCC ACT TTC GCT AGT GAG GAT TTT AGA AGC GTT TCT CCT	303
Glu Lys Asn Ala Thr Phe Ala Ser Glu Asp Phe Arg Ser Val Ser Pro	
65 70 75	
AGG TTT AAT CAA GAA AAT CTA GCC AAA AAT TAC GCC TTG GTG GAA TTA	351
Arg Phe Asn Gln Glu Asn Leu Ala Lys Asn Tyr Ala Leu Val Glu Leu	
80 85 90	
ATC CAA GAT CAT GCA CAC GCT AAA GGC GTT ACA CCA GCC CAA CTG GCT	399
Ile Gln Asp His Ala His Ala Lys Gly Val Thr Pro Ala Gln Leu Ala	
95 100 105 110	
CTC TCA TGG ATT TTG CAC ACG CAA AAA ATC ATT GTC CCT CTC TTT GGC	447
Leu Ser Trp Ile Leu His Thr Gln Lys Ile Ile Val Pro Leu Phe Gly	
115 120 125	
ACC ACC AAA GAA TCT AGG CTC ATA GAA AAT ATA GGG GCT TTG CAG GTT	495
Thr Thr Lys Glu Ser Arg Leu Ile Glu Asn Ile Gly Ala Leu Gln Val	
130 135 140	
TCT TGG AGT CAA AAA GAA TTG GAG ATT TTC CAA AAA GAA TTG ACT GCA	543
Ser Trp Ser Gln Lys Glu Leu Glu Ile Phe Gln Lys Glu Leu Thr Ala	
145 150 155	
ATC AAA ATA GAA GGG GCC CGC TAC CCT GAA AGA ATC AAT GAA ATG GTG	591
Ile Lys Ile Glu Gly Ala Arg Tyr Pro Glu Arg Ile Asn Glu Met Val	
160 165 170	
AAT CAA TAAAAGTATT GGGTATTTAT AATTGCATTG GCTCTTTTAA AA	639
Asn Gln	
175	

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 176 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Met Ser Glu Ala Gly Leu Ser Ser Ile Gln Lys Ala His Gln Ile Cys
 1           5           10           15
Pro Leu Ser Ala Leu Gln Ser Glu Tyr Ser Leu Trp Trp Arg Glu Pro
 20           25           30
Glu Lys Glu Ile Leu Gly Phe Leu Glu Lys Glu Lys Ile Gly Phe Val
 35           40           45
Ala Phe Ser Pro Leu Gly Lys Gly Phe Leu Gly Ala Lys Phe Glu Lys
 50           55           60
Asn Ala Thr Phe Ala Ser Glu Asp Phe Arg Ser Val Ser Pro Arg Phe
 65           70           75           80
Asn Gln Glu Asn Leu Ala Lys Asn Tyr Ala Leu Val Glu Leu Ile Gln
 85           90           95
Asp His Ala His Ala Lys Gly Val Thr Pro Ala Gln Leu Ala Leu Ser
100           105           110
Trp Ile Leu His Thr Gln Lys Ile Ile Val Pro Leu Phe Gly Thr Thr
115           120           125
Lys Glu Ser Arg Leu Ile Glu Asn Ile Gly Ala Leu Gln Val Ser Trp
130           135           140
Ser Gln Lys Glu Leu Glu Ile Phe Gln Lys Glu Leu Thr Ala Ile Lys
145           150           155           160
Ile Glu Gly Ala Arg Tyr Pro Glu Arg Ile Asn Glu Met Val Asn Gln
165           170           175
  
```

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 25...2088
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

TAATTTAAAA AAGGAACATT AAAT ATG GAT TTT ATC ACC ATC AAT TCT AGT      51
                      Met Asp Phe Ile Thr Ile Asn Ser Ser
                      1           5

AAC AAA ACC GAA GAG TTC GCT CTC AAA CAA GTG GCC AAA CAA GCC ACC      99
Asn Lys Thr Glu Glu Phe Ala Leu Lys Gln Val Ala Lys Gln Ala Thr
10           15           20           25
  
```


250	255	260	265	
TTG AGC GAG CGA GAA AAT GTT TTC AAT GAA ATT GCC AGA AAA ATC AGT	867			
Leu Ser Glu Arg Glu Asn Val Phe Asn Glu Ile Ala Arg Lys Ile Ser				
270 275 280				
GAA GCC CAC TCA GAA TTC AGT TTA GAA GAA ATT GAA TTG TCT TTA GAA	915			
Glu Ala His Ser Glu Phe Ser Leu Glu Glu Ile Glu Leu Ser Leu Glu				
285 290 295				
AAA GTG AAA AAG ACT GAG ATA AGA CGC ATG ATC ATT AAG GAT AAA ATC	963			
Lys Val Lys Lys Thr Glu Ile Arg Arg Met Ile Ile Lys Asp Lys Ile				
300 305 310				
CGC CCG GAT AAG CGC GCG TTA GAA GAA GTG CGG CCC ATT TTG ATA GAG	1011			
Arg Pro Asp Lys Arg Ala Leu Glu Glu Val Arg Pro Ile Leu Ile Glu				
315 320 325				
AGC GAT TTG CTC CCT ATG GCG CAT AGC TCC ATT TTA TTC ACT AGG GGG	1059			
Ser Asp Leu Leu Pro Met Ala His Ser Ser Ile Leu Phe Thr Arg Gly				
330 335 340 345				
CAA ACT CAA AGC TTA GTG GTA GGG GTT TTA GGC ACG GAT AAT GAC GCT	1107			
Gln Thr Gln Ser Leu Val Val Gly Val Leu Gly Thr Asp Asn Asp Ala				
350 355 360				
CAA ACC CAT GAG AGT TTG GAG CAT AAA GCT CCC ATT AAA GAG CGC TTC	1155			
Gln Thr His Glu Ser Leu Glu His Lys Ala Pro Ile Lys Glu Arg Phe				
365 370 375				
ATG TTT CAT TAT AAT TTC CCT CCT TTC TGC GTG GGC GAA GCG AGT TCT	1203			
Met Phe His Tyr Asn Phe Pro Pro Phe Cys Val Gly Glu Ala Ser Ser				
380 385 390				
ATT GGC GCG GCT TCA AGG CGT GAA TTA GGG CAT GGG AAT TTG GCT AAA	1251			
Ile Gly Ala Ala Ser Arg Arg Glu Leu Gly His Gly Asn Leu Ala Lys				
395 400 405				
AGA GCC TTA GAA ACG AGC ATT AAA AAT AAA GAG CAG GTG ATA CGA TTG	1299			
Arg Ala Leu Glu Thr Ser Ile Lys Asn Lys Glu Gln Val Ile Arg Leu				
410 415 420 425				
GTT TCT GAG ATT TTA GAA AGC AAT GGT TCA AGC TCA ATG GCG AGC GTG	1347			
Val Ser Glu Ile Leu Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val				
430 435 440				
TGC GCA GGC TCT TTA GCC CTT TAT GCA AGC GGT GTG GAA ATT TAC GAT	1395			
Cys Ala Gly Ser Leu Ala Leu Tyr Ala Ser Gly Val Glu Ile Tyr Asp				
445 450 455				
TTA GTC GCT GGG GTG GCT ATG GGC ATG GTG AGC GAA GGG CAA GAT CAC	1443			
Leu Val Ala Gly Val Ala Met Gly Met Val Ser Glu Gly Gln Asp His				
460 465 470				
GCT ATT TTA AGC GAT ATT AGC GGC TTA GAA GAC GCA GAA GGC GAT ATG	1491			
Ala Ile Leu Ser Asp Ile Ser Gly Leu Glu Asp Ala Glu Gly Asp Met				
475 480 485				

GAT TTT AAG ATT GCT GGG AAT TTA GAA GGC ATT ACG GCC ATG CAA ATG	1539
Asp Phe Lys Ile Ala Gly Asn Leu Glu Gly Ile Thr Ala Met Gln Met	
490 495 500 505	
GAT ACC AAA ATG AGC GGT ATC AAG CTA GAA ATT TTA TAC CAA GCC TTA	1587
Asp Thr Lys Met Ser Gly Ile Lys Leu Glu Ile Leu Tyr Gln Ala Leu	
510 515 520	
CTC CAA GCC AAA GAA GCA CGG AAA CAT ATT TTA AAA ATC ATG CAT GAA	1635
Leu Gln Ala Lys Glu Ala Arg Lys His Ile Leu Lys Ile Met His Glu	
525 530 535	
GCG AAA GAA AAG ATT GTG ATC AAT TTT TCC CAT TTG CCC ACA ACG GAG	1683
Ala Lys Glu Lys Ile Val Ile Asn Phe Ser His Leu Pro Thr Thr Glu	
540 545 550	
ATT TTT AAT GTC GCA CCC GAT AAA ATT GTA GAA ATT ATC GGT CAA GGG	1731
Ile Phe Asn Val Ala Pro Asp Lys Ile Val Glu Ile Ile Gly Gln Gly	
555 560 565	
GGG CGT GTG ATT AAA GAG ATA GTA GAA AAG TTT GAA GTT AAA ATT GAT	1779
Gly Arg Val Ile Lys Glu Ile Val Glu Lys Phe Glu Val Lys Ile Asp	
570 575 580 585	
TTG AAC AAA CCG AGC GGT GAA GTG AAA ATC ATG GGG AAT AAA GAG CGC	1827
Leu Asn Lys Pro Ser Gly Glu Val Lys Ile Met Gly Asn Lys Glu Arg	
590 595 600	
GTT TTA AAG ACT AAG GAA TTT ATT TTA AAC TAC TTG CAT TCT TTA GAT	1875
Val Leu Lys Thr Lys Glu Phe Ile Leu Asn Tyr Leu His Ser Leu Asp	
605 610 615	
CAA GAA TTG GAG CAA TAC GCT ATT GAT GAG GTA TTA GAA GCT CAA GTG	1923
Gln Glu Leu Glu Gln Tyr Ala Ile Asp Glu Val Leu Glu Ala Gln Val	
620 625 630	
AAA CGA ATC GTG GAT TTT GGG GCG TTT TTA AGC TTG CCT AAG GGG GGC	1971
Lys Arg Ile Val Asp Phe Gly Ala Phe Leu Ser Leu Pro Lys Gly Gly	
635 640 645	
GAA GGC TTG TTA AGA AAG CAA AAC ATG GAC AAG TGT CAA GTG GTT TTA	2019
Glu Gly Leu Leu Arg Lys Gln Asn Met Asp Lys Cys Gln Val Val Leu	
650 655 660 665	
AAA GAA GGC GAT AGC ATC AGG TGT AGG GTG ATT AGC TTC AAT AAG GGT	2067
Lys Glu Gly Asp Ser Ile Arg Cys Arg Val Ile Ser Phe Asn Lys Gly	
670 675 680	
AAA ATC GCT TTA GAT TTG GCT TAAAATTTTA AAAAGCGTTT TTTAAAAGCG TTTT	2122
Lys Ile Ala Leu Asp Leu Ala	
685	
TAAGCTAGTT T	2133

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 688 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Met	Asp	Phe	Ile	Thr	Ile	Asn	Ser	Ser	Asn	Lys	Thr	Glu	Glu	Phe	Ala
1				5					10					15	
Leu	Lys	Gln	Val	Ala	Lys	Gln	Ala	Thr	Ser	Ser	Leu	Leu	Tyr	Arg	Leu
		20						25					30		
Gly	Lys	Thr	Ile	Ile	Leu	Ala	Ser	Val	Cys	Val	Glu	Arg	Glu	Pro	Val
		35					40					45			
Ser	Glu	Asp	Phe	Leu	Pro	Leu	Val	Val	Gln	Phe	Leu	Glu	Lys	Ser	Tyr
	50					55				60					
Ala	Ala	Gly	Lys	Ile	Pro	Gly	Gly	Phe	Val	Lys	Arg	Glu	Gly	Arg	Ala
65				70					75						80
Gln	Asp	Phe	Glu	Ile	Leu	Thr	Ser	Arg	Leu	Ile	Asp	Arg	Thr	Leu	Arg
				85				90						95	
Pro	Leu	Phe	Pro	Lys	Asp	Tyr	Arg	Tyr	Pro	Thr	Gln	Ile	Thr	Leu	Met
		100					105						110		
Val	Leu	Ser	His	Asp	Ile	Glu	Asn	Asp	Leu	Gln	Val	Ser	Ala	Leu	Asn
		115					120					125			
Ala	Ala	Ser	Ala	Ala	Leu	Phe	Leu	Ala	His	Ile	Ala	Pro	Ile	Lys	Ser
	130					135					140				
Val	Ser	Ala	Cys	Arg	Ile	Ala	Arg	Met	Asp	Asn	Glu	Phe	Ile	Ile	Asn
145				150					155						160
Pro	Ser	Ala	Ser	Leu	Leu	Asn	Gln	Ser	Ser	Leu	Asp	Leu	Phe	Val	Ser
			165					170						175	
Gly	Thr	Lys	Glu	Ser	Leu	Asn	Met	Ile	Glu	Met	Arg	Ser	Leu	Gly	Gln
		180					185						190		
Lys	Leu	Asn	Ala	Leu	Glu	Glu	Pro	Leu	Met	Leu	Glu	Ala	Leu	Glu	Leu
		195					200					205			
Ala	Gln	Lys	Ser	Leu	Glu	Glu	Thr	Cys	Thr	Leu	Tyr	Glu	Glu	Ile	Phe
	210					215					220				
Thr	Pro	His	Gln	Asn	Glu	Leu	Phe	Phe	Lys	Glu	Ser	Gln	Gly	Ile	Val
225				230					235						240
Phe	Asn	Glu	Arg	Leu	Leu	Asp	Leu	Leu	Lys	Asn	Gln	Tyr	Phe	Asp	Glu
			245					250						255	
Ile	Ile	Lys	Gly	Ile	Glu	Ser	Ser	Ala	Leu	Ser	Glu	Arg	Glu	Asn	Val
		260					265						270		
Phe	Asn	Glu	Ile	Ala	Arg	Lys	Ile	Ser	Glu	Ala	His	Ser	Glu	Phe	Ser
	275					280					285				
Leu	Glu	Glu	Ile	Glu	Leu	Ser	Leu	Glu	Lys	Val	Lys	Lys	Thr	Glu	Ile
	290					295					300				
Arg	Arg	Met	Ile	Ile	Lys	Asp	Lys	Ile	Arg	Pro	Asp	Lys	Arg	Ala	Leu
305				310					315						320
Glu	Glu	Val	Arg	Pro	Ile	Leu	Ile	Glu	Ser	Asp	Leu	Leu	Pro	Met	Ala
			325						330					335	
His	Ser	Ser	Ile	Leu	Phe	Thr	Arg	Gly	Gln	Thr	Gln	Ser	Leu	Val	Val
			340				345						350		
Gly	Val	Leu	Gly	Thr	Asp	Asn	Asp	Ala	Gln	Thr	His	Glu	Ser	Leu	Glu
		355				360						365			
His	Lys	Ala	Pro	Ile	Lys	Glu	Arg	Phe	Met	Phe	His	Tyr	Asn	Phe	Pro
	370				375						380				
Pro	Phe	Cys	Val	Gly	Glu	Ala	Ser	Ser	Ile	Gly	Ala	Ala	Ser	Arg	Arg
385					390					395					400

09000007-061501

235	240	245	
GAG AAA CTT CAG GCT GAC Glu Lys Leu Gln Ala Asp 250	AAC ACG CCT TTT Asn Thr Pro Phe 255	AAA GGG GTT TTA CTC GCT Lys Gly Val Leu Leu Ala 260	819
GAA ATT GTA ATC ATA GAA Glu Ile Val Ile Ile Glu 270	GAA AAA GGC GTT TTA Glu Lys Gly Val Leu 275	GAG CCG TAT TTA TTG Glu Pro Tyr Leu Leu 280	867
GAT TTT AGC GTG CGT TTT Asp Phe Ser Val Arg Phe 285	AAA GAC ATT GAA TGC Lys Asp Ile Glu Cys 290	ACG ATT TTA CCC Thr Ile Leu Pro 295	915
CTT TTA GAA AGC TCG CTT Leu Leu Glu Ser Ser Leu 300	TTA GAT TTG TGT TTG Leu Asp Leu Cys Leu 305	GCC ACA GCC AAA GGG Ala Thr Ala Lys Gly 310	963
GAA TTA CAT TCT CTT GAA Glu Leu His Ser Leu Glu 315	TTG GTG TTT TCT AAA Leu Val Phe Ser Lys 320	GAA TTT GTG ATG AGT Glu Phe Val Met Ser 325	1011
GTG GCG CTT GTT TCT AGG Val Ala Leu Val Ser Arg 330	AAT TAC CCC ACT AGC Asn Tyr Pro Thr Ser 335	TCT TCG CCC AAA CAA Ser Ser Ser Pro Lys Gln 340	1059
ACC CTT TAT ATT GAT CCG Thr Leu Tyr Ile Asp Pro 350	GTT GAT GAA AAA AAG Val Asp Glu Lys Lys 355	GGT CAT TTG ATT TTA Gly His Leu Ile Leu 360	1107
GGG GAG GTG GAG CAG GAT Gly Glu Val Glu Gln Asp 365	AAT GGC GTG TTT GAA Asn Gly Val Phe Glu 370	AGC AGT GGG GGG AGG Ser Ser Gly Gly Arg 375	1155
GTG ATC TTT GCC ATT GGT Val Ile Phe Ala Ile Gly 380	AGG GGA AAA TCC TTA Arg Gly Lys Ser Leu 385	TTA GAA GCC AGA AAC Leu Glu Ala Arg Asn 390	1203
CAT GCT TAT GAA ATC GCT His Ala Tyr Glu Ile Ala 395	CAA AAG GTG CAT TTT Gln Lys Val His Phe 400	GAA GGC ATG TTT TAT Glu Gly Met Phe Tyr 405	1251
CGC AAG GAT ATT GGT TTT Arg Lys Asp Ile Gly Phe 410	AAG GTG TTA GAT TTG Lys Val Leu Asp Leu 415	AAA GAA TAT TCT TAAAG Lys Glu Tyr Ser 420	1301
GTAAAGTTT AAGACAAACC AAAGAGTTTG TCTTGTTTG			1340

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Met	Lys	Asp	Asn	Asn	Asn	Tyr	Asn	Val	Leu	Ile	Val	Gly	Asn	Lys	Gly	1	5	10	15
Arg	Glu	Tyr	Ala	Leu	Ala	Gln	Arg	Leu	Gln	Gln	Asp	Glu	Arg	Val	Asn	20	25	30	
Ala	Leu	Tyr	Phe	Cys	Leu	Gly	Asn	Gly	Gly	Thr	Gln	Asp	Leu	Gly	Glu	35	40	45	
Asn	Leu	Glu	Cys	Glu	His	Tyr	Glu	His	Ile	Val	Glu	Leu	Ala	Leu	Lys	50	55	60	
Lys	Gln	Ile	His	Leu	Ala	Ile	Ile	Ser	Glu	Glu	Glu	Phe	Leu	Val	Leu	65	70	75	80
Gly	Leu	Thr	Glu	Met	Leu	Glu	Lys	Ala	Gly	Ile	Leu	Val	Phe	Gly	Ala	85	90	95	
Ser	Lys	Glu	Ala	Ala	Lys	Leu	Glu	Ala	Ser	Lys	Ser	Tyr	Met	Lys	Ala	100	105	110	
Phe	Val	Lys	Glu	Cys	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Phe	Glu	Thr	Asn	115	120	125	
Asp	Leu	Lys	Glu	Ala	Leu	Ser	Tyr	Ile	Gln	Asn	Ala	Ser	Phe	Pro	Leu	130	135	140	
Val	Ile	Lys	Ala	Leu	Asn	Lys	Asn	Thr	Ser	Ile	Val	Tyr	Gln	Glu	Glu	145	150	155	160
Glu	Ala	Ile	Lys	Ile	Leu	Glu	Asp	Ala	Phe	Lys	Gln	Ser	Asn	Glu	Pro	165	170	175	
Val	Ile	Ile	Glu	Pro	Phe	Leu	Glu	Gly	Phe	Glu	Leu	Ser	Val	Thr	Ala	180	185	190	
Leu	Ile	Ala	Asn	Asp	Asp	Phe	Ile	Leu	Leu	Pro	Phe	Cys	Gln	Asn	Tyr	195	200	205	
Lys	Arg	Leu	Leu	Glu	Gly	Asp	Asn	Gly	Val	Asn	Thr	Gly	Gly	Met	Gly	210	215	220	
Ala	Ile	Ala	Pro	Ala	Asn	Phe	Phe	Ser	Asn	Glu	Leu	Glu	Glu	Lys	Ile	225	230	235	240
Lys	Asn	His	Ile	Phe	Lys	Pro	Thr	Leu	Glu	Lys	Leu	Gln	Ala	Asp	Asn	245	250	255	
Thr	Pro	Phe	Lys	Gly	Val	Leu	Leu	Ala	Glu	Ile	Val	Ile	Ile	Glu	Glu	260	265	270	
Lys	Gly	Val	Leu	Glu	Pro	Tyr	Leu	Leu	Asp	Phe	Ser	Val	Arg	Phe	Lys	275	280	285	
Asp	Ile	Glu	Cys	Gln	Thr	Ile	Leu	Pro	Leu	Leu	Glu	Ser	Ser	Leu	Leu	290	295	300	
Asp	Leu	Cys	Leu	Ala	Thr	Ala	Lys	Gly	Glu	Leu	His	Ser	Leu	Glu	Leu	305	310	315	320
Val	Phe	Ser	Lys	Glu	Phe	Val	Met	Ser	Val	Ala	Leu	Val	Ser	Arg	Asn	325	330	335	
Tyr	Pro	Thr	Ser	Ser	Ser	Pro	Lys	Gln	Thr	Leu	Tyr	Ile	Asp	Pro	Val	340	345	350	
Asp	Glu	Lys	Lys	Gly	His	Leu	Ile	Leu	Gly	Glu	Val	Glu	Gln	Asp	Asn	355	360	365	
Gly	Val	Phe	Glu	Ser	Ser	Gly	Gly	Arg	Val	Ile	Phe	Ala	Ile	Gly	Arg	370	375	380	
Gly	Lys	Ser	Leu	Leu	Glu	Ala	Arg	Asn	His	Ala	Tyr	Glu	Ile	Ala	Gln	385	390	395	400
Lys	Val	His	Phe	Glu	Gly	Met	Phe	Tyr	Arg	Lys	Asp	Ile	Gly	Phe	Lys	405	410	415	
Val	Leu	Asp	Leu	Lys	Glu	Tyr	Ser									420			

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 17...769
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TTAAAATGAA GTGAAA ATG AGA GAA ATA AAT ATG ATT TTA TAC ATT CAT ATC	52
Met Arg Glu Ile Asn Met Ile Leu Tyr Ile His Ile	
1 5 10	
CCC TTT TGT GAA AAT AAA TGC GGC TAT TGC GCT TTC AAT TCC TAT GAA	100
Pro Phe Cys Glu Asn Lys Cys Gly Tyr Cys Ala Phe Asn Ser Tyr Glu	
15 20 25	
AAC AAG CAT GGG TTA AAA GAA GAA TAC ACT CAA GCG TTA TGC CTG GAT	148
Asn Lys His Gly Leu Lys Glu Glu Tyr Thr Gln Ala Leu Cys Leu Asp	
30 35 40	
TTA AAG CAT GCG TTA AGT CAA ACT GAC GAA CCA ATT GAA AGC GTT TTT	196
Leu Lys His Ala Leu Ser Gln Thr Asp Glu Pro Ile Glu Ser Val Phe	
45 50 55 60	
ATT GGT GGC GGC ACG CCT AAC ACT TTA AGC GTG AAG GCT TTT GAA AGG	244
Ile Gly Gly Gly Thr Pro Asn Thr Leu Ser Val Lys Ala Phe Glu Arg	
65 70 75	
ATT TTT GAA AGC ATT TAT CAA CAT GCG AGC TTG AGC TTG GAT TGT GAG	292
Ile Phe Glu Ser Ile Tyr Gln His Ala Ser Leu Ser Leu Asp Cys Glu	
80 85 90	
ATC ACC ACT GAA GCT AAC CCC GAA TTG ATT ACT AAA GCT TGG TGT CAA	340
Ile Thr Thr Glu Ala Asn Pro Glu Leu Ile Thr Lys Ala Trp Cys Gln	
95 100 105	
GGC TTA AAA GGT TTA GGG ATC AAC CGC TTG AGT TTA GGG GTG CAA AGT	388
Gly Leu Lys Gly Leu Gly Ile Asn Arg Leu Ser Leu Gly Val Gln Ser	
110 115 120	
TTT AGG GAA GAT AAA TTA TTG TTT TTA GAG CGC CAA CAT TCC AAA AAT	436
Phe Arg Glu Asp Lys Leu Leu Phe Leu Glu Arg Gln His Ser Lys Asn	
125 130 135 140	
ATC GCT CCT GCG ATA GAA ACT ATT TTA AAA AGC GGG ATT GAA AAT ATC	484
Ile Ala Pro Ala Ile Glu Thr Ile Leu Lys Ser Gly Ile Glu Asn Ile	
145 150 155	
AGC ATT GAT TTG ATT TAT AAC ACC CCA TTA GAC AAT GAA AAC TCT CTA	532
Ser Ile Asp Leu Ile Tyr Asn Thr Pro Leu Asp Asn Glu Asn Ser Leu	

Lys	Leu	Ala	Lys	Glu	Leu	Pro	Ile	Asn	His	Leu	Ser	Ala	Tyr	Ala	Leu
			180					185					190		
Ser	Val	Glu	Lys	Asn	Thr	Asn	Leu	Glu	Lys	Asn	Ala	Lys	Lys	Pro	Ser
		195					200					205			
Cys	Ala	His	Phe	Asp	Asn	Val	Val	Arg	Glu	Ile	Leu	Glu	Gly	Phe	Ser
	210					215					220				
Phe	Lys	Gln	Tyr	Glu	Cys	Leu	Ile	Thr	Leu	Glu	Ile	Ile	Lys	Ser	Asn
	225				230					235					240
Thr	Thr	Trp	Leu	Thr	Gly	Gly	Leu	Lys	Ile	Ile					
			245						250						

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 76...1257
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

GCCAAGTCAT TGCTTATTTTC AAAAGAGAGG GGTATTTATA GGGTGTTAAT CGTTCAAAAA	60
TACGGCGGCA CGAGC ATG GGC AGC ATA GAA AGG ATC CAC AAT GTC GCT CAA	111
Met Gly Ser Ile Glu Arg Ile His Asn Val Ala Gln	
1 5 10	
AGG GTT TTA GAA AGC GTT ACA TTA GGG CAT CAA GTC GTG GTG GTG GTT	159
Arg Val Leu Glu Ser Val Thr Leu Gly His Gln Val Val Val Val Val	
15 20 25	
TCA GCG ATG AGC GGC GAA ACC GAC AGG CTT TTA GAA TTT GGC AAG AAT	207
Ser Ala Met Ser Gly Glu Thr Asp Arg Leu Leu Glu Phe Gly Lys Asn	
30 35 40	
TTT AGC CAT AAC CCT AAC AAG CGA GAG ATG GAC AGG ATT GTA AGC GTG	255
Phe Ser His Asn Pro Asn Lys Arg Glu Met Asp Arg Ile Val Ser Val	
45 50 55 60	
GGG GAA TTG GTT TCA AGT GCG GCT TTG AGC ATG GCG TTA GAA AGG TAT	303
Gly Glu Leu Val Ser Ser Ala Ala Leu Ser Met Ala Leu Glu Arg Tyr	
65 70 75	
GGG CAT AGA GCC ATT TCC TTG AGC GGG AAA GAA GCG GGC ATT TTA ACC	351
Gly His Arg Ala Ile Ser Leu Ser Gly Lys Glu Ala Gly Ile Leu Thr	
80 85 90	
AGC TCG CAT TTT CAA AAC GCC GTG ATC CAA TCC ATT GAC ACC AAA CGC	399
Ser Ser His Phe Gln Asn Ala Val Ile Gln Ser Ile Asp Thr Lys Arg	
95 100 105	

ATC Ile	ACA Thr	GAG Glu	CTT Leu	TTA Leu	GAA Glu	AAA Lys	AAC Asn	TAC Tyr	ATT Ile	GTG Val	GTG Val	ATC Ile	GCT Ala	GGG Gly	TTT Phe	447
110115120																
CAA Gln	GGC Gly	GCT Ala	GAT Asp	ATT Ile	CAA Gln	GGT Gly	GAA Glu	ACA Thr	ACG Thr	ACT Thr	TTA Leu	GGG Gly	CGT Arg	GGG Gly	GGG Gly	495
125130135140																
AGC Ser	GAT Asp	TTG Leu	AGC Ser	GCG Ala	GTT Val	GCT Ala	TTG Leu	GCC Ala	GGG Gly	GCT Ala	TTA Leu	AAA Lys	GCG Ala	CAT His	TTG Leu	543
145150155																
TGC Cys	GAA Glu	ATC Ile	TAT Tyr	ACG Thr	GAT Asp	GTG Val	GAT Asp	GGC Gly	GTT Val	TAT Tyr	ACC Thr	ACC Thr	GAT Asp	CCG Pro	CGC Arg	591
160165170																
ATT Ile	GAA Glu	GAA Glu	AAG Lys	GCT Ala	CAA Gln	AAA Lys	ATC Ile	GCG Ala	CAA Gln	ATC Ile	AGC Ser	TAT Tyr	GAT Asp	GAA Glu	ATG Met	639
175180185																
CTT Leu	GAA Glu	CTG Leu	GCT Ala	TCT Ser	ATG Met	GGG Gly	GCT Ala	AAA Lys	GTT Val	TTA Leu	TTA Leu	AAC Asn	CGC Arg	TCG Ser	GTG Val	687
190195200																
GAA Glu	TTA Leu	GCC Ala	AAA Lys	AAG Lys	CTC Leu	AGC Ser	GTG Val	AAG Lys	TTA Leu	GTG Val	ACT Thr	CGC Arg	AAT Asn	TCG Ser	TTT Phe	735
205210215220																
AAC Asn	CAT His	AGC Ser	GAA Glu	GGC Gly	ACG Thr	CTC Leu	ATT Ile	GTG Val	GCT Ala	GAA Glu	AAA Lys	GAC Asp	TTT Phe	AAA Lys	GGA Gly	783
225230235																
GAA Glu	CGC Arg	ATG Met	GAA Glu	ACC Thr	CCT Pro	ATA Ile	GTG Val	AGT Ser	GGG Gly	ATC Ile	GCA Ala	TTG Leu	GAT Asp	AAA Lys	AAT Asn	831
240245250																
CAG Gln	GCT Ala	CGT Arg	GTG Val	AGC Ser	ATG Met	GAG Glu	GGC Gly	GTG Val	GAA Glu	GAT Asp	CGG Arg	CCA Pro	GGC Gly	ATT Ile	GCC Ala	879
255260265																
GCT Ala	GAA Glu	ATC Ile	TTT Phe	GGC Gly	GCT Ala	TTA Leu	GCG Ala	GAG Glu	TAT Tyr	CGC Arg	ATT Ile	AAC Asn	GTG Val	GAT Asp	ATG Met	927
270275280																
ATC Ile	GTC Val	CAA Gln	ACG Thr	ATC Ile	GGC Gly	AGA Arg	GAC Asp	GGC Gly	AAA Lys	ACC Thr	GAT Asp	TTG Leu	GAT Asp	TTT Phe	ACG Thr	975
285290295300																
ATC Ile	GTT Val	AAA Lys	ACC Thr	CAA Gln	ATA Ile	GAA Glu	GAA Glu	ACC Thr	AAG Lys	CAA Gln	GCC Ala	TTA Leu	AAG Lys	CCT Pro	TTT Phe	1023
305310315																
TTA Leu	GCG Ala	CAA Gln	ATG Met	GAT Asp	TCC Ser	ATT Ile	GAT Asp	TAT Tyr	GAT Asp	GAA Glu	AAT Asn	ATC Ile	GCT Ala	AAA Lys	GTC Val	1071
320325330																
TCC Ser	ATA Ile	GTG Val	GGC Gly	GTG Val	GGC Gly	ATG Met	AAG Lys	TCG Ser	CAT His	TCT Ser	GGG Gly	GTG Val	GCG Ala	AGT Ser	ATC Ile	1119

335	340	345	
GCT TTT AAA GCC CTA GCC AAA GAC AAT ATC AAT ATC ATG ATG ATT TCT			1167
Ala Phe Lys Ala Leu Ala Lys Asp Asn Ile Asn Ile Met Met Ile Ser			
350	355	360	
ACA AGC GAG ATT AAA ATT TCG GTT TTG ATT GAC ATT AAA TAC GCT GAA			1215
Thr Ser Glu Ile Lys Ile Ser Val Leu Ile Asp Ile Lys Tyr Ala Glu			
365	370	375	380
TTA GCT GTT AGA ACT TTG CAT GCG GTG TAT CAA TTA GAT CAA TGAAAAATT			1266
Leu Ala Val Arg Thr Leu His Ala Val Tyr Gln Leu Asp Gln			
385	390		
TCTACGATTG GATCAAGGAA TTTGT			1291

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Met	Gly	Ser	Ile	Glu	Arg	Ile	His	Asn	Val	Ala	Gln	Arg	Val	Leu	Glu
1				5					10					15	
Ser	Val	Thr	Leu	Gly	His	Gln	Val	Val	Val	Val	Ser	Ala	Met	Ser	
			20					25				30			
Gly	Glu	Thr	Asp	Arg	Leu	Leu	Glu	Phe	Gly	Lys	Asn	Phe	Ser	His	Asn
			35				40					45			
Pro	Asn	Lys	Arg	Glu	Met	Asp	Arg	Ile	Val	Ser	Val	Gly	Glu	Leu	Val
			50			55					60				
Ser	Ser	Ala	Ala	Leu	Ser	Met	Ala	Leu	Glu	Arg	Tyr	Gly	His	Arg	Ala
65				70					75					80	
Ile	Ser	Leu	Ser	Gly	Lys	Glu	Ala	Gly	Ile	Leu	Thr	Ser	Ser	His	Phe
			85					90						95	
Gln	Asn	Ala	Val	Ile	Gln	Ser	Ile	Asp	Thr	Lys	Arg	Ile	Thr	Glu	Leu
			100					105					110		
Leu	Glu	Lys	Asn	Tyr	Ile	Val	Val	Ile	Ala	Gly	Phe	Gln	Gly	Ala	Asp
			115				120					125			
Ile	Gln	Gly	Glu	Thr	Thr	Thr	Leu	Gly	Arg	Gly	Gly	Ser	Asp	Leu	Ser
			130			135					140				
Ala	Val	Ala	Leu	Ala	Gly	Ala	Leu	Lys	Ala	His	Leu	Cys	Glu	Ile	Tyr
145				150					155					160	
Thr	Asp	Val	Asp	Gly	Val	Tyr	Thr	Thr	Asp	Pro	Arg	Ile	Glu	Glu	Lys
			165						170					175	
Ala	Gln	Lys	Ile	Ala	Gln	Ile	Ser	Tyr	Asp	Glu	Met	Leu	Glu	Leu	Ala
			180				185					190			
Ser	Met	Gly	Ala	Lys	Val	Leu	Leu	Asn	Arg	Ser	Val	Glu	Leu	Ala	Lys
			195				200					205			
Lys	Leu	Ser	Val	Lys	Leu	Val	Thr	Arg	Asn	Ser	Phe	Asn	His	Ser	Glu
			210			215					220				
Gly	Thr	Leu	Ile	Val	Ala	Glu	Lys	Asp	Phe	Lys	Gly	Glu	Arg	Met	Glu
225				230					235						240

TAT GGT ATA GAA GCC CAA AAC GCG CTT TTA AAA ATC TTA GAA GAA CCC	288
Tyr Gly Ile Glu Ala Gln Asn Ala Leu Leu Lys Ile Leu Glu Glu Pro	
85 90 95	
CCG AAT AAC GTT TGT TTT ATC ATG TTC GCT AAA AGC CAA AAC CAT GTG	336
Pro Asn Asn Val Cys Phe Ile Met Phe Ala Lys Ser Gln Asn His Val	
100 105 110	
TTA GCC ACC ATT AAA TCC CGC CTA ATT AAA GAA GAC AAA CGC CAA AAA	384
Leu Ala Thr Ile Lys Ser Arg Leu Ile Lys Glu Asp Lys Arg Gln Lys	
115 120 125	
ATC CCC CTA AAA CCT TTA GAT TTG GAT TTA TCC AAG CTG GAT TTG AAA	432
Ile Pro Leu Lys Pro Leu Asp Leu Asp Leu Ser Lys Leu Asp Leu Lys	
130 135 140	
GAC ATT TAT GCG TTT TTA AAA AAT TTA GAC AAA GAA AAT TTT GAT TCC	480
Asp Ile Tyr Ala Phe Leu Lys Asn Leu Asp Lys Glu Asn Phe Asp Ser	
145 150 155 160	
AGA GAA AAT CAG AGG GAA AGG ATT GAA AGC CTG TTA GAG AGC GTT AAC	528
Arg Glu Asn Gln Arg Glu Arg Ile Glu Ser Leu Leu Glu Ser Val Asn	
165 170 175	
AGG CAT AAG ATC CCC TTA AAC GAG CAA GAA TTG CAA GCC TTT GAT TTA	576
Arg His Lys Ile Pro Leu Asn Glu Gln Glu Leu Gln Ala Phe Asp Leu	
180 185 190	
GCG ATC AAG GCT AAC AGC TCT TAT TAC AAG CTC AGC TAT AAT CTT TTA	624
Ala Ile Lys Ala Asn Ser Ser Tyr Tyr Lys Leu Ser Tyr Asn Leu Leu	
195 200 205	
CCC CTG CTT TTA AGC CTT TTA TCC AAA AAG AAA ACG CCA TGATTGTAAA AC	675
Pro Leu Leu Leu Ser Leu Leu Ser Lys Lys Lys Thr Pro	
210 215 220	
GCCTTAACCC TGATGCGCTC AAAAACGCTC T	706

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Gly Tyr Ser Val Lys Asn Ser Asn Arg Leu Ile Tyr Thr Asp Asn Leu	
1 5 10 15	
Glu Glu Ser Leu Glu Glu Thr Ala Ser Leu Phe Glu His His Ile Lys	
20 25 30	
Phe Tyr Thr Glu Ile Ile Glu Lys Asp Lys Lys Val Ile Lys Thr Phe	
35 40 45	
Asn Lys Asp Phe Lys Ile Glu His Ala Lys Glu Val Ile Ser Lys Ala	
50 55 60	

His	Leu	Lys	His	Ser	Glu	Leu	Asn	Ala	Phe	Leu	Ile	Ala	Ala	Pro	Ser
65					70					75				80	
Tyr	Gly	Ile	Glu	Ala	Gln	Asn	Ala	Leu	Leu	Lys	Ile	Leu	Glu	Glu	Pro
			85						90					95	
Pro	Asn	Asn	Val	Cys	Phe	Ile	Met	Phe	Ala	Lys	Ser	Gln	Asn	His	Val
			100					105					110		
Leu	Ala	Thr	Ile	Lys	Ser	Arg	Leu	Ile	Lys	Glu	Asp	Lys	Arg	Gln	Lys
		115					120					125			
Ile	Pro	Leu	Lys	Pro	Leu	Asp	Leu	Asp	Leu	Ser	Lys	Leu	Asp	Leu	Lys
	130					135					140				
Asp	Ile	Tyr	Ala	Phe	Leu	Lys	Asn	Leu	Asp	Lys	Glu	Asn	Phe	Asp	Ser
145					150					155					160
Arg	Glu	Asn	Gln	Arg	Glu	Arg	Ile	Glu	Ser	Leu	Leu	Glu	Ser	Val	Asn
			165						170					175	
Arg	His	Lys	Ile	Pro	Leu	Asn	Glu	Gln	Glu	Leu	Gln	Ala	Phe	Asp	Leu
			180					185					190		
Ala	Ile	Lys	Ala	Asn	Ser	Ser	Tyr	Tyr	Lys	Leu	Ser	Tyr	Asn	Leu	Leu
		195					200					205			
Pro	Leu	Leu	Leu	Ser	Leu	Leu	Ser	Lys	Lys	Lys	Thr	Pro			
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...1059
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

TATTCTCTCG	CAATAATTGT	TATTGTTATT	GCGACAAAAC	TTTTAGAAGG	AGTTATT	ATG	60
						Met	
						1	
GGA AGT ATC	GGT AGT ATG	GGC AAA CCT	ATT GAA GGG	TTT TTA GTG	GCA		108
Gly Ser Ile	Gly Ser Met	Gly Lys Pro	Ile Glu Gly	Phe Leu Val	Ala		
	5		10		15		
GCC ATT CAG	TTT CCT GTG	CCA ATT GTC	AAT AGC CGT	AAG GAT ATT	GAT		156
Ala Ile Gln	Phe Pro Val	Pro Ile Val	Asn Ser Arg	Lys Asp Ile	Asp		
	20		25		30		
CAC AAT ATT	GAA AGC ATT	ATT AGA ACC	TTG CAT GCG	ACT AAA GCG	GGG		204
His Asn Ile	Glu Ser Ile	Ile Arg Thr	Leu His Ala	Thr Lys Ala	Gly		
	35		40		45		
TAT CCG GGA	GTG GAG CTT	ATC ATT TTC	CCT GAG TAT	AGC ACG CAA	GGT		252
Tyr Pro Gly	Val Glu Ile	Ile Phe Pro	Glu Tyr Ser	Thr Gln Gly			
	50		55		60		65

Glu	Asn	Asn	Ile	Tyr	Asn	Leu	Gly	His	Arg	Gly	Tyr	Val	Ala	Lys	Pro
	275						280					285			
Gly	Gly	Glu	His	Asp	Ala	Gly	Leu	Thr	Tyr	Ile	Lys	Asp	Leu	Ala	Ala
	290					295				300					
Gly	Lys	Tyr	Lys	Leu	Pro	Trp	Glu	Asp	His	Met	Lys	Ile	Lys	Asp	Gly
305				310						315					320
Ser	Ile	Tyr	Gly	Tyr	Pro	Thr	Thr	Gly	Gly	Arg	Phe	Gly	Lys		
			325					330							

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1095
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

TAGCTATGGA TTTTCGCCGT ATTTGTGGTG GATAAAAGAA AAGGATCTTC A ATG ATT	57
Met Ile	
1	
GCT TAC ATT CTC AAA CGC TTG CTT TTG ATT ATC CCT ACT TTA TTA GCT	105
Ala Tyr Ile Leu Lys Arg Leu Leu Leu Ile Ile Pro Thr Leu Leu Ala	
5 10 15	
ATC ATG ACC ATT AAT TTC TTT TTG ATC CAA TCG GCT CCT GGA GGC CCT	153
Ile Met Thr Ile Asn Phe Phe Leu Ile Gln Ser Ala Pro Gly Gly Pro	
20 25 30	
ATA GAG CAG ATG ATG GCT AAA ATC AAT AAC ACG CAG TCC AAA GAG ATT	201
Ile Glu Gln Met Met Ala Lys Ile Asn Asn Thr Gln Ser Lys Glu Ile	
35 40 45 50	
CAA GGC GTT GTT AAA GAG CGT TCG TAT AGG GCG TCT CAA GGG TTG GAG	249
Gln Gly Val Val Lys Glu Arg Ser Tyr Arg Ala Ser Gln Gly Leu Glu	
55 60 65	
AGC GAT TTG TTA GAA AAT TTA AAA AAA CTC TAT GGT TTT GAC AAG CCC	297
Ser Asp Leu Leu Glu Asn Leu Lys Lys Leu Tyr Gly Phe Asp Lys Pro	
70 75 80	
ATA GGG GAG CGC TAC CTT CTC ATG CTC AAA AAA TAT CTG CAA TTT GAT	345
Ile Gly Glu Arg Tyr Leu Leu Met Leu Lys Lys Tyr Leu Gln Phe Asp	
85 90 95	
TTT GGG GAG AGC TTT TAT CGC CAG ATT AAA GTG ATA GAT TTG ATT AAG	393
Phe Gly Glu Ser Phe Tyr Arg Gln Ile Lys Val Ile Asp Leu Ile Lys	
100 105 110	

ATGAAATCTT CTTTAAAACT TTTTATGCGG CCTT

1152

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```

Met Ile Ala Tyr Ile Leu Lys Arg Leu Leu Leu Ile Ile Pro Thr Leu
 1           5           10           15
Leu Ala Ile Met Thr Ile Asn Phe Phe Leu Ile Gln Ser Ala Pro Gly
          20           25           30
Gly Pro Ile Glu Gln Met Met Ala Lys Ile Asn Asn Thr Gln Ser Lys
          35           40           45
Glu Ile Gln Gly Val Val Lys Glu Arg Ser Tyr Arg Ala Ser Gln Gly
          50           55           60
Leu Glu Ser Asp Leu Leu Glu Asn Leu Lys Lys Leu Tyr Gly Phe Asp
65           70           75           80
Lys Pro Ile Gly Glu Arg Tyr Leu Leu Met Leu Lys Lys Tyr Leu Gln
          85           90           95
Phe Asp Phe Gly Glu Ser Phe Tyr Arg Gln Ile Lys Val Ile Asp Leu
          100          105          110
Ile Lys Glu Lys Leu Pro Val Ser Ile Ser Leu Gly Leu Phe Ser Thr
          115          120          125
Leu Leu Ile Tyr Leu Ile Ser Ile Pro Leu Gly Ile Phe Lys Ala Lys
          130          135          140
Arg Asn Asn Glu Pro Leu Asp Val Leu Ser Ser Val Val Ile Ile Val
145          150          155          160
Ala Asn Ala Ile Pro Ala Phe Leu Phe Ala Val Val Leu Ile Val Phe
          165          170          175
Phe Ala Gly Gly Asn Tyr Trp His Trp Phe Pro Leu Lys Gly Leu Val
          180          185          190
Ser Asp Asn Phe Glu Ser Leu Ser Ala Leu Gly Lys Ile Lys Asp Tyr
          195          200          205
Leu Trp His Ile Thr Leu Pro Val Leu Cys Ile Ser Leu Gly Gly Phe
          210          215          220
Ala Ser Leu Thr Leu Leu Val Lys Asn Ser Phe Leu Asp Glu Met Gly
225          230          235          240
Lys Leu Tyr Val Leu Ser Ala Lys Ala Lys Gly Cys Ser Val Gly Arg
          245          250          255
Ile Phe Tyr Ala His Val Phe Arg Asn Ala Ile Leu Leu Val Val Ala
          260          265          270
Gly Phe Pro Gln Ala Phe Leu Gly Met Phe Phe Ser Ser Ser Leu Leu
          275          280          285
Ile Glu Ile Val Phe Ser Leu Asp Gly Leu Gly Leu Leu Gly Tyr Glu
          290          295          300
Ser Ile Val Ser Arg Asp Tyr Pro Val Val Phe Gly Ser Leu Tyr Ile
305          310          315          320
Phe Thr Leu Leu Gly Leu Val Ala Ser Leu Ile Ser Asp Leu Leu Cys
          325          330          335

```

Val Val Ile Asp Pro Arg Ile Asp Phe Glu Lys Arg
 340 345

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...618
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

TTAAAGGTCT AAACC ATG GAT ATT AAG GCA TGT TAT CAA AAC GCT AAA GCG	51
Met Asp Ile Lys Ala Cys Tyr Gln Asn Ala Lys Ala	
1 5 10	
TTA TTA GAG GGG CAT TTC TTG CTC AGC AGT GGG TTT CAT TCC AAT TAT	99
Leu Leu Glu Gly His Phe Leu Leu Ser Ser Gly Phe His Ser Asn Tyr	
15 20 25	
TAT TTG CAA TCC GCT AAA GTT TTA GAA GAT CCC AAA CTA GCC GAA CAA	147
Tyr Leu Gln Ser Ala Lys Val Leu Glu Asp Pro Lys Leu Ala Glu Gln	
30 35 40	
TTA GCG CTA GAA TTA GCC AAA CAA ATC CAA GAA GCT CAT TTG AAT ATT	195
Leu Ala Leu Glu Leu Ala Lys Gln Ile Gln Glu Ala His Leu Asn Ile	
45 50 55 60	
GAA TGC GTG TGC TCA CCG GCT ATT GGG GGG ATT TTG GCT GGG TAT GAG	243
Glu Cys Val Cys Ser Pro Ala Ile Gly Gly Ile Leu Ala Gly Tyr Glu	
65 70 75	
CTT GCA AGG GCT TTG GGC GTG CGT TTT ATC TTC ACC GAA AGG GTG GAT	291
Leu Ala Arg Ala Leu Gly Val Arg Phe Ile Phe Thr Glu Arg Val Asp	
80 85 90	
AAT ACC ATG GCG TTA AGG CGT GGC TTT GAA GTC AAA AAA AAC GAA AAA	339
Asn Thr Met Ala Leu Arg Arg Gly Phe Glu Val Lys Lys Asn Glu Lys	
95 100 105	
ATT TTA GTG TGT GAG GAC ATT ATC ACT ACG GGA AAA TCC GCT ATG GAA	387
Ile Leu Val Cys Glu Asp Ile Ile Thr Thr Gly Lys Ser Ala Met Glu	
110 115 120	
TGC GCT AAA GTT TTA GAA GAA AAG GGT GCT CAA ATC GTG GCT TTT GGT	435
Cys Ala Lys Val Leu Glu Glu Lys Gly Ala Gln Ile Val Ala Phe Gly	
125 130 135 140	
GCT TTA GCT AAT CGG GGC ATT TGC AAG CGT GCT CAT TCT CAT TTA AAA	483

Ala Leu Ala Asn Arg Gly Ile Cys Lys Arg Ala His Ser His Leu Lys
145 150 155

GCC CAA GAG GGA GCG TGT TTG CCT AGC CAT TTG CCC CTT TTT GCT TTA 531
Ala Gln Glu Gly Ala Cys Leu Pro Ser His Leu Pro Leu Phe Ala Leu
160 165 170

GAA GAT TTT GTT TTT GAC ATG CAC AAG CCT AGT TCT TGC CCT TTA TGC 579
Glu Asp Phe Val Phe Asp Met His Lys Pro Ser Ser Cys Pro Leu Cys
175 180 185

GCT ACT AGC GTT GCT ATA AAG CCA GGA AGT CGT GGC AAC TAAAAAACA AA 630
Ala Thr Ser Val Ala Ile Lys Pro Gly Ser Arg Gly Asn
190 195 200

AAAAAATAAA ACCCCAAAAA AAAAGCAAGC GT 662

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Met Asp Ile Lys Ala Cys Tyr Gln Asn Ala Lys Ala Leu Leu Glu Gly
1 5 10 15
His Phe Leu Leu Ser Ser Gly Phe His Ser Asn Tyr Tyr Leu Gln Ser
20 25 30
Ala Lys Val Leu Glu Asp Pro Lys Leu Ala Glu Gln Leu Ala Leu Glu
35 40 45
Leu Ala Lys Gln Ile Gln Glu Ala His Leu Asn Ile Glu Cys Val Cys
50 55 60
Ser Pro Ala Ile Gly Gly Ile Leu Ala Gly Tyr Glu Leu Ala Arg Ala
65 70 75 80
Leu Gly Val Arg Phe Ile Phe Thr Glu Arg Val Asp Asn Thr Met Ala
85 90 95
Leu Arg Arg Gly Phe Glu Val Lys Lys Asn Glu Lys Ile Leu Val Cys
100 105 110
Glu Asp Ile Ile Thr Thr Gly Lys Ser Ala Met Glu Cys Ala Lys Val
115 120 125
Leu Glu Glu Lys Gly Ala Gln Ile Val Ala Phe Gly Ala Leu Ala Asn
130 135 140
Arg Gly Ile Cys Lys Arg Ala His Ser His Leu Lys Ala Gln Glu Gly
145 150 155 160
Ala Cys Leu Pro Ser His Leu Pro Leu Phe Ala Leu Glu Asp Phe Val
165 170 175
Phe Asp Met His Lys Pro Ser Ser Cys Pro Leu Cys Ala Thr Ser Val
180 185 190
Ala Ile Lys Pro Gly Ser Arg Gly Asn
195 200

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...384
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

CTCTCTTTGC GCCTAAAGGC CTTTATCACC GATATTTTT ATG ATT TAT ACC CCC	54
Met Ile Tyr Thr Pro	
1 5	
ATG CTT TAT ATA ATG ACT TAT GCG ATT TTA GGG AGC GCG AAG GAT TTT	102
Met Leu Tyr Ile Met Thr Tyr Ala Ile Leu Gly Ser Ala Lys Asp Phe	
10 15 20	
AGG GAA AAC CAG AGC GCG ATT TTT TTA TGC CTG CTT TTT TAC GCC CTA	150
Arg Glu Asn Gln Ser Ala Ile Phe Leu Cys Leu Leu Phe Tyr Ala Leu	
25 30 35	
ACA CAC AGC TTT TTT ATC GCT TTT AAA TCC CAA AGC CCT GGC ATG CGT	198
Thr His Ser Phe Phe Ile Ala Phe Lys Ser Gln Ser Pro Gly Met Arg	
40 45 50	
TAC GCT CGG TTT AAA TTA ATC AAA AAT AAT GGC GAA AAA GTG GGC TTT	246
Tyr Ala Arg Phe Lys Leu Ile Lys Asn Asn Gly Glu Lys Val Gly Phe	
55 60 65	
TTT TTA GCT TTG TGG CGC TTT GTT TTG TGG GTG TTG AGC ATG GGG TTA	294
Phe Leu Ala Leu Trp Arg Phe Val Leu Trp Val Leu Ser Met Gly Leu	
70 75 80 85	
CTC ATA GGG TTT GTT ACG CCT TTT ATT TTT AAG TTT TTT TTG CAT GAC	342
Leu Ile Gly Phe Val Thr Pro Phe Ile Phe Lys Phe Phe Leu His Asp	
90 95 100	
AAA CTC AGC GGC ACT CAT ATT GAA ACC ATC AAG GAG GCA ACA TGAAAAATT	393
Lys Leu Ser Gly Thr His Ile Glu Thr Ile Lys Glu Ala Thr	
105 110 115	
TAGTAATC	401

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met Ile Tyr Thr Pro Met Leu Tyr Ile Met Thr Tyr Ala Ile Leu Gly
1 5 10 15
Ser Ala Lys Asp Phe Arg Glu Asn Gln Ser Ala Ile Phe Leu Cys Leu
20 25 30
Leu Phe Tyr Ala Leu Thr His Ser Phe Phe Ile Ala Phe Lys Ser Gln
35 40 45
Ser Pro Gly Met Arg Tyr Ala Arg Phe Lys Leu Ile Lys Asn Asn Gly
50 55 60
Glu Lys Val Gly Phe Phe Leu Ala Leu Trp Arg Phe Val Leu Trp Val
65 70 75 80
Leu Ser Met Gly Leu Ile Gly Phe Val Thr Pro Phe Ile Phe Lys
85 90 95
Phe Phe Leu His Asp Lys Leu Ser Gly Thr His Ile Glu Thr Ile Lys
100 105 110
Glu Ala Thr
115

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...667
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

AGCGGGGCTG GTATTTTCAGC AGAAAGCGGG ATTAAACCT TTAGAGACGC TG ATG GCT 58
Met Ala
1
TGT GGG AAA GGG CAT GAC ATC ATG GAA GTT GCC TCG CCT TAT GGC TGG 106
Cys Gly Lys Gly His Asp Ile Met Glu Val Ala Ser Pro Tyr Gly Trp
5 10 15
AAA AAG AAC CCG CAA AAG GTG TTG GAT TTT TAC AAC CAA AGG CGC CGA 154
Lys Lys Asn Pro Gln Lys Val Leu Asp Phe Tyr Asn Gln Arg Arg Arg
20 25 30

CAG CTT TTT GAA GTT TAT CCT AAC AAA GCC CAT AAG GCT TTA GCG GAA	202
Gln Leu Phe Glu Val Tyr Pro Asn Lys Ala His Lys Ala Leu Ala Glu	
35 40 45 50	
TTG GAA AAA CAC TAT CAA GTC AAT ATC ATC ACC CAA AAT GTA GAT GAT	250
Leu Glu Lys His Tyr Gln Val Asn Ile Ile Thr Gln Asn Val Asp Asp	
55 60 65	
TTG CAT GAA AGA GCG GGT TCT TCT CGC ATT TTG CAC TTG CAT GGG GAA	298
Leu His Glu Arg Ala Gly Ser Ser Arg Ile Leu His Leu His Gly Glu	
70 75 80	
TTA TTG AGC GTT CGC AGC GAG AAA GAT CCT AAT TTA GTT TAT AGG TGG	346
Leu Leu Ser Val Arg Ser Glu Lys Asp Pro Asn Leu Val Tyr Arg Trp	
85 90 95	
GAA AAG GAC TTG AAT TTA GGC GAC TTG GCC AAA GAC AAA TCG CAA TTA	394
Glu Lys Asp Leu Asn Leu Gly Asp Leu Ala Lys Asp Lys Ser Gln Leu	
100 105 110	
CGC CCT GAT ATT GTG TGG TTT GGC GAA GCG GTG CCT TTG CTT AAA GAA	442
Arg Pro Asp Ile Val Trp Phe Gly Glu Ala Val Pro Leu Leu Lys Glu	
115 120 125 130	
GCG ATT TCT TTA GTC AAA CAA GCG CAT CTT TTA ATC ATC ATT GGC ACT	490
Ala Ile Ser Leu Val Lys Gln Ala His Leu Leu Ile Ile Ile Gly Thr	
135 140 145	
TCT TTG CAA GTC TAT CCC GCC GCT AGC CTC TAC ACG CAT GCG CAT AAA	538
Ser Leu Gln Val Tyr Pro Ala Ala Ser Leu Tyr Thr His Ala His Lys	
150 155 160	
GAC GCT CTC ATT TAT TAC ATT GAC CCT AAG GCT AAA AAC GCC CAT TTA	586
Asp Ala Leu Ile Tyr Tyr Ile Asp Pro Lys Ala Lys Asn Ala His Leu	
165 170 175	
CCC CAG AAT GTC CAA TGC ATT AAT GAA AGC GCG GTG CAT GCC ATG CAA	634
Pro Gln Asn Val Gln Cys Ile Asn Glu Ser Ala Val His Ala Met Gln	
180 185 190	
GAT TTA ATG CCC AAA CTC ATA GAA ATG GCT TCT TAAGAAATGT TAAAATAATT	687
Asp Leu Met Pro Lys Leu Ile Glu Met Ala Ser	
195 200 205	
TTTATTTTTT CAGCTAACGA TTAGCAAAAA	717

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Met	Ala	Cys	Gly	Lys	Gly	His	Asp	Ile	Met	Glu	Val	Ala	Ser	Pro	Tyr
1				5					10					15	
Gly	Trp	Lys	Lys	Asn	Pro	Gln	Lys	Val	Leu	Asp	Phe	Tyr	Asn	Gln	Arg
		20						25					30		
Arg	Arg	Gln	Leu	Phe	Glu	Val	Tyr	Pro	Asn	Lys	Ala	His	Lys	Ala	Leu
		35					40					45			
Ala	Glu	Leu	Glu	Lys	His	Tyr	Gln	Val	Asn	Ile	Ile	Thr	Gln	Asn	Val
	50					55					60				
Asp	Asp	Leu	His	Glu	Arg	Ala	Gly	Ser	Ser	Arg	Ile	Leu	His	Leu	His
65				70					75					80	
Gly	Glu	Leu	Leu	Ser	Val	Arg	Ser	Glu	Lys	Asp	Pro	Asn	Leu	Val	Tyr
			85					90					95		
Arg	Trp	Glu	Lys	Asp	Leu	Asn	Leu	Gly	Asp	Leu	Ala	Lys	Asp	Lys	Ser
		100						105					110		
Gln	Leu	Arg	Pro	Asp	Ile	Val	Trp	Phe	Gly	Glu	Ala	Val	Pro	Leu	Leu
		115				120						125			
Lys	Glu	Ala	Ile	Ser	Leu	Val	Lys	Gln	Ala	His	Leu	Leu	Ile	Ile	Ile
	130					135					140				
Gly	Thr	Ser	Leu	Gln	Val	Tyr	Pro	Ala	Ala	Ser	Leu	Tyr	Thr	His	Ala
145				150					155					160	
His	Lys	Asp	Ala	Leu	Ile	Tyr	Tyr	Ile	Asp	Pro	Lys	Ala	Lys	Asn	Ala
			165					170					175		
His	Leu	Pro	Gln	Asn	Val	Gln	Cys	Ile	Asn	Glu	Ser	Ala	Val	His	Ala
		180				185							190		
Met	Gln	Asp	Leu	Met	Pro	Lys	Leu	Ile	Glu	Met	Ala	Ser			
	195					200						205			

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 23...421
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

ATTAAAGGAG TTTGAGAGTC TG ATG CAA CAA GCC ACA GAA GCA TTG AAT CAC	52
Met Gln Gln Ala Thr Glu Ala Leu Asn His	
1 5 10	
CCC TAT TTT GGC GTT TTT GTT TTA TTG GTA TTC ACC TTT TGG GTG TTT	100
Pro Tyr Phe Gly Val Phe Val Leu Leu Val Phe Thr Phe Trp Val Phe	
15 20 25	
AAC TTA ACC TTA AGG ATC CAA AGG TTT TTA AGC CGT AAA ATG GCT CAA	148
Asn Leu Thr Leu Arg Ile Gln Arg Phe Leu Ser Arg Lys Met Ala Gln	
30 35 40	
AAA AAG GGC GAA AAG CTC AAG CTC GCT CCC TAT GAA TGC GGG CCT GTG	196

Lys Lys Gly Glu Lys Leu Lys Leu Ala Pro Tyr Glu Cys Gly Pro Val
 45 50 55
 GCT CTC AAA CAG CCT AAT AGG GTG TCG CAC CAT TTC TAT ATC ATG GCC 244
 Ala Leu Lys Gln Pro Asn Arg Val Ser His His Phe Tyr Ile Met Ala
 60 65 70
 ATG CTT TTT ATT TTA TTT GAT GTA GAA ATC GTT TTC ATG TTC CCT TGG 292
 Met Leu Phe Ile Leu Phe Asp Val Glu Ile Val Phe Met Phe Pro Trp
 75 80 85 90
 GCG ATT GGT TTT AAA AAA TTA GGC TTG TTT GGA CTC GTT GAA ATG CTA 340
 Ala Ile Gly Phe Lys Lys Leu Gly Leu Phe Gly Leu Val Glu Met Leu
 95 100 105
 GGC TTT GTC TTC TTT TTA ACC ATT GGT TTT ATT TAC GCT TTA AAG CGA 388
 Gly Phe Val Phe Phe Leu Thr Ile Gly Phe Ile Tyr Ala Leu Lys Arg
 110 115 120
 AAC GCT TTG AGC TGG CAA AAA TTA GAG GTG AAA TAATGCAACA AGCACCGGTT 441
 Asn Ala Leu Ser Trp Gln Lys Leu Glu Val Lys
 125 130
 GTTCTAAGCA CTTTGGATAA ATTATTG 468

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met Gln Gln Ala Thr Glu Ala Leu Asn His Pro Tyr Phe Gly Val Phe
 1 5 10 15
 Val Leu Leu Val Phe Thr Phe Trp Val Phe Asn Leu Thr Leu Arg Ile
 20 25 30
 Gln Arg Phe Leu Ser Arg Lys Met Ala Gln Lys Lys Gly Glu Lys Leu
 35 40 45
 Lys Leu Ala Pro Tyr Glu Cys Gly Pro Val Ala Leu Lys Gln Pro Asn
 50 55 60
 Arg Val Ser His His Phe Tyr Ile Met Ala Met Leu Phe Ile Leu Phe
 65 70 75 80
 Asp Val Glu Ile Val Phe Met Phe Pro Trp Ala Ile Gly Phe Lys Lys
 85 90 95
 Leu Gly Leu Phe Gly Leu Val Glu Met Leu Gly Phe Val Phe Phe Leu
 100 105 110
 Thr Ile Gly Phe Ile Tyr Ala Leu Lys Arg Asn Ala Leu Ser Trp Gln
 115 120 125
 Lys Leu Glu Val Lys
 130

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...831
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

AGCGATCAAA	CAAGACGCTC	CCAAAAGGTT	AGTGTG	ATG	GTA	AGA	AAA	CAA	TCC		54					
				Met	Val	Arg	Lys	Gln	Ser							
				1				5								
CCC	TAT	GAA	GAT	GTG	CAA	AAA	CAA	TCG	CGC	CAG	CAT	GAC	CCC	TAT	AAA	102
Pro	Tyr	Glu	Asp	Val	Gln	Lys	Gln	Ser	Arg	Gln	His	Asp	Pro	Tyr	Lys	
			10					15					20			
ATC	ATA	GAA	CCC	ACC	CCT	AAA	AAA	TAT	TTA	GAG	GGC	AGC	GCT	TAT	GAG	150
Ile	Ile	Glu	Pro	Thr	Pro	Lys	Lys	Tyr	Leu	Glu	Gly	Ser	Ala	Tyr	Glu	
		25					30					35				
GTC	ATT	TAC	AAC	CAC	CTT	TCT	TAC	AAA	CAT	GAG	ATT	TTA	GAC	AAA	TAC	198
Val	Ile	Tyr	Asn	His	Leu	Ser	Tyr	Lys	His	Glu	Ile	Leu	Asp	Lys	Tyr	
	40					45					50					
ATA	GAG	ACT	AAC	ACG	GCT	GTG	TTT	TGG	ATC	AAA	AAA	GAC	GAT	ATT	TTT	246
Ile	Glu	Thr	Asn	Thr	Ala	Val	Phe	Trp	Ile	Lys	Lys	Asp	Asp	Ile	Phe	
55					60					65					70	
TCT	GTC	GCT	ACG	ATT	TTA	AGG	CAT	TTG	GGT	TAT	GAG	TGT	TTG	AGC	GAA	294
Ser	Val	Ala	Thr	Ile	Leu	Arg	His	Leu	Gly	Tyr	Glu	Cys	Leu	Ser	Glu	
			75						80					85		
ATG	AGC	GCG	ATA	GAT	TTG	TGC	GCT	AAA	AAA	GGG	CAT	TTT	GAA	TTG	TTT	342
Met	Ser	Ala	Ile	Asp	Leu	Cys	Ala	Lys	Lys	Gly	His	Phe	Glu	Leu	Phe	
			90					95					100			
TAT	CAG	TTC	GTG	GGC	TTT	AGC	GAT	AGC	TGC	AAG	AAC	CGC	CGT	AGG	NTG	390
Tyr	Gln	Phe	Val	Gly	Phe	Ser	Asp	Ser	Cys	Lys	Asn	Arg	Arg	Arg	Xaa	
		105					110					115				
CGC	GTG	AAG	TGC	GTT	TTG	TTG	CCT	AAT	GAG	AGC	GTG	GAT	TCT	TTG	AGT	438
Arg	Val	Lys	Cys	Val	Leu	Leu	Pro	Asn	Glu	Ser	Val	Asp	Ser	Leu	Ser	
		120				125						130				
TTT	TTA	TAC	CGA	TCG	GCT	AAT	TGG	AGC	GAA	AGG	GAA	GCG	TAT	GAC	ATG	486
Phe	Leu	Tyr	Arg	Ser	Ala	Asn	Trp	Ser	Glu	Arg	Glu	Ala	Tyr	Asp	Met	
135					140					145					150	
CTT	GGT	ATT	GTG	TTT	GAC	AAA	CAC	CCC	TAT	TTG	AAA	CGC	CTT	ATT	ATG	534
Leu	Gly	Ile	Val	Phe	Asp	Lys	His	Pro	Tyr	Leu	Lys	Arg	Leu	Ile	Met	

155										160					165					
CCG	CAT	GAT	TGG	GTA	GGC	CAC	CCA	TTA	TTG	CGC	TCT	TAC	CCG	CTC	AAA	582				
Pro	His	Asp	Trp	Val	Gly	His	Pro	Leu	Leu	Arg	Ser	Tyr	Pro	Leu	Lys					
			170				175				180									
GGC	GAT	GAA	TTC	GCC	CAA	TGG	TAT	GAA	GTG	GAT	AAA	ATT	TTT	GGT	AAA	630				
Gly	Asp	Glu	Phe	Ala	Gln	Trp	Tyr	Glu	Val	Asp	Lys	Ile	Phe	Gly	Lys					
			185				190				195									
GAA	TAC	CGA	GAA	GTG	GTG	GGT	AAA	GAG	CAG	AGA	GAC	AGC	GCA	AGA	GTG	678				
Glu	Tyr	Arg	Glu	Val	Val	Gly	Lys	Glu	Gln	Arg	Asp	Ser	Ala	Arg	Val					
			200				205				210									
GAT	GAA	AAA	GAC	ACT	TTC	AAT	TTT	GCA	AAA	ATT	GGC	TAT	GAA	CAG	GGC	726				
Asp	Glu	Lys	Asp	Thr	Phe	Asn	Phe	Ala	Lys	Ile	Gly	Tyr	Glu	Gln	Gly					
215				220				225				230								
AAG	GGC	GAA	GAA	TTA	AAA	GAA	GTA	GAA	GAA	AAG	CAT	GCG	TTT	AAG	AAA	774				
Lys	Gly	Glu	Glu	Leu	Lys	Glu	Val	Glu	Glu	Lys	His	Ala	Phe	Lys	Lys					
			235				240				245									
ATC	CCT	TTT	GTC	AAA	GAT	TTG	CAC	AAA	ATC	GCC	CCC	ACT	ATC	TTA	AAA	822				
Ile	Pro	Phe	Val	Lys	Asp	Leu	His	Lys	Ile	Ala	Pro	Thr	Ile	Leu	Lys					
			250				255				260									
AAG	AGG	CTA	TAAAATGGCT CAAAATTTC ACGAACTCAA CCC										864							
Lys	Arg	Leu																		
			265																	

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met	Val	Arg	Lys	Gln	Ser	Pro	Tyr	Glu	Asp	Val	Gln	Lys	Gln	Ser	Arg
1				5				10				15			
Gln	His	Asp	Pro	Tyr	Lys	Ile	Ile	Glu	Pro	Thr	Pro	Lys	Lys	Tyr	Leu
			20				25				30				
Glu	Gly	Ser	Ala	Tyr	Glu	Val	Ile	Tyr	Asn	His	Leu	Ser	Tyr	Lys	His
			35				40				45				
Glu	Ile	Leu	Asp	Lys	Tyr	Ile	Glu	Thr	Asn	Thr	Ala	Val	Phe	Trp	Ile
			50				55				60				
Lys	Lys	Asp	Asp	Ile	Phe	Ser	Val	Ala	Thr	Ile	Leu	Arg	His	Leu	Gly
65				70				75				80			
Tyr	Glu	Cys	Leu	Ser	Glu	Met	Ser	Ala	Ile	Asp	Leu	Cys	Ala	Lys	Lys
			85				90				95				
Gly	His	Phe	Glu	Leu	Phe	Tyr	Gln	Phe	Val	Gly	Phe	Ser	Asp	Ser	Cys
			100				105				110				
Lys	Asn	Arg	Arg	Arg	Xaa	Arg	Val	Lys	Cys	Val	Leu	Leu	Pro	Asn	Glu

GCC Ala	ACC Thr	ATT Ile	CTC Leu	ACT Thr	AAC Asn	ACC Thr	CCA Pro	ACG Thr	CTC Leu	ATG Met	GAT Asp	GAA Glu	AGA Arg	AAA Lys	AGC Ser	297
	70						75					80				
ATC Ile	ATG Met	CAA Gln	ACT Thr	TAT Tyr	GAT Asp	GTC Val	AAC Asn	CAC His	CCC Pro	CTA Leu	GAG Glu	TGT Cys	GGC Gly	GTG Val	TGC Cys	345
	85					90					95					
GAT Asp	AAG Lys	AGT Ser	GGG Gly	GAG Glu	TGC Cys	GAA Glu	TTG Leu	CAA Gln	GAC Asp	ATG Met	ACG Thr	CAT His	TTA Leu	ACC Thr	GGC Gly	393
100					105					110					115	
GTA Val	GAG Glu	CAC His	CAA Gln	CCC Pro	TAT Tyr	GCG Ala	GTG Val	GCT Ala	GAT Asp	GAT Asp	TTT Phe	AAA Lys	GCA Ala	CTG Leu	GAT Asp	441
					120				125					130		
TTT Phe	TGG Trp	GCA Ala	AAA Lys	GCC Ala	TTG Leu	TAT Tyr	GAT Asp	CCT Pro	AAT Asn	TTG Leu	TGC Cys	ATC Ile	ATG Met	TGT Cys	GAA Glu	489
			135					140					145			
AGG Arg	TGC Cys	GTA Val	ACC Thr	ACT Thr	TGT Cys	AAG Lys	GAC Asp	AAT Asn	GTG Val	GGC Gly	GAA Glu	AAC Asn	AAC Asn	CTT Leu	AAA Lys	537
			150				155					160				
GCC Ala	ACT Thr	AAA Lys	GCC Ala	GAC Asp	TTG Leu	CAT His	GCT Ala	CCG Pro	GAT Asp	AAA Lys	TTT Phe	AAA Lys	GAC Asp	AGC Ser	ATG Met	585
	165					170					175					
TCC Ser	AAA Lys	GAC Asp	GCT Ala	TTT Phe	AGC Ser	GTG Val	TGG Trp	AGT Ser	CGT Arg	AAG Lys	CAA Gln	AAA Lys	GGC Gly	ATT Ile	ATT Ile	633
180					185					190					195	
TCT Ser	TTT Phe	GTG Val	GGC Gly	AGC Ser	GTG Val	CCT Pro	TGC Cys	TAT Tyr	GAT Asp	TGC Cys	GGG Gly	GAA Glu	TGC Cys	ATT Ile	GCA Ala	681
				200					205					210		
GTA Val	TGC Cys	CCT Pro	GTG Val	GGC Gly	GCT Ala	TTG Leu	AGC Ser	TAT Tyr	AAA Lys	GAT Asp	TTC Phe	GCT Ala	TAC Tyr	ACG Thr	GCT Ala	729
			215					220					225			
AAC Asn	GCA Ala	TGG Trp	GAG Glu	TTA Leu	AAA Lys	AAG Lys	ATC Ile	CAT His	TCT Ser	ACT Thr	TGT Cys	TCG Ser	CAT His	TGC Cys	TCG Ser	777
		230					235					240				
GCC Ala	GGG Gly	TGT Cys	TTG Leu	ATT Ile	TCT Ser	TAT Tyr	GAT Asp	GTG Val	CGC Arg	CAT His	TTT Phe	GAT Asp	ACT Thr	CTA Leu	GGC Gly	825
	245					250					255					
GAA Glu	GAA Glu	TCT Ser	AAA Lys	ATT Ile	TTT Phe	AGA Arg	GTG Val	CTT Leu	AAT Asn	GAT Asp	TTT Phe	TAC Tyr	CAT His	AAC Asn	CCT Pro	873
260					265					270					275	
ATT Ile	TGT Cys	GGG Gly	GCA Ala	GGC Gly	CGT Arg	TTC Phe	GCT Ala	TTT Phe	GAT Asp	GTG Val	AGC Ser	TCT Ser	AGC Ser	CCT Pro	AAA Lys	921
				280					285					290		
GGC Gly	AGT Ser	GCT Ala	AAT Asn	CTT Leu	AAA Lys	GAA Glu	GCG Ala	CAA Gln	AAC Asn	GCC Ala	CTC Leu	AAA Lys	GAA Glu	TGC Cys	GAA Glu	969

295				300				305								
GCG Ala	GTG Val	CGA Arg 310	ATA Ile	GGT Gly	GGG Gly	GAT Asp 315	ATT Ile	ACG Thr	AAT Asn	GAA Glu	GAG Glu	GCG Ala 320	TTT Phe	TTA Leu	ATA Ile	1017
GAG Glu	CGT Arg 325	TTA Leu	AGA Arg	AAA Lys	GAG Glu	CTT Leu 330	GAT Asp	TTT Phe	AAA Lys	ATC Ile	TAC Tyr 335	AAT Asn	CAA Gln	GAA Glu	GCG Ala	1065
TAT Tyr 340	CGT Arg	TTC Phe	CAG Gln	CAA Gln 345	TTC Phe	TTA Leu	AAA Lys	GTA Val	TTG Leu	GGC Gly 350	GAA Glu	ATT Ile	AAA Lys	CGC Arg	CCC Pro 355	1113
AGC Ser	GTT Val	GAA Glu	GAG Glu 360	ATT Ile	AAA Lys	ACT Thr	TCT Ser	CAT His 365	TTA Leu	GTC Val	GTT Val	ACG Thr	ATA Ile	GGA Gly 370	TCT Ser	1161
TCT Ser	ATC Ile	AAA Lys 375	ACA Thr	GAA Glu	AAC Asn	CCT Pro	TTG Leu	GTG Val 380	CGC Arg	TAT Tyr	GCC Ala	ATC Ile 385	AAT Asn	AAC Asn	GCT Ala	1209
CTC Leu	AAA Lys 390	CTC Leu	AAT Asn	AAA Lys	GCT Ala	TCT Ser	TTA Leu 395	ATC Ile	GCT Ala	ATG Met	CAC His	CCT Pro 400	ATT Ile	AAG Lys	GAT Asp	1257
AAC Asn 405	GCG Ala	CTA Leu	GCG Ala	AAT Asn	TTG Leu	TGC Cys 410	CGA Arg	AGC Ser	TCT Ser	TTT Phe	TGC Cys 415	ATC Ile	ACC Thr	CAT His	GAA Glu	1305
GTG Val 420	GGG Gly	GCT Ala	GAA Glu	GAA Glu 425	ATC Ile	CTT Leu	TTA Leu	GGC Gly	ATG Met 430	CTT Leu	TTA Leu	AAA Lys	ATG Met	CTT Leu	AAC Asn 435	1353
ATT Ile	GAA Glu	AGC Ser	GCG Ala 440	GCC Ala	CTA Leu	AAA Lys	AGC Ser	TTA Leu	GAA Glu 445	GAT Asp	TCC Ser	AAG Lys	CAA Gln	AAT Asn 450	ATT Ile	1401
GTA Val	GAT Asp	GAA Glu 455	GCG Ala	GCT Ala	CTT Leu	AAA Lys	GCC Ala	TTA Leu 460	GAA Glu	GAA Glu	GAG Glu	CGA Arg 465	AAA Lys	AAA Lys	GCT Ala	1449
TTA Leu	GAA Glu 470	CAA Gln	GCC Ala	GAG Glu	CAA Gln	GGG Gly 475	TGC Cys	AGT Ser	ATT Ile	GGA Gly	GAA Glu 480	AAT Asn	AAG Lys	GCA Ala	GAA Glu	1497
AAT Asn 485	CAA Gln	GAA Glu	GAG Glu	AAT Asn	AAA Lys	ACA Thr 490	GAA Glu	GCG Ala	ACT Thr	ACC Thr 495	CCA Pro	AAA Lys	GAA Glu	GAA Glu	AAT Asn	1545
CAA Gln 500	GAA Glu	GAA Glu	AAC Asn	AAG Lys 505	ACA Thr	GAG Glu	GTT Val	AAA Lys	GAA Glu 510	GAA Glu	AAA Lys	ATT Ile	GAA Glu	GTC Val	CCT Pro 515	1593
ACC Thr	AAA Lys	ACC Thr	ACT Thr 520	TAT Tyr	TTG Leu	CTG Leu	CTT Leu	GAA Glu 525	GAA Glu	GCG Ala	GGC Gly	ATC Ile 530	AAT Asn	TTA Leu 530	GAA Glu	1641

ACT Thr	TAT Tyr	GAA Glu	AAA Lys 535	ATT Ile	CTG Leu	GCT Ala	CTT Leu	TTG Leu	CAA Gln	AAA Lys	TCA Ser	AAT Asn	AAC Asn 545	ACC Thr	CTG Leu	1689
CTA Leu	GTG Val	GTT Val 550	GGC Gly	GAA Glu	GAA Glu	ATC Ile	TAT Tyr 555	AGC Ser	CAT His	AAG Lys	CAA Gln	GCC Ala 560	CAC His	AAT Asn	ATC Ile	1737
GCT Ala	AAA Lys 565	ATG Met	TTG Leu	CGT Arg	TTG Leu	CTA Leu 570	GCC Ala	CAA Gln	AAA Lys	AGC Ser	GCT Ala 575	ATT Ile	AAA Lys	CTC Leu	ATT Ile	1785
CTT Leu 580	ATC Ile	CCC Pro	CCA Pro	AGC Ser	GCC Ala 585	AAC Asn	GCT Ala	TTA Leu	GGC Gly	ATC Ile 590	GCT Ala	TCT Ser	ATT Ile	TGT Cys	CAA Gln 595	1833
TTG Leu	AGC Ser	GAA Glu	GAA Glu	ATT Ile 600	TTT Phe	GAA Glu	CAT His	GAA Glu	AAA Lys 605	ATT Ile	GTA Val	GGC Gly	ATT Ile	CGC Arg 610	GCT Ala	1881
CAA Gln	GGG Gly	GAT Asp	TTC Phe 615	ACT Thr	ATC Ile	AAT Asn	AGC Ser	GAT Asp 620	GAT Asp	AGG Arg	GTT Val	TTT Phe	GGA Gly 625	AAA Lys	GAC Asp	1929
GCT Ala	GCC Ala	AGC Ser 630	AAA Lys	GTG Val	GAT Asp	TTT Phe	ATT Ile 635	TTA Leu	CCC Pro	AGT Ser	CTC Leu	AAC Asn 640	CAG Gln	CTA Leu	GAA Glu	1977
GGC Gly	ACG Thr 645	ATC Ile	ACC Thr	AAT Asn	ATT Ile	GAA Glu 650	GGG Gly	CGT Arg	GTG Val	TTG Leu	CCC Pro 655	TTA Leu	AAA Lys	CCG Pro	GCT Ala	2025
TTG Leu 660	AGG Arg	TTT Phe	GAG Glu	GGC Gly	TAT Tyr 665	GAT Asp	TTG Leu	AGC Ser	GAT Asp	ATT Ile 670	ATG Met	CAA Gln	GGC Gly	TTT Phe	GGC Gly 675	2073
TTT Phe	GTG Val	GAA Glu	GAA Glu	AAC Asn 680	CTC Leu	ATA Ile	GAA Glu	TGC Cys	ACC Thr 685	CAC His	AAA Lys	CTC Leu	CCT Pro	ACA Thr 690	GAA Glu	2121
GCG Ala	GGC Gly	TTT Phe	AAA Lys 695	GCC Ala	ATA Ile	GAA Glu	TTT Phe	GAT Asp 700	TAT Tyr	TTA Leu	ACC Thr	AAC Asn	TAT Tyr 705	TTC Phe	GCT Ala	2169
AAC Asn	GAC Asp	AGA Arg 710	GTC Val	AAC Asn	CAC His	AGA Arg	GGC Gly 715	TAT Tyr	CTG Leu	CTA Leu	GGA Gly	ACA Thr 720	AGC Ser	CAT His	TTT Phe	2217
GAA Glu	AAG Lys 725	AGC Ser	GCT Ala	AAA Lys	GAA Glu	TGC Cys 730	GAA Glu	ACC Thr	ATA Ile	GAA Glu	TGC Cys 735	GAG Glu	CCT Pro	ATC Ile	AAG Lys	2265
CCT Pro 740	TTA Leu	AAA Lys	GAA Glu	AAA Lys	ATC Ile 745	GCT Ala	TTC Phe	AAC Asn	GCG Ala	TAT Tyr 750	TTA Leu	AAA Lys	TAC Tyr	CCA Pro	GAA Glu 755	2313
ACG Thr	CAA Gln	TTC Phe	AAT Asn	AAC Asn	GCT Ala	ACT Thr	AAT Asn	AAA Lys	AGC Ser	GAG Glu	AAT Asn	TTG Leu	CAA Gln	TTA Leu	AAA Lys	2361

760												765				770				
GCC	GGT	GTC	TAT	GTG	TCT	AAA	GCT	TTC	TTA	AAG	AAA	TTG	AAT	AAA	GAA	2409				
Ala	Gly	Val	Tyr	Val	Ser	Lys	Ala	Phe	Leu	Lys	Lys	Leu	Asn	Lys	Glu					
			775						780					785						
GTG	GGG	CAA	AAC	ATC	ACT	TTA	TCT	AAA	GAA	GAA	GAG	GAA	TTA	ACA	GGC	2457				
Val	Gly	Gln	Asn	Ile	Thr	Leu	Ser	Lys	Glu	Glu	Glu	Glu	Leu	Thr	Gly					
			790						795					800						
GTT	TTG	TAT	CTT	GAT	GAG	AGC	TTG	GAT	CAG	GAA	GTG	TTT	GTT	ATC	TCG	2505				
Val	Leu	Tyr	Leu	Asp	Glu	Ser	Leu	Asp	Gln	Glu	Val	Phe	Val	Ile	Ser					
			805					810						815						
CCT	TCT	CTT	TTG	AAA	AAC	CAT	TCT	GGC	TTT	TTT	AGA	GAG	GGC	GTG	TTT	2553				
Pro	Ser	Leu	Leu	Lys	Asn	His	Ser	Gly	Phe	Phe	Arg	Glu	Gly	Val	Phe					
			820			825					830				835					
GAT	AGC	GTG	GAT	TTA	AAG	GAG	CAA	GCA	TGAGCGCTTA	TATCATTGAA	ACCCTGA					2607				
Asp	Ser	Val	Asp	Leu	Lys	Glu	Gln	Ala												
						840														
TTAAAATTTT	GATTTT															2623				

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met	Ile	Thr	Met	Asn	Ile	Asn	Gly	Lys	Thr	Ile	Glu	Cys	Gln	Glu	Gly
1				5					10					15	
Gln	Ser	Val	Leu	Glu	Ala	Ala	Arg	Ser	Ala	Gly	Ile	Tyr	Ile	Pro	Thr
			20					25					30		
Ile	Cys	Tyr	Leu	Ser	Gly	Cys	Ser	Pro	Thr	Val	Ala	Cys	Lys	Met	Cys
		35					40					45			
Met	Val	Glu	Met	Asp	Gly	Lys	Arg	Val	Tyr	Ser	Cys	Asn	Thr	Lys	Ala
		50				55					60				
Lys	Asn	Asn	Ala	Thr	Ile	Leu	Thr	Asn	Thr	Pro	Thr	Leu	Met	Asp	Glu
65					70					75				80	
Arg	Lys	Ser	Ile	Met	Gln	Thr	Tyr	Asp	Val	Asn	His	Pro	Leu	Glu	Cys
				85					90					95	
Gly	Val	Cys	Asp	Lys	Ser	Gly	Glu	Cys	Glu	Leu	Gln	Asp	Met	Thr	His
			100					105					110		
Leu	Thr	Gly	Val	Glu	His	Gln	Pro	Tyr	Ala	Val	Ala	Asp	Asp	Phe	Lys
			115				120					125			
Ala	Leu	Asp	Phe	Trp	Ala	Lys	Ala	Leu	Tyr	Asp	Pro	Asn	Leu	Cys	Ile
			130			135					140				
Met	Cys	Glu	Arg	Cys	Val	Thr	Thr	Cys	Lys	Asp	Asn	Val	Gly	Glu	Asn
145					150					155				160	
Asn	Leu	Lys	Ala	Thr	Lys	Ala	Asp	Leu	His	Ala	Pro	Asp	Lys	Phe	Lys
				165					170					175	

Asp	Ser	Met	Ser	Lys	Asp	Ala	Phe	Ser	Val	Trp	Ser	Arg	Lys	Gln	Lys
			180					185					190		
Gly	Ile	Ile	Ser	Phe	Val	Gly	Ser	Val	Pro	Cys	Tyr	Asp	Cys	Gly	Glu
		195					200					205			
Cys	Ile	Ala	Val	Cys	Pro	Val	Gly	Ala	Leu	Ser	Tyr	Lys	Asp	Phe	Ala
	210					215					220				
Tyr	Thr	Ala	Asn	Ala	Trp	Glu	Leu	Lys	Lys	Ile	His	Ser	Thr	Cys	Ser
225					230					235					240
His	Cys	Ser	Ala	Gly	Cys	Leu	Ile	Ser	Tyr	Asp	Val	Arg	His	Phe	Asp
				245					250					255	
Thr	Leu	Gly	Glu	Glu	Ser	Lys	Ile	Phe	Arg	Val	Leu	Asn	Asp	Phe	Tyr
			260					265					270		
His	Asn	Pro	Ile	Cys	Gly	Ala	Gly	Arg	Phe	Ala	Phe	Asp	Val	Ser	Ser
		275					280					285			
Ser	Pro	Lys	Gly	Ser	Ala	Asn	Leu	Lys	Glu	Ala	Gln	Asn	Ala	Leu	Lys
	290					295					300				
Glu	Cys	Glu	Ala	Val	Arg	Ile	Gly	Gly	Asp	Ile	Thr	Asn	Glu	Glu	Ala
305					310					315					320
Phe	Leu	Ile	Glu	Arg	Leu	Arg	Lys	Glu	Leu	Asp	Phe	Lys	Ile	Tyr	Asn
				325					330					335	
Gln	Glu	Ala	Tyr	Arg	Phe	Gln	Gln	Phe	Leu	Lys	Val	Leu	Gly	Glu	Ile
			340					345					350		
Lys	Arg	Pro	Ser	Val	Glu	Glu	Ile	Lys	Thr	Ser	His	Leu	Val	Val	Thr
		355					360					365			
Ile	Gly	Ser	Ser	Ile	Lys	Thr	Glu	Asn	Pro	Leu	Val	Arg	Tyr	Ala	Ile
	370					375					380				
Asn	Asn	Ala	Leu	Lys	Leu	Asn	Lys	Ala	Ser	Leu	Ile	Ala	Met	His	Pro
385					390					395					400
Ile	Lys	Asp	Asn	Ala	Leu	Ala	Asn	Leu	Cys	Arg	Ser	Ser	Phe	Cys	Ile
			405						410					415	
Thr	His	Glu	Val	Gly	Ala	Glu	Glu	Ile	Leu	Leu	Gly	Met	Leu	Leu	Lys
			420					425					430		
Met	Leu	Asn	Ile	Glu	Ser	Ala	Ala	Leu	Lys	Ser	Leu	Glu	Asp	Ser	Lys
		435					440					445			
Gln	Asn	Ile	Val	Asp	Glu	Ala	Ala	Leu	Lys	Ala	Leu	Glu	Glu	Glu	Arg
	450					455					460				
Lys	Lys	Ala	Leu	Glu	Gln	Ala	Glu	Gln	Gly	Cys	Ser	Ile	Gly	Glu	Asn
465					470					475					480
Lys	Ala	Glu	Asn	Gln	Glu	Glu	Asn	Lys	Thr	Glu	Ala	Thr	Thr	Pro	Lys
			485						490					495	
Glu	Glu	Asn	Gln	Glu	Glu	Asn	Lys	Thr	Glu	Val	Lys	Glu	Glu	Lys	Ile
			500					505					510		
Glu	Val	Pro	Thr	Lys	Thr	Thr	Tyr	Leu	Leu	Leu	Glu	Glu	Ala	Gly	Ile
		515					520					525			
Asn	Leu	Glu													

Ile Met Leu Asn Ala Ile Asn Ile Gly Phe Val Ala Ile Ser Lys Tyr	
40 45 50	
ACG CAT AAT TTA GAC GGG CAG ATG TTT GCG CTC TTT ATT ATC TCT ATT	247
Thr His Asn Leu Asp Gly Gln Met Phe Ala Leu Phe Ile Ile Ser Ile	
55 60 65	
GCC GCT AGT GAG GTG GCT ATT GGT TTG GGC TTG GTG ATT TTG TGG TTT	295
Ala Ala Ser Glu Val Ala Ile Gly Leu Gly Leu Val Ile Leu Trp Phe	
70 75 80	
AAG AAA TTC AAA AGC TTA GAT ATT GAT TCT TTA AAC GCT ATG AAA GGT T	344
Lys Lys Phe Lys Ser Leu Asp Ile Asp Ser Leu Asn Ala Met Lys Gly	
85 90 95 100	
GAGCATGCAA TATTCTTCTT TGCTGTCACT GGTG	378

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Met Ile Gly Leu Asn His Tyr Leu Ile Val Ser Gly Leu Leu Phe Cys	
1 5 10 15	
Ile Gly Leu Ala Gly Met Leu Lys Arg Lys Asn Ile Leu Leu Phe	
20 25 30	
Phe Ser Thr Glu Ile Met Leu Asn Ala Ile Asn Ile Gly Phe Val Ala	
35 40 45	
Ile Ser Lys Tyr Thr His Asn Leu Asp Gly Gln Met Phe Ala Leu Phe	
50 55 60	
Ile Ile Ser Ile Ala Ala Ser Glu Val Ala Ile Gly Leu Gly Leu Val	
65 70 75 80	
Ile Leu Trp Phe Lys Lys Phe Lys Ser Leu Asp Ile Asp Ser Leu Asn	
85 90 95	
Ala Met Lys Gly	
100	

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...627
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

CCGGT	GGAAT	AAGTC	ATG	CAA	GCA	GTG	ATT	TTA	GCG	AAT	GGG	GAG	TTT	CCT	51		
			Met	Gln	Ala	Val	Ile	Leu	Ala	Asn	Gly	Glu	Phe	Pro			
			1				5					10					
AAA	TCT	CAA	AAA	TGC	TTA	GAC	CTT	TTA	AAA	AAC	GCT	CCC	TTT	TTA	ATC	99	
Lys	Ser	Gln	Lys	Cys	Leu	Asp	Leu	Leu	Lys	Asn	Ala	Pro	Phe	Leu	Ile		
			15				20					25					
GCA	TGC	GAT	GGG	GCT	GTT	ACC	TCA	TTA	CAT	GCG	CTT	CAA	TTC	AAA	CCC	147	
Ala	Cys	Asp	Gly	Ala	Val	Thr	Ser	Leu	His	Ala	Leu	Gln	Phe	Lys	Pro		
			30				35				40						
AGC	GTT	GTT	ATA	GGC	GAT	CTA	GAT	AGC	ATT	GAT	TCG	CAT	TTG	AAA	GCT	195	
Ser	Val	Val	Ile	Gly	Asp	Leu	Asp	Ser	Ile	Asp	Ser	His	Leu	Lys	Ala		
			45			50				55					60		
TTG	TAT	AAC	CCT	ATA	CGC	ATG	AGT	GAA	CAA	AAC	AGC	AAC	GAT	TTG	TCC	243	
Leu	Tyr	Asn	Pro	Ile	Arg	Met	Ser	Glu	Gln	Asn	Ser	Asn	Asp	Leu	Ser		
				65				70						75			
AAA	GCC	TTT	TTT	TAT	GCT	TTA	AAT	AAA	GGC	TGT	GAT	GAC	TTT	ATT	TTT	291	
Lys	Ala	Phe	Phe	Tyr	Ala	Leu	Asn	Lys	Gly	Cys	Asp	Asp	Phe	Ile	Phe		
			80					85					90				
TTA	GGG	TTG	AAT	GGC	AAG	CGA	GAA	GAT	CAC	GCT	TTA	GCG	AAC	ACT	TTT	339	
Leu	Gly	Leu	Asn	Gly	Lys	Arg	Glu	Asp	His	Ala	Leu	Ala	Asn	Thr	Phe		
			95				100					105					
TTA	TTG	TTG	GAA	TAT	TTT	AAA	TTT	TGC	CAA	AAA	ATC	CAA	GCC	ATA	AGC	387	
Leu	Leu	Leu	Glu	Tyr	Phe	Lys	Phe	Cys	Gln	Lys	Ile	Gln	Ala	Ile	Ser		
			110			115					120						
GAC	TAT	GGT	CTT	TTT	AGG	GTG	TTA	GAA	ACC	CCT	TTC	ACT	TTG	CCC	AGT	435	
Asp	Tyr	Gly	Leu	Phe	Arg	Val	Leu	Glu	Thr	Pro	Phe	Thr	Leu	Pro	Ser		
			125			130				135					140		
TTT	AAA	GGG	GAA	CAA	ATC	TCG	CTT	TTT	AGC	CTG	GAT	CTT	AAA	GCC	CAA	483	
Phe	Lys	Gly	Glu	Gln	Ile	Ser	Leu	Phe	Ser	Leu	Asp	Leu	Lys	Ala	Gln		
				145					150					155			
TTC	ACT	TCT	AAA	AAC	CTC	AAA	TAC	CCC	TTA	AAA	AAC	TTG	CGT	TTA	AAA	531	
Phe	Thr	Ser	Lys	Asn	Leu	Lys	Tyr	Pro	Leu	Lys	Asn	Leu	Arg	Leu	Lys		
			160					165					170				
ACG	CTC	TTT	TCT	GGC	TCG	CTC	AAT	GAA	GCT	ACA	GAT	AGT	TAT	TTT	AGC	579	
Thr	Leu	Phe	Ser	Gly	Ser	Leu	Asn	Glu	Ala	Thr	Asp	Ser	Tyr	Phe	Ser		
			175				180					185					
CTT	AGC	TCT	ACA	CCT	AAA	TCG	GTG	GTG	TTG	GTG	TAT	CAA	AAA	TTC	TTA	T	628
Leu	Ser	Ser	Thr	Pro	Lys	Ser	Val	Val	Leu	Val	Tyr	Gln	Lys	Phe	Leu		
			190			195					200						
AAGCGGGTTT	TGTTAGGCAA	GTGTTTGTCT	GTATA													663	

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

```

Met Gln Ala Val Ile Leu Ala Asn Gly Glu Phe Pro Lys Ser Gln Lys
 1           5           10           15
Cys Leu Asp Leu Leu Lys Asn Ala Pro Phe Leu Ile Ala Cys Asp Gly
          20           25           30
Ala Val Thr Ser Leu His Ala Leu Gln Phe Lys Pro Ser Val Val Ile
          35           40           45
Gly Asp Leu Asp Ser Ile Asp Ser His Leu Lys Ala Leu Tyr Asn Pro
 50           55           60
Ile Arg Met Ser Glu Gln Asn Ser Asn Asp Leu Ser Lys Ala Phe Phe
 65           70           75           80
Tyr Ala Leu Asn Lys Gly Cys Asp Asp Phe Ile Phe Leu Gly Leu Asn
          85           90           95
Gly Lys Arg Glu Asp His Ala Leu Ala Asn Thr Phe Leu Leu Leu Glu
          100          105          110
Tyr Phe Lys Phe Cys Gln Lys Ile Gln Ala Ile Ser Asp Tyr Gly Leu
          115          120          125
Phe Arg Val Leu Glu Thr Pro Phe Thr Leu Pro Ser Phe Lys Gly Glu
          130          135          140
Gln Ile Ser Leu Phe Ser Leu Asp Leu Lys Ala Gln Phe Thr Ser Lys
          145          150          155          160
Asn Leu Lys Tyr Pro Leu Lys Asn Leu Arg Leu Lys Thr Leu Phe Ser
          165          170          175
Gly Ser Leu Asn Glu Ala Thr Asp Ser Tyr Phe Ser Leu Ser Ser Thr
          180          185          190
Pro Lys Ser Val Val Leu Val Tyr Gln Lys Phe Leu
          195          200

```

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 17...1048
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

225	230	235	
AGA CCC ATT GCT AAC ACG GAG TAT TCA GGC GAT TAC GCT CAA AGA GAT			772
Arg Pro Ile Ala Asn Thr Glu Tyr Ser Gly Asp Tyr Ala Gln Arg Asp			
240	245	250	
GAC GCT AAA GAC TTG AGC GCT AAG ATT GAA AGC ATG AAT TTG AGC GCT			820
Asp Ala Lys Asp Leu Ser Ala Lys Ile Glu Ser Met Asn Leu Ser Ala			
255	260	265	
AGG TGT TTT AAT TGC TTG GAT AAA ATC GGC ATC AAG TAT GTG GGC GAA			868
Arg Cys Phe Asn Cys Leu Asp Lys Ile Gly Ile Lys Tyr Val Gly Glu			
270	275	280	
CTC GTG TTG ATG AGC GAA GAA GAG CTT AAG GGC GTG AAA AAC ATG GGT			916
Leu Val Leu Met Ser Glu Glu Glu Leu Lys Gly Val Lys Asn Met Gly			
285	290	295	300
AAA AAA TCC TAT GAT GAA ATC GCT GAA AAA TTG AAT GAT TTG GGC TAT			964
Lys Lys Ser Tyr Asp Glu Ile Ala Glu Lys Leu Asn Asp Leu Gly Tyr			
305	310	315	
CCG GTA GGC ACA GAA TTA AGC CCT GAA CAA AGA GAG AGT TTA AAG AAA			1012
Pro Val Gly Thr Glu Leu Ser Pro Glu Gln Arg Glu Ser Leu Lys Lys			
320	325	330	
AGA TTA GAA AAA TTA GAA GAT AAA GGA GGT AAC GAC TGATGAGACA CAAACA			1064
Arg Leu Glu Lys Leu Glu Asp Lys Gly Gly Asn Asp			
335	340		
CGGATACCGC AAGCTTGGGA GAACCAGCTC GCACAGAAAG GC			1106

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Met	Lys	Val	Ile	Lys	Thr	Ala	Pro	Leu	Ile	Pro	Ser	Glu	Ile	Lys	Val
1				5					10					15	
Leu	Glu	Lys	Glu	Gly	Asn	Arg	Val	Lys	Ile	Ser	Leu	Ala	Pro	Phe	Glu
			20					25					30		
Phe	Gly	Tyr	Ala	Val	Thr	Leu	Ala	His	Pro	Ile	Arg	Arg	Leu	Leu	Leu
		35					40					45			
Leu	Ser	Ser	Val	Gly	Tyr	Ala	Pro	Val	Gly	Leu	Lys	Ile	Glu	Gly	Val
	50					55				60					
His	His	Glu	Phe	Asp	Ser	Leu	Arg	Gly	Val	Thr	Glu	Asp	Val	Ser	Leu
65					70				75					80	
Phe	Ile	Met	Asn	Leu	Lys	Asn	Ile	Arg	Phe	Ile	Ala	Lys	Ala	Leu	Val
			85					90					95		
Gly	Gln	Asp	Ser	Ser	Leu	Glu	Asn	Gln	Ser	Val	Val	Val	Asp	Tyr	Ser
			100				105						110		

(A) LENGTH: 649 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 19...621
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AAGCGTAGGG TGTTTTTA ATG ATT TTT TAT AGA AAG GAA GCT ACA ATG AAC	51
Met Ile Phe Tyr Arg Lys Glu Ala Thr Met Asn	
1 5 10	
GCA TTG AAA AAA TTA AGT TTC TGC GCC TTG TTA TCC CTA GGC CTC TTC	99
Ala Leu Lys Lys Leu Ser Phe Cys Ala Leu Leu Ser Leu Gly Leu Phe	
15 20 25	
GCT CAA ACA GCG CAT GCT AAG CAT TTA AAG GGC ACG ATT AAC TAT CCT	147
Ala Gln Thr Ala His Ala Lys His Leu Lys Gly Thr Ile Asn Tyr Pro	
30 35 40	
GAT TGG CTT GAA ATC AAT TTT TTT GAC GAA AAA AAC CCG CCC AAT CAA	195
Asp Trp Leu Glu Ile Asn Phe Phe Asp Glu Lys Asn Pro Pro Asn Gln	
45 50 55	
TAT GTC GGA TCG GCT TCA ATT TCT GGT AAA AGG AAC GAT TTT TAC GCC	243
Tyr Val Gly Ser Ala Ser Ile Ser Gly Lys Arg Asn Asp Phe Tyr Ala	
60 65 70 75	
AAT TAC ATC CCC TAT GAT GAC CAA TTG CCC CCT GAA CAA AAC GCT GAA	291
Asn Tyr Ile Pro Tyr Asp Asp Gln Leu Pro Pro Glu Gln Asn Ala Glu	
80 85 90	
AAA ATC GCT CTT TTA AGG GCC AGA ATA AAC GCT TAC AGC ACT TTA GAG	339
Lys Ile Ala Leu Leu Arg Ala Arg Ile Asn Ala Tyr Ser Thr Leu Glu	
95 100 105	
AGC ATT TTA CTC ACT AAA ATG CAC AAT CGT ATT GTT AAG GTG CTT CAA	387
Ser Ile Leu Leu Thr Lys Met His Asn Arg Ile Val Lys Val Leu Gln	
110 115 120	
GTT AAA AAT AAT GTT ATC AGC CAT TTA TTC GGG CTT GTT GAT TTT TTA	435
Val Lys Asn Asn Val Ile Ser His Leu Phe Gly Leu Val Asp Phe Leu	
125 130 135	
ACC TCT AAA TCC ATT TTG GCT AAA AGG TTC GTG GAT ACC ACA AAT CAT	483
Thr Ser Lys Ser Ile Leu Ala Lys Arg Phe Val Asp Thr Thr Asn His	
140 145 150 155	
CGT GTG TAT GTC ATG GTG CAA TTC CCT TTC ATT CAG CCT GAA GAC TTG	531
Arg Val Tyr Val Met Val Gln Phe Pro Phe Ile Gln Pro Glu Asp Leu	
160 165 170	

ATC GCT TAC TTT AAA GCC AAA CGC ATC GAC CTT TCT TCA GCG AGC GCT 579
 Ile Ala Tyr Phe Lys Ala Lys Arg Ile Asp Leu Ser Ser Ala Ser Ala
 175 180 185

ACC CAT CTC AGC GCC CTT TTA AAT AAG GCG TTG TTC CAC CTC TAAGAGTTT 630
 Thr His Leu Ser Ala Leu Leu Asn Lys Ala Leu Phe His Leu
 190 195 200

GGGATTTAAG ATGCGGTTT 649

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met	Ile	Phe	Tyr	Arg	Lys	Glu	Ala	Thr	Met	Asn	Ala	Leu	Lys	Lys	Leu
1				5					10					15	
Ser	Phe	Cys	Ala	Leu	Leu	Ser	Leu	Gly	Leu	Phe	Ala	Gln	Thr	Ala	His
			20					25					30		
Ala	Lys	His	Leu	Lys	Gly	Thr	Ile	Asn	Tyr	Pro	Asp	Trp	Leu	Glu	Ile
			35				40					45			
Asn	Phe	Phe	Asp	Glu	Lys	Asn	Pro	Pro	Asn	Gln	Tyr	Val	Gly	Ser	Ala
			50			55					60				
Ser	Ile	Ser	Gly	Lys	Arg	Asn	Asp	Phe	Tyr	Ala	Asn	Tyr	Ile	Pro	Tyr
65					70				75					80	
Asp	Asp	Gln	Leu	Pro	Pro	Glu	Gln	Asn	Ala	Glu	Lys	Ile	Ala	Leu	Leu
			85					90						95	
Arg	Ala	Arg	Ile	Asn	Ala	Tyr	Ser	Thr	Leu	Glu	Ser	Ile	Leu	Leu	Thr
			100					105					110		
Lys	Met	His	Asn	Arg	Ile	Val	Lys	Val	Leu	Gln	Val	Lys	Asn	Asn	Val
			115				120					125			
Ile	Ser	His	Leu	Phe	Gly	Leu	Val	Asp	Phe	Leu	Thr	Ser	Lys	Ser	Ile
			130			135					140				
Leu	Ala	Lys	Arg	Phe	Val	Asp	Thr	Thr	Asn	His	Arg	Val	Tyr	Val	Met
145					150				155						160
Val	Gln	Phe	Pro	Phe	Ile	Gln	Pro	Glu	Asp	Leu	Ile	Ala	Tyr	Phe	Lys
				165				170						175	
Ala	Lys	Arg	Ile	Asp	Leu	Ser	Ser	Ala	Ser	Ala	Thr	His	Leu	Ser	Ala
			180					185					190		
Leu	Leu	Asn	Lys	Ala	Leu	Phe	His	Leu							
			195				200								

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...513
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GCATGCTCTT AGAGT ATG TCT GTA TCG CAT GTT GCT TTA ATC TTA AGG AAA	51
Met Ser Val Ser His Val Ala Leu Ile Leu Arg Lys	
1 5 10	
TTG TTT TAT CAT AGA CAA GGA GTT TTT ATG GGC GGT TTT TCA GTG GGA	99
Leu Phe Tyr His Arg Gln Gly Val Phe Met Gly Gly Phe Ser Val Gly	
15 20 25	
ATG TTG AAA GAT TAT GTG GAC ATA TTT GTT TTT GCG GTG CTT GGC GTG	147
Met Leu Lys Asp Tyr Val Asp Ile Phe Val Phe Ala Val Leu Gly Val	
30 35 40	
GCC AGT TTT TTA GCT TTG TGG TTT GCG ATT GAA AGG GTT ATT TTT TAT	195
Ala Ser Phe Leu Ala Leu Trp Phe Ala Ile Glu Arg Val Ile Phe Tyr	
45 50 55 60	
TCT AAA GTC GAT TTG AAA GCT TAT GAC GAT ATA GAT GCC CTG AAT TTG	243
Ser Lys Val Asp Leu Lys Ala Tyr Asp Asp Ile Asp Ala Leu Asn Leu	
65 70 75	
GAT TTA ACC AAG AAT CTA ACC ATT CTC TAT GTG ATT TTT TCT AAC GCG	291
Asp Leu Thr Lys Asn Leu Thr Ile Leu Tyr Val Ile Phe Ser Asn Ala	
80 85 90	
CCT TAT GTG GGC TTA TTA GGG ACG GTT TTA GGG ATT ATG GTG ATT TTC	339
Pro Tyr Val Gly Leu Leu Gly Thr Val Leu Gly Ile Met Val Ile Phe	
95 100 105	
TAT GAC ATG GGC GTG AGC GGC GGG ATG GAC GCT AAA ACG ATC ATG GTA	387
Tyr Asp Met Gly Val Ser Gly Gly Met Asp Ala Lys Thr Ile Met Val	
110 115 120	
GGT TTG TCT TTG GCT TTA AAA GCG ACC GCT CTA GGG CTT GCT GTG GCG	435
Gly Leu Ser Leu Ala Leu Lys Ala Thr Ala Leu Gly Leu Ala Val Ala	
125 130 135 140	
ATT CCC ACT TTG ATC GCT TAT AAT AGC TTG TTG AGA AAA TCC GAT GTT	483
Ile Pro Thr Leu Ile Ala Tyr Asn Ser Leu Leu Arg Lys Ser Asp Val	
145 150 155	
TTG AGC GAA AAA TTC AGG ATC ATG AAA AAA TGAAAAGCAT CAGAAGAGGC GAT	536
Leu Ser Glu Lys Phe Arg Ile Met Lys Lys	
160 165	
GGGC	540

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Met	Ser	Val	Ser	His	Val	Ala	Leu	Ile	Leu	Arg	Lys	Leu	Phe	Tyr	His
1				5					10					15	
Arg	Gln	Gly	Val	Phe	Met	Gly	Gly	Phe	Ser	Val	Gly	Met	Leu	Lys	Asp
			20					25					30		
Tyr	Val	Asp	Ile	Phe	Val	Phe	Ala	Val	Leu	Gly	Val	Ala	Ser	Phe	Leu
		35					40					45			
Ala	Leu	Trp	Phe	Ala	Ile	Glu	Arg	Val	Ile	Phe	Tyr	Ser	Lys	Val	Asp
		50				55					60				
Leu	Lys	Ala	Tyr	Asp	Asp	Ile	Asp	Ala	Leu	Asn	Leu	Asp	Leu	Thr	Lys
65					70					75					80
Asn	Leu	Thr	Ile	Leu	Tyr	Val	Ile	Phe	Ser	Asn	Ala	Pro	Tyr	Val	Gly
				85					90					95	
Leu	Leu	Gly	Thr	Val	Leu	Gly	Ile	Met	Val	Ile	Phe	Tyr	Asp	Met	Gly
			100					105					110		
Val	Ser	Gly	Gly	Met	Asp	Ala	Lys	Thr	Ile	Met	Val	Gly	Leu	Ser	Leu
		115					120					125			
Ala	Leu	Lys	Ala	Thr	Ala	Leu	Gly	Leu	Ala	Val	Ala	Ile	Pro	Thr	Leu
		130				135					140				
Ile	Ala	Tyr	Asn	Ser	Leu	Leu	Arg	Lys	Ser	Asp	Val	Leu	Ser	Glu	Lys
145					150					155					160
Phe	Arg	Ile	Met	Lys	Lys										
				165											

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...723
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

TCATGAATTA	AACCCTAGCG	AACA	ATG	AAG	CTT	TTT	GAC	TAC	GCT	CCT	TTG		51			
			Met	Lys	Leu	Phe	Asp	Tyr	Ala	Pro	Leu					
			1				5									
AGT	TTG	GCT	TGG	CGG	GAG	TTT	TTG	CAA	AGC	GAA	TTT	AAA	AAG	CCT	TAT	99
Ser	Leu	Ala	Trp	Arg	Glu	Phe	Leu	Gln	Ser	Glu	Phe	Lys	Lys	Pro	Tyr	
10				15					20					25		

[illegible]

(i) SEQUENCE CHARACTERISTICS:

-429-

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

```

Met Lys Leu Phe Asp Tyr Ala Pro Leu Ser Leu Ala Trp Arg Glu Phe
 1          5          10          15
Leu Gln Ser Glu Phe Lys Lys Pro Tyr Phe Leu Glu Ile Glu Lys Arg
 20          25          30
Tyr Leu Glu Ala Leu Lys Ile Pro Lys Thr Ile Phe Pro Lys Ser Ser
 35          40          45
Asn Leu Phe Tyr Ala Leu Asn Leu Thr Pro Pro Cys Ala Val Lys Ile
 50          55          60
Ile Leu Leu Gly Gln Asp Pro Tyr His Ser Thr Tyr Leu Glu Asn Asp
 65          70          75          80
Gln Glu Leu Pro Val Ala Met Gly Leu Ser Phe Ser Val Glu Lys Asn
 85          90          95
Ala Pro Ile Pro Pro Ser Leu Lys Asn Ile Phe Lys Glu Leu His Ala
100          105          110
Asn Leu Gly Val Pro Val Pro Cys Gly Asp Leu Ser Ala Trp Ala
115          120          125
Lys Arg Gly Met Leu Leu Leu Asn Ala Ile Leu Ser Val Glu Lys Asn
130          135          140
Gln Ala Ala Ser His Gln Tyr Ile Gly Trp Glu Ala Phe Ser Asp Gln
145          150          155          160
Ile Leu Met Arg Leu Phe Glu Thr Thr Ala Pro Leu Ile Val Val Leu
165          170          175
Leu Gly Lys Val Ala Gln Lys Lys Ile Ala Leu Ile Pro Lys Asn Lys
180          185          190
His Ile Ile Ile Thr Ala Pro His Pro Ser Pro Leu Ser Arg Gly Phe
195          200          205
Leu Gly Ser Gly Val Phe Thr Ser Val Gln Lys Ala Tyr Arg Glu Val
210          215          220
Tyr Arg Lys Asp Phe Asp Phe Ser Leu
225          230

```

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1179
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

AAGAAGAAAT AAAAAGCTC ATG GGG TTT TTA TTT GAA AAA TCG TTA ATG AGT

51

Met Gly Phe Leu Phe Glu Lys Ser Leu Met Ser																
1 5 10																
TTT	TTC	GCT	CAT	CCA	ATC	AAA	ATC	CTT	AAA	ATC	ATC	AGT	TTG	ATT	TTA	99
Phe	Phe	Ala	His	Pro	Ile	Lys	Ile	Leu	Lys	Ile	Ile	Ser	Leu	Ile	Leu	
15 20 25																
AGT	TTT	TTG	GTA	AGC	TTT	TTG	GTT	GCT	GAA	AAC	GCT	CAT	GAG	CCA	GAA	147
Ser	Phe	Leu	Val	Ser	Phe	Leu	Val	Ala	Glu	Asn	Ala	His	Glu	Pro	Glu	
30 35 40																
GAA	ATC	AAG	GCT	AAA	GTG	GCT	TAT	GTG	AAA	ATC	CCC	CAA	TTA	GAA	GAT	195
Glu	Ile	Lys	Ala	Lys	Val	Ala	Tyr	Val	Lys	Ile	Pro	Gln	Leu	Glu	Asp	
45 50 55																
TTG	GAA	AAC	AAC	CCG	GTT	TAT	ATC	GGT	CAA	ATT	ATA	GGC	GTA	ACT	TAT	243
Leu	Glu	Asn	Asn	Pro	Val	Tyr	Ile	Gly	Gln	Ile	Ile	Gly	Val	Thr	Tyr	
60 65 70 75																
GAT	TTA	TTG	CTG	TTT	GAC	GCT	GAG	TTT	TTG	GAA	GCC	AAA	ATC	AAA	GAC	291
Asp	Leu	Leu	Leu	Phe	Asp	Ala	Glu	Phe	Leu	Glu	Ala	Lys	Ile	Lys	Asp	
80 85 90																
GGG	TTG	GAT	AAA	ACC	CAA	ATT	GAG	CTT	TTA	AAC	AAG	ATG	CCT	AAA	TGG	339
Gly	Leu	Asp	Lys	Thr	Gln	Ile	Glu	Leu	Leu	Asn	Lys	Met	Pro	Lys	Trp	
95 100 105																
AAA	AAG	GTG	GAA	AAA	GAG	CTT	TTC	AGA	GCG	ACT	TAT	TAT	TAC	AAG	ATT	387
Lys	Lys	Val	Glu	Lys	Glu	Leu	Phe	Arg	Ala	Thr	Tyr	Tyr	Tyr	Lys	Ile	
110 115 120																
AAG	GGC	ATA	AAA	GCG	ATT	ATT	CCG	TCC	TTA	GAA	GTG	AGC	GCG	TTT	TCC	435
Lys	Gly	Ile	Lys	Ala	Ile	Ile	Pro	Ser	Leu	Glu	Val	Ser	Ala	Phe	Ser	
125 130 135																
AAT	AAA	GAC	AAA	TAC	ATA	GAT	CAT	TCC	ATA	GCC	CCA	AAA	GTT	ACT	TTG	483
Asn	Lys	Asp	Lys	Tyr	Ile	Asp	His	Ser	Ile	Ala	Pro	Lys	Val	Thr	Leu	
140 145 150 155																
CAG	GTA	ACG	GAT	TTG	TCC	AAA	AAC	CCT	CGT	TAT	GCG	AAT	GTC	ATG	GCT	531
Gln	Val	Thr	Asp	Leu	Ser	Lys	Asn	Pro	Arg	Tyr	Ala	Asn	Val	Met	Ala	
160 165 170																
AAA	GAT	TTA	CAA	GTC	TTG	CAA	TAC	AAA	ACC	AAA	GAT	TAT	GAC	GAT	AAA	579
Lys	Asp	Leu	Gln	Val	Leu	Gln	Tyr	Lys	Thr	Lys	Asp	Tyr	Asp	Asp	Lys	
175 180 185																
AAC	AAT	ATT	TTG	GTG	ATG	GAA	ATA	GCG	TTC	AAA	GAA	GCC	ACT	TGG	GAA	627
Asn	Asn	Ile	Leu	Val	Met	Glu	Ile	Ala	Phe	Lys	Glu	Ala	Thr	Trp	Glu	
190 195 200																
GAT	TTT	CAC	ATC	AAA	GAA	GCG	ATC	AAG	CAA	GGG	TTT	GAT	AAC	GCC	TCT	675
Asp	Phe	His	Ile	Lys	Glu	Ala	Ile	Lys	Gln	Gly	Phe	Asp	Asn	Ala	Ser	
205 210 215																
TTA	AAC	CAG	ATC	AAG	GCT	AAA	GAA	GGG	AGC	GTT	TTT	TAT	TAT	TGC	GTG	723
Leu	Asn	Gln	Ile	Lys	Ala	Lys	Glu	Gly	Ser	Val	Phe	Tyr	Tyr	Cys	Val	
220 225 230 235																

Phe	Leu	Val	Ala	Glu	Asn	Ala	His	Glu	Pro	Glu	Glu	Ile	Lys	Ala	Lys
		35					40					45			
Val	Ala	Tyr	Val	Lys	Ile	Pro	Gln	Leu	Glu	Asp	Leu	Glu	Asn	Asn	Pro
	50					55					60				
Val	Tyr	Ile	Gly	Gln	Ile	Ile	Gly	Val	Thr	Tyr	Asp	Leu	Leu	Leu	Phe
65					70					75					80
Asp	Ala	Glu	Phe	Leu	Glu	Ala	Lys	Ile	Lys	Asp	Gly	Leu	Asp	Lys	Thr
				85					90					95	
Gln	Ile	Glu	Leu	Leu	Asn	Lys	Met	Pro	Lys	Trp	Lys	Lys	Val	Glu	Lys
			100					105					110		
Glu	Leu	Phe	Arg	Ala	Thr	Tyr	Tyr	Tyr	Lys	Ile	Lys	Gly	Ile	Lys	Ala
		115						120				125			
Ile	Ile	Pro	Ser	Leu	Glu	Val	Ser	Ala	Phe	Ser	Asn	Lys	Asp	Lys	Tyr
	130					135					140				
Ile	Asp	His	Ser	Ile	Ala	Pro	Lys	Val	Thr	Leu	Gln	Val	Thr	Asp	Leu
145					150					155					160
Ser	Lys	Asn	Pro	Arg	Tyr	Ala	Asn	Val	Met	Ala	Lys	Asp	Leu	Gln	Val
				165					170					175	
Leu	Gln	Tyr	Lys	Thr	Lys	Asp	Tyr	Asp	Asp	Lys	Asn	Asn	Ile	Leu	Val
			180					185					190		
Met	Glu	Ile	Ala	Phe	Lys	Glu	Ala	Thr	Trp	Glu	Asp	Phe	His	Ile	Lys
		195					200					205			
Glu	Ala	Ile	Lys	Gln	Gly	Phe	Asp	Asn	Ala	Ser	Leu	Asn	Gln	Ile	Lys
	210					215					220				
Ala	Lys	Glu	Gly	Ser	Val	Phe	Tyr	Tyr	Cys	Val	Leu	Pro	Lys	Thr	Ile
225					230					235					240
Gln	Asn	Leu	Ser	Phe	Asp	Tyr	Phe	Ser	Leu	Ser	Asn	Lys	Gln	Phe	Lys
				245					250					255	
Thr	Leu	Ser	Phe	Ser	Thr	Ile	Pro	Thr	Gln	Asp	Thr	Thr	Gly	Ile	Gln
			260					265					270		
Ser	Asp	Leu	Ile	Pro	Lys	Asn	Asn	Phe	Leu	Val	Phe	Ser	Asn	Val	Ala
		275					280						285		
Leu	Leu	Ala	Leu	Cys	Val	Phe	Phe	Leu	Val	Leu	Phe	Phe	Ile	Phe	Gly
	290					295					300				
Arg	Lys	Leu	Ile	Phe	Leu	Gly	Leu	Gly	Ile	Leu	Cys	Leu	Gly	Phe	Val
305					310					315					320
Leu	Tyr	His	Leu	Leu	Phe	Thr	Gln	Lys	Ser	Ala	Leu	Leu	Leu	Ala	His
				325					330					335	
Lys	Lys	Ile	Arg	Ile	Leu	Pro	Thr	Gln	Asn	Ser	Thr	Ile	Leu	Gly	Leu
			340					345					350		
Ser	Lys	Asn	Glu	Met	Pro	Ile	Lys	Ile	Leu	Gly	Ser	His	Asp	Asp	Tyr
		355					360					365			
Tyr	Lys	Ile	Leu	Thr	Pro	His	Glu	Gln	Ile	Gly	Trp	Val	Lys	Lys	Asp
	370					375					380				
Glu	Val	Lys													
385															

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

AAG Lys 200	ATT Ile	AAA Lys	GAA Glu	ACC Thr	CCT Pro 205	TAT Tyr	CTG Leu	TAT Tyr	GTG Val	AGA Arg 210	GTG Val	AGT Ser	GGT Gly	TTT Phe	GAC Asp 215	678
AAG Lys	AAT Asn	GTT Val	ACC Thr	AAA Lys 220	TCG Ser	GTT Val	TTA Leu	GAA Glu	GGC Gly 225	TTA Leu	AAA Lys	GCT Ala	AAC Asn	CCT Pro 230	AAG Lys	726
GCT Ala	AAG Lys	GGG Gly	ATC Ile 235	GTG Val	TTG Leu	GAT Asp	TTA Leu	AGG Arg 240	GGC Gly	AAT Asn	CCT Pro	GGA Gly	GGG Gly 245	CTA Leu	TTA Leu	774
AAC Asn	CAA Gln	GCG Ala 250	GTG Val	GGC Gly	TTG Leu	TCT Ser	AAC Asn 255	CTC Leu	TTC Phe	ATT Ile	AAA Lys	GAG Glu 260	GGG Gly	GTT Val	TTA Leu	822
GTC Val	TCT Ser 265	CAA Gln	AAA Lys	GGC Gly	AAA Lys	AAT Asn 270	AAA Lys	GAA Glu	GAA Glu	AAT Asn	TTA Leu 275	GAA Glu	TAC Tyr	AAG Lys	GCT Ala	870
AAC Asn 280	GGC Gly	AGA Arg	GCC Ala	CCT Pro	TAT Tyr 285	ACC Thr	AAT Asn	TTG Leu	CCT Pro	ATT Ile 290	GCG Ala	GTG Val	TTA Leu	GTC Val	AAT Asn 295	918
GGC Gly	GGT Gly	TCA Ser	GCG Ala	AGC Ser 300	GCG Ala	AGC Ser	GAG Glu	ATC Ile	GTC Val 305	GCA Ala	GGG Gly	GCA Ala	CTG Leu	CAA Gln 310	GAT Asp	966
CAC His	AAA Lys	CGG Arg	GCC Ala 315	GTG Val	ATT Ile	ATC Ile	GGT Gly	GAA Glu 320	AAA Lys	ACC Thr	TTT Phe	GGT Gly	AAG Lys 325	GGA Gly	AGC Ser	1014
GTG Val	CAG Gln 330	ATG Met	CTG Leu	CTC Leu	CCT Pro	GTC Val	AAT Asn 335	AAA Lys	GAC Asp	GAA Glu	GCC Ala	ATT Ile 340	AAA Lys	ATC Ile	ACA Thr	1062
ACC Thr	GCA Ala 345	CGC Arg	TAC Tyr	TAT Tyr	TTG Leu	CCG Pro 350	AGC Ser	GGG Gly	CGT Arg	ACC Thr	ATT Ile 355	CAA Gln	GCT Ala	AAG Lys	GGG Gly	1110
ATC Ile 360	ACG Thr	CCT Pro	GAT Asp	ATT Ile	GTG Val 365	ATT Ile	TAT Tyr	CCG Pro	GGT Gly	AAA Lys 370	GTG Val	CCA Pro	GAA Glu	AAT Asn	GAA Glu 375	1158
AAC Asn	AAA Lys	TTC Phe	AGC Ser	TTG Leu 380	AAA Lys	GAA Glu	GCG Ala	GAT Asp	CTA Leu 385	AAA Lys	CAC His	CAT His	TTA Leu	GAG Glu 390	CAA Gln	1206
GAG Glu	CTT Leu	AAA Lys	AAG Lys 395	ATT Ile	GAT Asp	GAT Asp	AAA Lys	ACC Thr 400	CCC Pro	AAT Asn	TCC Ser	AAA Lys	GAG Glu 405	GCG Ala	GAT Asp	1254
AAA Lys	GAC Asp	AAG Lys 410	AAA Lys	AAC Asn	GAA Glu	GAG Glu	GAA Glu 415	AAA Lys	GAG Glu	ATT Ile	ACT Thr	CCT Pro 420	AAA Lys	ATG Met	ATC Ile	1302
AAC Asn	GAT Asp	GAT Asp	ATT Ile	CAG Gln	CTA Leu	AAA Lys	ACC Thr	GCT Ala	ATT Ile	GAC Asp	AGC Ser	TTG Leu	AAA Lys	ACC Thr	TGG Trp	1350

425

430

435

TCT ATC GTT GAT GAG AAA ATG GAT GAA AAA GCG CCT AAG AAG AAA TAAAA 1400
 Ser Ile Val Asp Glu Lys Met Asp Glu Lys Ala Pro Lys Lys Lys
 440 445 450

ACTCATGGGG TTTTATTTG AAAAATCGTT AATGAGTTTT TTCGCTCATC CAATC 1455

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Met	Thr	Lys	Arg	Leu	Phe	Lys	Gly	Leu	Leu	Ala	Val	Ser	Leu	Ala	Val	1	5	10	15
Ser	Leu	His	Gly	Glu	Val	Lys	Glu	Lys	Lys	Pro	Val	Lys	Pro	Val		20	25	30	
Lys	Glu	Asp	Pro	Gln	Glu	Leu	Ala	Ala	Lys	Arg	Val	Glu	Ala	Phe	Ser	35	40	45	
Arg	Phe	Ser	Asn	Val	Val	Ser	Glu	Ile	Glu	Lys	Lys	Tyr	Val	Asp	Lys	50	55	60	
Ile	Ser	Ile	Ser	Glu	Ile	Met	Thr	Lys	Ala	Ile	Glu	Gly	Leu	Leu	Ser	65	70	75	80
Asn	Leu	Asp	Ala	His	Ser	Ala	Tyr	Leu	Asn	Glu	Lys	Lys	Phe	Lys	Glu	85	90	95	
Phe	Gln	Ala	Gln	Thr	Glu	Gly	Glu	Phe	Gly	Gly	Leu	Gly	Ile	Thr	Val	100	105	110	
Gly	Met	Arg	Asp	Gly	Val	Leu	Thr	Val	Ile	Ala	Pro	Leu	Glu	Gly	Thr	115	120	125	
Pro	Ala	Tyr	Lys	Ala	Gly	Val	Lys	Ser	Gly	Asp	Asn	Ile	Leu	Lys	Ile	130	135	140	
Asn	Asn	Glu	Ser	Thr	Leu	Ser	Met	Ser	Ile	Asp	Asp	Ala	Ile	Asn	Leu	145	150	155	160
Met	Arg	Gly	Lys	Pro	Lys	Thr	Pro	Ile	Gln	Ile	Thr	Val	Val	Arg	Lys	165	170	175	
Asn	Glu	Pro	Lys	Pro	Leu	Val	Phe	Asn	Ile	Ile	Arg	Asp	Ile	Ile	Lys	180	185	190	
Leu	Pro	Ser	Val	Tyr	Val	Lys	Lys	Ile	Lys	Glu	Thr	Pro	Tyr	Leu	Tyr	195	200	205	
Val	Arg	Val	Ser	Gly	Phe	Asp	Lys	Asn	Val	Thr	Lys	Ser	Val	Leu	Glu	210	215	220	
Gly	Leu	Lys	Ala	Asn	Pro	Lys	Ala	Lys	Gly	Ile	Val	Leu	Asp	Leu	Arg	225	230	235	240
Gly	Asn	Pro	Gly	Gly	Leu	Leu	Asn	Gln	Ala	Val	Gly	Leu	Ser	Asn	Leu	245	250	255	
Phe	Ile	Lys	Glu	Gly	Val	Leu	Val	Ser	Gln	Lys	Gly	Lys	Asn	Lys	Glu	260	265	270	
Glu	Asn	Leu	Glu	Tyr	Lys	Ala	Asn	Gly	Arg	Ala	Pro	Tyr	Thr	Asn	Leu	275	280	285	
Pro	Ile	Ala	Val	Leu	Val	Asn	Gly	Gly	Ser	Ala	Ser	Ala	Ser	Glu	Ile	290	295	300	

GGT Gly 75	TGG Trp	TTG Leu	AAA Lys	GAA Glu	TGC Cys 80	CAA Gln	AGG Arg	ATT Ile	TTA Leu	AAA Lys 85	GAT Asp	AAT Asn	GGC Gly	AGT Ser	ATT Ile 90	291
TGT Cys	GTG Val	ATA Ile	GGG Gly	AGT Ser 95	TTT Phe	CAA Gln	AAT Asn	ATT Ile	TTT Phe 100	AGA Arg	ATT Ile	GGT Gly	TTT Phe	CAT His 105	TTG Leu	339
CAA Gln	AAT Asn	TTA Leu	GGG Gly 110	TTT Phe	TGG Trp	ATA Ile	CTC Leu	AAT Asn 115	GAT Asp	ATT Ile	ATT Ile	TGG Trp	CAC His 120	AAG Lys	AGT Ser	387
AAT Asn	CCG Pro	GTG Val 125	CCT Pro	AAT Asn	TTT Phe	GCT Ala	GGC Gly 130	AAG Lys	AGA Arg	TTA Leu	TGC Cys	AAC Asn 135	GCC Ala	CAT His	GAG Glu	435
ACG Thr	CTT Leu 140	ATT Ile	TGG Trp	TGT Cys	GCT Ala	AAA Lys 145	CAC His	AAA Lys	AAC Asn	AGC Ser	AAA Lys 150	GTT Val	GCC Ala	TTT Phe	AAT Asn	483
TAT Tyr 155	AAA Lys	ACA Thr	ATG Met	AAG Lys	TAC Tyr 160	CTC Leu	AAT Asn	AAC Asn	GAC Asp	AAA Lys 165	CAA Gln	GAA Glu	AAA Lys	TCG Ser	GTT Val 170	531
TGG Trp	CAA Gln	ATC Ile	CCT Pro	ATT Ile 175	TGC Cys	ATG Met	GGT Gly	AAC Asn	GAA Glu 180	AGA Arg	CTA Leu	AAA Lys	GAT Asp	GCG Ala 185	CAA Gln	579
GGT Gly	AAA Lys	AAA Lys	GTG Val 190	CAT His	TCC Ser	ACG Thr	CAA Gln	AAA Lys 195	CCA Pro	GAA Glu	GCG Ala	CTT Leu	TTA Leu 200	AAA Lys	AAA Lys	627
ATC Ile	ATT Ile	TTA Leu 205	AGC Ser	GCG Ala	ACT Thr	AAA Lys	CCT Pro 210	AAA Lys	GAT Asp	ATT Ile	ATT Ile	TTA Leu 215	GAT Asp	CCC Pro	TTT Phe	675
TTT Phe	GGC Gly 220	ACA Thr	GGC Gly	ACA Thr	ACA Thr	GGG Gly 225	GCT Ala	GTG Val	GCT Ala	AAA Lys	TCC Ser 230	ATG Met	AAC Asn	AGG Arg	TAT Tyr	723
TTT Phe 235	ATT Ile	GGT Gly	ATT Ile	GAA Glu	AAA Lys 240	GAT Asp	TCT Ser	TTT Phe	TAT Tyr	ATT Ile 245	AAA Lys	GAA Glu	GCG Ala	GCA Ala	AAA Lys 250	771
CGC Arg	CTG Leu	AAT Asn	AAC Asn	ACT Thr 255	AGG Arg	GAT Asp	AAA Lys	AGC Ser	GAT Asp 260	TTT Phe	ATC Ile	ACT Thr	AAT Asn	TTA Leu 265	GAT Asp	819
TTA Leu	GAA Glu	ACT Thr	AAA Lys 270	CCC Pro	CCA Pro	AAA Lys	ATA Ile	CCT Pro 275	ATG Met	AGT Ser	CTT Leu	TTA Leu	ATT Ile	TCT Ser	AAA Lys	867
CAA Gln	TTA Leu	TTA Leu 285	AAA Lys	ATC Ile	GGG Gly	GAT Asp	TTT Phe 290	TTA Leu	TAC Tyr	TCA Ser	CCT Pro	AAC Asn 295	AAA Lys	GAA Glu	AAA Lys	915
ATT Ile	TGT Cys	CAA Gln	GTT Val	TTA Leu	GAA Glu	AAC Asn	GGA Gly	CAA Gln	GTG Val	AGG Arg	GAT Asp	AAT Asn	GAA Glu	AAC Asn	TAT Tyr	963

GCA Ala	AGC Ser	CCC Pro 90	ATA Ile	GAT Asp	AAT Asn	ATT Ile	GAA Glu 95	GCC Ala	TAT Tyr	GTG Val	GAA Glu	GAG Glu 100	ATT Ile	AAA Lys	AAC Asn	342
GCT Ala	TCC Ser 105	ATT Ile	AAA Lys	CGA Arg	AAA Lys	CTT Leu 110	TTT Phe	GGC Gly	TTG Leu	GCT Ala	AAC Asn 115	ACC Thr	ATT Ile	AGA Arg	GAG Glu	390
CAA Gln 120	GCC Ala	CTA Leu	GAA Glu	AGC Ser	GCG Ala 125	CAA Gln	AAA Lys	TCC Ser	AGC Ser	GAT Asp 130	ATT Ile	TTA Leu	GGC Gly	GCT Ala	GTG Val 135	438
GAG Glu	CGA Arg	GAA Glu	GTC Val	TAT Tyr 140	GCG Ala	TTA Leu	TTG Leu	AAT Asn	GGC Gly 145	AGC Ser	ACC Thr	ATA Ile	GAA Glu	GGC Gly	TTT Phe	486
AGG Arg	AAT Asn	ATT Ile	AAA Lys 155	GAA Glu	GTG Val	CTT Leu	GAA Glu	AGC Ser 160	GCA Ala	ATG Met	GAT Asp	CTC Leu	ATT Ile	ACA Thr	GAA Glu	534
AAC Asn	CAA Gln 170	AGA Arg	AAG Lys	GGG Gly	AGT Ser	TTG Leu	GAA Glu 175	GTT Val	ACT Thr	GGC Gly	ATA Ile	CCG Pro 180	ACT Thr	GGC Gly	TTT Phe	582
GTC Val 185	CAA Gln	TTG Leu	GAT Asp	AAC Asn	TAT Tyr 190	ACG Thr	AGC Ser	GGT Gly	TTC Phe	AAT Asn	AAG Lys 195	GGG Gly	AGT Ser	TTA Leu	GTC Val	630
ATT Ile 200	ATA Ile	GGG Gly	GCA Ala	AGG Arg	CCG Pro 205	TCT Ser	ATG Met	GGT Gly	AAA Lys	ACT Thr 210	AGT Ser	TTG Leu	ATG Met	ATG Met	AAC Asn 215	678
ATG Met	GTC Val	TTA Leu	AGC Ser	GCG Ala 220	CTC Leu	AAT Asn	GAC Asp	GAT Asp	AGG Arg 225	GGG Gly	GTA Val	GCG Ala	GTT Val	TTT Phe	AGT Ser	726
TTA Leu	GAA Glu	ATG Met	TCC Ser 235	GCA Ala	GAG Glu	CAA Gln	CTC Leu	GCT Ala 240	TTA Leu	AGG Arg	GCG Ala	TTA Leu	TCG Ser	GAT Asp	CTC Leu	774
ACC Thr	TCT Ser	ATT Ile 250	AAC Asn	ATG Met	CAT His	GAT Asp	TTA Leu 255	GAA Glu	AGC Ser	GGG Gly	AGG Arg	CTT Leu 260	GAT Asp	GAT Asp	GAT Asp	822
CAA Gln 265	TGG Trp	GAA Glu	AAT Asn	TTA Leu	GCC Ala 270	AAA Lys	TGC Cys	TTT Phe	GAT Asp	CAC His	CTT Leu 275	TCG Ser	CAA Gln	AAA Lys	AAA Lys	870
CTC Leu 280	TTT Phe	TTC Phe	TAC Tyr	GAT Asp	AAA Lys 285	AGT Ser	TAT Tyr	GTG Val	AGG Arg	ATA Ile 290	GAG Glu	CAA Gln	ATC Ile	CGC Arg	TTG Leu 295	918
CAA Gln	CTA Leu	CGA Arg	AAG Lys	CTT Leu 300	AAA Lys	TCC Ser	CAA Gln	CAC His	AAG Lys 305	GAA Glu	TTG Leu	GGT Gly	ATC Ile	GCT Ala 310	TTT Phe	966
ATT Ile	GAC Asp	TAT Tyr	TTG Leu	CAG Gln	CTC Leu	ATG Met	TCA Ser	GGG Gly	AGT Ser	AAA Lys	GCC Ala	ACT Thr	AAA Lys	GAG Glu	CGC Arg	1014

315	320	325	
CAT GAG CAA ATC GCT GAA ATT TCA AGG GAG CTT AAA ACT TTA GCC AGA His Glu Gln Ile Ala Glu Ile Ser Arg Glu Leu Lys Thr Leu Ala Arg 330 335 340			1062
GAA TTA GAA ATC CCT ATC ATA GCG TTA GTG CAA CTC AAC CGC AGC CTA Glu Leu Glu Ile Pro Ile Ile Ala Leu Val Gln Leu Asn Arg Ser Leu 345 350 355			1110
GAA AAC CGA GAC GAT AAA CGG CCC ATT CTT TCG GAT ATC AAA GAC AGC Glu Asn Arg Asp Asp Lys Arg Pro Ile Leu Ser Asp Ile Lys Asp Ser 360 365 370 375			1158
GGG GGG ATT GAA CAA GAC GCT GAT ATT GTT TTA TTT TTA TAT AGA GGC Gly Gly Ile Glu Gln Asp Ala Asp Ile Val Leu Phe Leu Tyr Arg Gly 380 385 390			1206
TAT ATC TAT CAA ATG AGG GCT GAA GAC AAC AAA ATA GAC AAA CTC AAA Tyr Ile Tyr Gln Met Arg Ala Glu Asp Asn Lys Ile Asp Lys Leu Lys 395 400 405			1254
AAA GAA GGT AAA ATT GAA GAG GCG CAA GAG TTG TAC TTA AAA GTT AAT Lys Glu Gly Lys Ile Glu Glu Ala Gln Glu Leu Tyr Leu Lys Val Asn 410 415 420			1302
GAA GAA AGG CGT ATC CAC AAG CAA AAT GGC AGC ATT GAA GAG GCT GAA Glu Glu Arg Arg Ile His Lys Gln Asn Gly Ser Ile Glu Glu Ala Glu 425 430 435			1350
ATC ATT GTG GCT AAA AAC AGG AAT GGG GCT ACA GGA ACG GTT TAT ACG Ile Ile Val Ala Lys Asn Arg Asn Gly Ala Thr Gly Thr Val Tyr Thr 440 445 450 455			1398
CGC TTT AAC GCT CCT TTC ACG CGC TAT GAA GAC ATG CCC ATA GAT TCC Arg Phe Asn Ala Pro Phe Thr Arg Tyr Glu Asp Met Pro Ile Asp Ser 460 465 470			1446
CAT TTA GAA GAA GGG CAA GAA ACT AAA GTG GAT TAT GAT ATA GTT ACA His Leu Glu Glu Gly Gln Glu Thr Lys Val Asp Tyr Asp Ile Val Thr 475 480 485			1494
ACT TGAAAGACAA AACTTTTTCAG GGGGCGTTTG AACTTCTTA Thr			1536

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Met	Asp	His	Leu	Lys	His	Leu	Gln	Gln	Leu	Gln	Asn	Ile	Glu	Arg	Ile
1				5				10						15	
Val	Leu	Ser	Gly	Ile	Val	Leu	Ala	Asn	His	Lys	Ile	Glu	Glu	Val	His
			20					25					30		
Ser	Val	Leu	Glu	Pro	Ser	Asp	Phe	Tyr	Tyr	Pro	Pro	Asn	Gly	Leu	Phe
		35					40					45			
Phe	Glu	Ile	Ala	Leu	Lys	Leu	His	Glu	Glu	Asp	Cys	Pro	Ile	Asp	Glu
	50					55					60				
Asn	Phe	Ile	Arg	Gln	Lys	Met	Pro	Lys	Asp	Lys	Gln	Ile	Lys	Glu	Glu
65					70					75					80
Asp	Leu	Val	Ala	Ile	Phe	Ala	Ala	Ser	Pro	Ile	Asp	Asn	Ile	Glu	Ala
				85					90					95	
Tyr	Val	Glu	Glu	Ile	Lys	Asn	Ala	Ser	Ile	Lys	Arg	Lys	Leu	Phe	Gly
			100					105					110		
Leu	Ala	Asn	Thr	Ile	Arg	Glu	Gln	Ala	Leu	Glu	Ser	Ala	Gln	Lys	Ser
			115					120					125		
Ser	Asp	Ile	Leu	Gly	Ala	Val	Glu	Arg	Glu	Val	Tyr	Ala	Leu	Leu	Asn
	130					135					140				
Gly	Ser	Thr	Ile	Glu	Gly	Phe	Arg	Asn	Ile	Lys	Glu	Val	Leu	Glu	Ser
145					150					155					160
Ala	Met	Asp	Leu	Ile	Thr	Glu	Asn	Gln	Arg	Lys	Gly	Ser	Leu	Glu	Val
				165					170					175	
Thr	Gly	Ile	Pro	Thr	Gly	Phe	Val	Gln	Leu	Asp	Asn	Tyr	Thr	Ser	Gly
			180					185					190		
Phe	Asn	Lys	Gly	Ser	Leu	Val	Ile	Ile	Gly	Ala	Arg	Pro	Ser	Met	Gly
		195					200					205			
Lys	Thr	Ser	Leu	Met	Met	Asn	Met	Val	Leu	Ser	Ala	Leu	Asn	Asp	Asp
	210					215					220				
Arg	Gly	Val	Ala	Val	Phe	Ser	Leu	Glu	Met	Ser	Ala	Glu	Gln	Leu	Ala
225					230					235					240
Leu	Arg	Ala	Leu	Ser	Asp	Leu	Thr	Ser	Ile	Asn	Met	His	Asp	Leu	Glu
				245					250					255	
Ser	Gly	Arg	Leu	Asp	Asp	Asp	Gln	Trp	Glu	Asn	Leu	Ala	Lys	Cys	Phe
			260					265					270		
Asp	His	Leu	Ser	Gln	Lys	Lys	Leu	Phe	Phe	Tyr	Asp	Lys	Ser	Tyr	Val
		275					280					285			
Arg	Ile	Glu	Gln	Ile	Arg	Leu	Gln	Leu	Arg	Lys	Leu	Lys	Ser	Gln	His
	290					295					300				
Lys	Glu	Leu	Gly	Ile	Ala	Phe	Ile	Asp	Tyr	Leu	Gln	Leu	Met	Ser	Gly
305					310					315					320
Ser	Lys	Ala	Thr	Lys	Glu	Arg	His	Glu	Gln	Ile	Ala	Glu	Ile	Ser	Arg
				325					330					335	
Glu	Leu	Lys	Thr	Leu	Ala	Arg	Glu	Leu	Glu	Ile	Pro	Ile	Ile	Ala	Leu
			340					345					350		
Val	Gln	Leu	Asn	Arg	Ser	Leu	Glu	Asn	Arg	Asp	Asp	Lys	Arg	Pro	Ile
			355				360					365			
Leu	Ser	Asp	Ile	Lys	Asp	Ser	Gly	Gly	Ile	Glu	Gln	Asp	Ala	Asp	Ile
	370					375						380			
Val	Leu	Phe	Leu	Tyr	Arg	Gly	Tyr	Ile	Tyr	Gln	Met	Arg	Ala	Glu	Asp
385					390					395					400
Asn	Lys	Ile	Asp	Lys	Leu	Lys	Lys	Glu	Gly	Lys	Ile	Glu	Glu	Ala	Gln
				405					410					415	
Glu	Leu	Tyr	Leu	Lys	Val	Asn	Glu	Glu	Arg	Arg	Ile	His	Lys	Gln	Asn
			420					425					430		
Gly	Ser	Ile	Glu	Glu	Ala	Glu	Ile	Ile	Val	Ala	Lys	Asn	Arg	Asn	Gly
		435					440					445			
Ala	Thr	Gly	Thr	Val	Tyr	Thr	Arg	Phe	Asn	Ala	Pro	Phe	Thr	Arg	Tyr
	450					455					460				

Glu Asp Met Pro Ile Asp Ser His Leu Glu Glu Gly Gln Glu Thr Lys
 465 470 475 480
 Val Asp Tyr Asp Ile Val Thr Thr
 485

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 98...1207
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GAAACGCATA AGGGGGTTGG CTATCGCTTT AACCCACTAT GAAAAAAAAAT CCCTTAAACT	60
CTTTTATAGGG ATTTATTTAG GCTCTTCGTT TGTGTTG ATG CTA GTG ATT AGC GTT	115
Met Leu Val Ile Ser Val	
1 5	
TTA GCG TTT AAC TAT GAA AAA AAC GAA AAA ATC AAA ATG ATA CGC ATG	163
Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Met Ile Arg Met	
10 15 20	
GAC ATG GAC AAA ATG GCT TCT AAG ATC GCT AGC GAA GTG ATT GCC TTG	211
Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Val Ile Ala Leu	
25 30 35	
CAC ATG CAA ACG CAT GGG GAT TAT CAA AAC GCT TTA AAC GCT CTC ATT	259
His Met Gln Thr His Gly Asp Tyr Gln Asn Ala Leu Asn Ala Leu Ile	
40 45 50	
TCA CGC TAT AAA GAC GCT TCC ATA GCC CTT TTT GAT AGT AAA AAG CGT	307
Ser Arg Tyr Lys Asp Ala Ser Ile Ala Leu Phe Asp Ser Lys Lys Arg	
55 60 65 70	
GTT TTG TAT TCT AAT ATC CCT GAA AGC GCC AAT TTG ATT AAA AAC CAT	355
Val Leu Tyr Ser Asn Ile Pro Glu Ser Ala Asn Leu Ile Lys Asn His	
75 80 85	
AAA GAA GCG GGC TTT TTT AGT TTT AGG GGA GAG TAT TAC CTA TTG AGC	403
Lys Glu Ala Gly Phe Phe Ser Phe Arg Gly Glu Tyr Tyr Leu Leu Ser	
90 95 100	
GAT GAA ACT TTC GCT CAC TTA GGC GTG GCT AAA ATG CTT TTT AAA AAT	451
Asp Glu Thr Phe Ala His Leu Gly Val Ala Lys Met Leu Phe Lys Asn	
105 110 115	
TCT AAA CCC CTT CAT TTT TCT TCT TTG TAT CGT AAC ATT GTT TTA GTG	499
Ser Lys Pro Leu His Phe Ser Ser Leu Tyr Arg Asn Ile Val Leu Val	

120				125				130								
TTT Phe 135	GTT Val	GTA Val	GCG Ala	TTT Phe	TTA Leu	TGC Cys	GTG Val	ATA Ile	GGG Gly	GTT Val	TCT Ser	GTG Val	TTT Phe	TTG Leu	GGG Gly	547
CGT Arg	TTG Leu	TTT Phe	TTA Leu	AAG Lys	CCC Pro	ATT Ile	AGG Arg	AAT Asn	GAA Glu	ATC Ile	ACC Thr	CGC Arg	ATT Ile	GAT Asp	CAT His	595
TTT Phe	TTA Leu	AAA Lys	AAC Asn	ACC Thr	ACG Thr	CAT His	GAA Glu	TTA Leu	AAC Asn	ACC Thr	CCC Pro	ATG Met	AGC Ser	GCT Ala	TTA Leu	643
GTC Val	TTG Leu	TCT Ser	TTA Leu	AAA Lys	ACC Thr	TTA Leu	GAA Glu	GAC Asp	AAC Asn	CAA Gln	CAA Gln	CAC His	CGC Arg	CGC Arg	ATT Ile	691
AAA Lys	ATC Ile	GCT Ala	ATC Ile	CAG Gln	CGC Arg	ATG Met	AGT Ser	TTT Phe	TTA Leu	TAC Tyr	CGC Arg	TCG Ser	CTC Leu	TCG Ser	TAT Tyr	739
TTA Leu	GTG Val	ATG Met	CAA Gln	GAT Asp	ATT Ile	GAG Glu	CGC Arg	GAA Glu	TCT Ser	TTT Phe	GTG Val	CTT Leu	TTA Leu	GAT Asp	TTA Leu	787
AAA Lys	GCC Ala	CTG Leu	ATT Ile	ATT Ile	AAA Lys	GAA Glu	AAC Asn	ACG Thr	CTT Leu	TTT Phe	AGC Ser	GAG Glu	ATG Met	ATA Ile	GAC Asp	835
TAC Tyr	CAC His	AAG Lys	CTG Leu	GAA Glu	TTT Phe	AAA Lys	AGC Ser	GAT Asp	TTA Leu	GTG Val	GAA Glu	GTG Val	GAA Glu	CTT Leu	AAA Lys	883
GCT Ala	AAA Lys	GAG Glu	CAG Gln	GAT Asp	TTC Phe	ATT Ile	TCG Ser	CTT Leu	TAT Tyr	AGC Ser	AAT Asn	TTG Leu	CTC Leu	ATG Met	AAC Asn	931
GCG Ala	ATC Ile	AAA Lys	TAC Tyr	AGC Ser	GTC Val	ATG Met	AAT Asn	GGG Gly	TAT Tyr	ATC Ile	CAC His	ATA Ile	GAG Glu	CTA Leu	ACG Thr	979
CAT His	GCG Ala	TTT Phe	TTG Leu	AAA Lys	GTG Val	AAA Lys	AAT Asn	TTA Leu	GGG Gly	TAT Tyr	GAA Glu	ATC Ile	CCT Pro	AAA Lys	GAC Asp	1027
AAG Lys	ATC Ile	ACA Thr	GAA Glu	TTA Leu	AGC Ser	GTT Val	CGT Arg	TAT Tyr	GTG Val	CGT Arg	TTC Phe	AAT Asn	TCT Ser	GGC Gly	GTG Val	1075
TTG Leu	GGT Gly	TAT Tyr	GGT Gly	ATA Ile	GGG Gly	TTA Leu	GGT Gly	TTG Leu	GTG Val	AAA Lys	AAA Lys	GTG Val	TGC Cys	GAA Glu	AAG Lys	1123
TAT Tyr	AAA Lys	ATG Met	CGT Arg	TTA Leu	GAA Glu	ATT Ile	CAT His	AGC Ser	GAA Glu	CCC Pro	TCT Ser	TTA Leu	AAG Lys	GGA Gly	TCG Ser	1171

TTT TAT GAA AAT TCG TTT TGC GTT CAA TTT CAA GGA TAAAGATGCT TTCAGT 1223
Phe Tyr Glu Asn Ser Phe Cys Val Gln Phe Gln Gly
360 365 370

GTATGAAAAA GTGAATGCTC TAG

1246

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Met	Leu	Val	Ile	Ser	Val	Leu	Ala	Phe	Asn	Tyr	Glu	Lys	Asn	Glu	Lys	1	5	10	15
Ile	Lys	Met	Ile	Arg	Met	Asp	Met	Asp	Lys	Met	Ala	Ser	Lys	Ile	Ala	20	25	30	
Ser	Glu	Val	Ile	Ala	Leu	His	Met	Gln	Thr	His	Gly	Asp	Tyr	Gln	Asn	35	40	45	
Ala	Leu	Asn	Ala	Leu	Ile	Ser	Arg	Tyr	Lys	Asp	Ala	Ser	Ile	Ala	Leu	50	55	60	
Phe	Asp	Ser	Lys	Lys	Arg	Val	Leu	Tyr	Ser	Asn	Ile	Pro	Glu	Ser	Ala	65	70	75	80
Asn	Leu	Ile	Lys	Asn	His	Lys	Glu	Ala	Gly	Phe	Phe	Ser	Phe	Arg	Gly	85	90	95	
Glu	Tyr	Tyr	Leu	Leu	Ser	Asp	Glu	Thr	Phe	Ala	His	Leu	Gly	Val	Ala	100	105	110	
Lys	Met	Leu	Phe	Lys	Asn	Ser	Lys	Pro	Leu	His	Phe	Ser	Ser	Leu	Tyr	115	120	125	
Arg	Asn	Ile	Val	Leu	Val	Phe	Val	Val	Ala	Phe	Leu	Cys	Val	Ile	Gly	130	135	140	
Val	Ser	Val	Phe	Leu	Gly	Arg	Leu	Phe	Leu	Lys	Pro	Ile	Arg	Asn	Glu	145	150	155	160
Ile	Thr	Arg	Ile	Asp	His	Phe	Leu	Lys	Asn	Thr	Thr	His	Glu	Leu	Asn	165	170	175	
Thr	Pro	Met	Ser	Ala	Leu	Val	Leu	Ser	Leu	Lys	Thr	Leu	Glu	Asp	Asn	180	185	190	
Gln	Gln	His	Arg	Arg	Ile	Lys	Ile	Ala	Ile	Gln	Arg	Met	Ser	Phe	Leu	195	200	205	
Tyr	Arg	Ser	Leu	Ser	Tyr	Leu	Val	Met	Gln	Asp	Ile	Glu	Arg	Glu	Ser	210	215	220	
Phe	Val	Leu	Leu	Asp	Leu	Lys	Ala	Leu	Ile	Ile	Lys	Glu	Asn	Thr	Leu	225	230	235	240
Phe	Ser	Glu	Met	Ile	Asp	Tyr	His	Lys	Leu	Glu	Phe	Lys	Ser	Asp	Leu	245	250	255	
Val	Glu	Val	Glu	Leu	Lys	Ala	Lys	Glu	Gln	Asp	Phe	Ile	Ser	Leu	Tyr	260	265	270	
Ser	Asn	Leu	Leu	Met	Asn	Ala	Ile	Lys	Tyr	Ser	Val	Met	Asn	Gly	Tyr	275	280	285	
Ile	His	Ile	Glu	Leu	Thr	His	Ala	Phe	Leu	Lys	Val	Lys	Asn	Leu	Gly	290	295	300	
Tyr	Glu	Ile	Pro	Lys	Asp	Lys	Ile	Thr	Glu	Leu	Ser	Val	Arg	Tyr	Val	305	310	315	320

Arg Phe Asn Ser Gly Val Leu Gly Tyr Gly Ile Gly Leu Gly Leu Val
 325 330 335
 Lys Lys Val Cys Glu Lys Tyr Lys Met Arg Leu Glu Ile His Ser Glu
 340 345 350
 Pro Ser Leu Lys Gly Ser Phe Tyr Glu Asn Ser Phe Cys Val Gln Phe
 355 360 365
 Gln Gly
 370

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...665
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GGGATAGTTT TAAAAATGAT GAAGAGTTTT TAACATTTTC TTACGCTTGG ATTGATAAA A 60
 Me

TGC TGC CCA AAC TTA AAG ACA CAG GGA GTT TTT ATA TCT TTA ATA CCC 108
 t Leu Pro Lys Leu Lys Asp Thr Gly Ser Phe Tyr Ile Phe Asn Thr Pr
 1 5 10 15

CTT TTA ATT GCG CTT TAT TTT TAG CGT ATT TGC ACC ATA AAA AAG TGC 156
 o Phe Asn Cys Ala Leu Phe Leu Ala Tyr Leu His His Lys Lys Val Hi
 20 25 30

ATT TTT TAA ATT TTA TCA CTT GGG TTA AAA AAG ATG GGT TTG CCA ACG 204
 s Phe Leu Asn Phe Ile Thr Trp Val Lys Lys Asp Gly Phe Ala Asn Al
 35 40 45

CCA AAA AGC GTT ATA ACC ACG CGC AAG AAA GCA TTT TAT TTT ATA GCA 252
 a Lys Lys Arg Tyr Asn His Ala Gln Glu Ser Ile Leu Phe Tyr Ser Me
 50 55 60 6

TGC ACA AGA AAA ACT ACA CCT TTA ATG CCG ATG AGA TTC GCA TCG CTT 300
 t His Lys Lys Asn Tyr Thr Phe Asn Ala Asp Glu Ile Arg Ile Ala Ty
 5 70 75 80

ATG AAT CCG CTG AAC GCA TCA AAC ATG CTC AAA GTA AGG GGA TTT TAA 348
 r Glu Ser Ala Glu Arg Ile Lys His Ala Gln Ser Lys Gly Ile Leu Ly
 85 90 95

AAA ATA ACA AAC GCT GGT TCC CTA ACC CTA AGG GCA AAT TAT GCC TTG 396
 s Asn Asn Lys Arg Trp Phe Pro Asn Pro Lys Gly Lys Leu Cys Leu As
 100 105 110

GAC Asp	AGC Ser	AAT Asn	GTG Val 130	GAG Glu	TTA Leu	GAG Glu	CAT His	TTA Leu 135	GAA Glu	GAA Glu	GTG Val	GAG Glu	TTG Leu 140	AGC Ser	AAG Lys	492
TCT Ser	AAT Asn	ATT Ile 145	TTA Leu	CTA Leu	ATC Ile	GGC Gly	CCT Pro 150	ACA Thr	GGA Gly	TCA Ser	GGC Gly	AAA Lys 155	ACT Thr	TTA Leu	ATG Met	540
GCG Ala 160	CAA Gln	ACT Thr	CTG Leu	GCC Ala	AAG Lys	CAT His 165	TTG Leu	GAT Asp	ATT Ile	CCT Pro	ATC Ile 170	GCC Ala	ATT Ile	AGC Ser	GAT Asp	588
GCG Ala 175	ACT Thr	AGC Ser	TTG Leu	ACT Thr	GAA Glu 180	GCG Ala	GGC Gly	TAT Tyr	GTG Val	GGC Gly 185	GAA Glu	GAC Asp	GTG Val	GAA Glu	AAT Asn 190	636
ATT Ile	CTC Leu	ACA Thr	AGA Arg 195	TTG Leu	TTG Leu	CAA Gln	GCG Ala	AGC Ser 200	GAC Asp	TGG Trp	AAT Asn	GTC Val	CAA Gln 205	AAA Lys	GCC Ala	684
CAA Gln	AAA Lys	GGC Gly 210	ATT Ile	GTG Val	TTT Phe	ATT Ile	GAT Asp 215	GAG Glu 215	ATT Ile	GAT Asp	AAA Lys	ATC Ile 220	AGC Ser 220	CGT Arg	TTG Leu	732
TCA Ser	GAA Glu	AAC Asn 225	CGC Arg	TCT Ser	ATC Ile	ACT Thr 230	AGA Arg	GAT Asp	GTT Val	TCT Ser	GGC Gly 235	GAG Glu 235	GGC Gly	GTT Val	CAG Gln	780
CAA Gln 240	GCG Ala	TTG Leu	TTG Leu	AAA Lys	ATC Ile	GTT Val 245	GAA Glu	GGT Gly	TCT Ser	TTA Leu	GTG Val 250	AAT Asn	ATC Ile	CCC Pro	CCC Pro	828
AAA Lys 255	GGC Gly	GGC Gly	AGA Arg	AAG Lys	CAC His 260	CCT Pro	GAG Glu	GGC Gly	AAT Asn	TTC Phe 265	ATT Ile	CAA Gln	ATT Ile	GAC Asp	ACG Thr 270	876
AGC Ser	GAT Asp	ATT Ile	TTA Leu 275	TTC Phe	ATT Ile	TGT Cys	GCT Ala	GGA Gly 280	GCG Ala	TTT Phe	GAT Asp	GGG Gly	TTA Leu 285	GCT Ala	GAA Glu	924
ATC Ile	ATT Ile	AAA Lys	AAA Lys 290	CGC Arg	ACC Thr	ACG Thr	CAG Gln	AAT Asn 295	GTG Val	TTG Leu	GGT Gly	TTC Phe 300	ACT Thr	CAA Gln	GAA Glu	972
AAG Lys	ATG Met	AGC Ser 305	AAA Lys	AAA Lys	GAG Glu	CAA Gln 310	GAA Glu	GCG Ala	ATC Ile	TTG Leu	CAT His 315	TTA Leu 315	GTC Val	CAA Gln	ACC Thr	1020
CAT His	GAC Asp 320	CTG Leu	GTT Val	ACT Thr	TAT Tyr	GGG Gly 325	CTT Leu	ATC Ile	CCT Pro	GAG Glu 330	CTT Leu 330	ATT Ile	GGC Gly	CGT Arg	TTG Leu	1068
CCG Pro 335	GTT Val	TTA Leu	AGC Ser	ACG Thr	CTA Leu 340	GAT Asp	AGC Ser	ATC Ile	AGT Ser	TTA Leu 345	GAA Glu	GCG Ala	ATG Met	GTG Val	GAT Asp 350	1116
ATT Ile	TTA Leu	CAA Gln	AAA Lys	CCT Pro	AAA Lys	AAC Asn	GCT Ala	CTT Leu	ATC Ile	AAG Lys	CAA Gln	TAC Tyr	CAG Gln	CAG Gln	CTT Leu	1164


```

Ser Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu Asn Ile Leu
180 185 190
Thr Arg Leu Leu Gln Ala Ser Asp Trp Asn Val Gln Lys Ala Gln Lys
195 200 205
Gly Ile Val Phe Ile Asp Glu Ile Asp Lys Ile Ser Arg Leu Ser Glu
210 215 220
Asn Arg Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val Gln Gln Ala
225 230 235 240
Leu Leu Lys Ile Val Glu Gly Ser Leu Val Asn Ile Pro Pro Lys Gly
245 250 255
Gly Arg Lys His Pro Glu Gly Asn Phe Ile Gln Ile Asp Thr Ser Asp
260 265 270
Ile Leu Phe Ile Cys Ala Gly Ala Phe Asp Gly Leu Ala Glu Ile Ile
275 280 285
Lys Lys Arg Thr Thr Gln Asn Val Leu Gly Phe Thr Gln Glu Lys Met
290 295 300
Ser Lys Lys Glu Gln Glu Ala Ile Leu His Leu Val Gln Thr His Asp
305 310 315 320
Leu Val Thr Tyr Gly Leu Ile Pro Glu Leu Ile Gly Arg Leu Pro Val
325 330 335
Leu Ser Thr Leu Asp Ser Ile Ser Leu Glu Ala Met Val Asp Ile Leu
340 345 350
Gln Lys Pro Lys Asn Ala Leu Ile Lys Gln Tyr Gln Gln Leu Phe Lys
355 360 365
Met Asp Glu Val Asp Leu Ile Phe Glu Glu Glu Ala Ile Lys Glu Ile
370 375 380
Ala Gln Leu Ala Leu Glu Arg Lys Thr Gly Ala Arg Gly Leu Arg Ala
385 390 395 400
Ile Ile Glu Asp Phe Cys Leu Asp Ile Met Phe Asp Leu Pro Lys Leu
405 410 415
Lys Gly Ser Glu Val Arg Ile Thr Lys Asp Cys Val Leu Lys Gln Ala
420 425 430
Glu Pro Leu Ile Ile Ala Lys Thr His Ser Lys Ile Leu Pro
435 440 445

```

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...858
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```

AGTGTTAGAA AAAACTTTGC TTTGAAATTT GGC ATG AAA GCA GGC ATT ATT GGT      54
Met Lys Ala Gly Ile Ile Gly
1 5
TTA GGG CTT ATG GGG GGG AGT TTA GGG CTA GCC TTG CAA GAA TGG GGG      102

```

Leu Gly Leu Met Gly Gly Ser Leu Gly Leu Ala Leu Gln Glu Trp Gly	
10 15 20	
CGT TTT AAA AGC GTT ATA GGC TAT GAT CAT AAC GCT TTG CAT GCT AAA	150
Arg Phe Lys Ser Val Ile Gly Tyr Asp His Asn Ala Leu His Ala Lys	
25 30 35	
TTG GCT TTG ACT TTG GGG CTT GTA GAT GAA TGC GTG GGA TTT GAA AAG	198
Leu Ala Leu Thr Leu Gly Leu Val Asp Glu Cys Val Gly Phe Glu Lys	
40 45 50 55	
ATT TTA GAA TGC GAT GTG ATT TTT TTG GCC ATT CCG GTT GAG GGC ATC	246
Ile Leu Glu Cys Asp Val Ile Phe Leu Ala Ile Pro Val Glu Gly Ile	
60 65 70	
ATT GGA TGT CTG AAA AAA ATG ACC TCT ATC AAA AAA AGC GCG ACC ATT	294
Ile Gly Cys Leu Lys Lys Met Thr Ser Ile Lys Lys Ser Ala Thr Ile	
75 80 85	
ATT GAT TTA GGG GGC GCT AAA GCG CAA ATC ATT CGC AAT ATC CCT AAA	342
Ile Asp Leu Gly Gly Ala Lys Ala Gln Ile Ile Arg Asn Ile Pro Lys	
90 95 100	
AGC ATT CGT AAG AAT TTC ATC GCT GCG CAC CCC ATG TGC GGG ACA GAG	390
Ser Ile Arg Lys Asn Phe Ile Ala Ala His Pro Met Cys Gly Thr Glu	
105 110 115	
TTT TAT GGC CCT AAA GCG AGC GTT AAG GGG CTG TAT GAA AAC GCT CTA	438
Phe Tyr Gly Pro Lys Ala Ser Val Lys Gly Leu Tyr Glu Asn Ala Leu	
120 125 130 135	
GTG ATA TTG TGC GAT TTA GAA GAT TCA GGG ACT GAG CAA GTA GAG ATC	486
Val Ile Leu Cys Asp Leu Glu Asp Ser Gly Thr Glu Gln Val Glu Ile	
140 145 150	
GCT AAA GAA ATC TTT TTA GGC GTT AAA GCG CGC TTG ATT AAA ATG AAA	534
Ala Lys Glu Ile Phe Leu Gly Val Lys Ala Arg Leu Ile Lys Met Lys	
155 160 165	
TCC AAT GAG CAT GAC ACC CAT GTG GCT TAT ATC AGC CAT TTA CCC CAT	582
Ser Asn Glu His Asp Thr His Val Ala Tyr Ile Ser His Leu Pro His	
170 175 180	
GTT TTG AGC TAT GCG TTA GCC AAT AGC GTT TTA AAG CAA AAC GAC CCA	630
Val Leu Ser Tyr Ala Leu Ala Asn Ser Val Leu Lys Gln Asn Asp Pro	
185 190 195	
GAG ATG ATT TTA TCT TTA GCG GGT GGG GGT TTT AGG GAT ATG AGC CGT	678
Glu Met Ile Leu Ser Leu Ala Gly Gly Gly Phe Arg Asp Met Ser Arg	
200 205 210 215	
CTG TCC AAA AGC TCG CCT TTA ATG TGG AAA GAT ATT TTC AAA CAA AAC	726
Leu Ser Lys Ser Ser Pro Leu Met Trp Lys Asp Ile Phe Lys Gln Asn	
220 225 230	
CGA GAC AAT GTC TTA GAA GCG ATT AAA AAA TGC GAA AAA GAA ATC GTG	774
Arg Asp Asn Val Leu Glu Ala Ile Lys Lys Cys Glu Lys Glu Ile Val	
235 240 245	

CAA GCT AAG GCG TGG ATA GAA AAT AAC GAT TAT GAA AGC CTT GCA GAA 822
 Gln Ala Lys Ala Trp Ile Glu Asn Asn Asp Tyr Glu Ser Leu Ala Glu
 250 255 260

TGG ATG GCG CAA GCG AAC AAA CTC CAG GAG TTC ATG TAAAGTAAAA TGATGT 874
 Trp Met Ala Gln Ala Asn Lys Leu Gln Glu Phe Met
 265 270 275

AAAATAATTT AAAATTTTTT ATATTGTTGT TTTTAGG 911

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Met	Lys	Ala	Gly	Ile	Ile	Gly	Leu	Gly	Leu	Met	Gly	Gly	Ser	Leu	Gly
1				5					10					15	
Leu	Ala	Leu	Gln	Glu	Trp	Gly	Arg	Phe	Lys	Ser	Val	Ile	Gly	Tyr	Asp
			20					25					30		
His	Asn	Ala	Leu	His	Ala	Lys	Leu	Ala	Leu	Thr	Leu	Gly	Leu	Val	Asp
			35				40					45			
Glu	Cys	Val	Gly	Phe	Glu	Lys	Ile	Leu	Glu	Cys	Asp	Val	Ile	Phe	Leu
	50					55				60					
Ala	Ile	Pro	Val	Glu	Gly	Ile	Ile	Gly	Cys	Leu	Lys	Lys	Met	Thr	Ser
65					70					75				80	
Ile	Lys	Lys	Ser	Ala	Thr	Ile	Ile	Asp	Leu	Gly	Gly	Ala	Lys	Ala	Gln
			85						90					95	
Ile	Ile	Arg	Asn	Ile	Pro	Lys	Ser	Ile	Arg	Lys	Asn	Phe	Ile	Ala	Ala
			100					105					110		
His	Pro	Met	Cys	Gly	Thr	Glu	Phe	Tyr	Gly	Pro	Lys	Ala	Ser	Val	Lys
		115					120					125			
Gly	Leu	Tyr	Glu	Asn	Ala	Leu	Val	Ile	Leu	Cys	Asp	Leu	Glu	Asp	Ser
	130					135				140					
Gly	Thr	Glu	Gln	Val	Glu	Ile	Ala	Lys	Glu	Ile	Phe	Leu	Gly	Val	Lys
145					150					155				160	
Ala	Arg	Leu	Ile	Lys	Met	Lys	Ser	Asn	Glu	His	Asp	Thr	His	Val	Ala
			165						170					175	
Tyr	Ile	Ser	His	Leu	Pro	His	Val	Leu	Ser	Tyr	Ala	Leu	Ala	Asn	Ser
			180					185					190		
Val	Leu	Lys	Gln	Asn	Asp	Pro	Glu	Met	Ile	Leu	Ser	Leu	Ala	Gly	Gly
		195					200						205		
Gly	Phe	Arg	Asp	Met	Ser	Arg	Leu	Ser	Lys	Ser	Ser	Pro	Leu	Met	Trp
	210					215						220			
Lys	Asp	Ile	Phe	Lys	Gln	Asn	Arg	Asp	Asn	Val	Leu	Glu	Ala	Ile	Lys
225					230					235				240	
Lys	Cys	Glu	Lys	Glu	Ile	Val	Gln	Ala	Lys	Ala	Trp	Ile	Glu	Asn	Asn
			245						250					255	
Asp	Tyr	Glu	Ser	Leu	Ala	Glu	Trp	Met	Ala	Gln	Ala	Asn	Lys	Leu	Gln
			260					265					270		
Glu	Phe	Met													
		275													

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...267
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```

AATAATTTTAA AATTTTTTTAT ATTGTTGTTT TTAGGGGTGC GAGGAGCGAA ATGGGGTATT      60
TGGATTGTTT TT ATG GAT TAT AGG CTG TTT CAT ATG GAT AGC ATG GAT TTA      111
      Met Asp Tyr Arg Leu Phe His Met Asp Ser Met Asp Leu
        1              5              10

CCC AGC AAC CAG CAA ACA ACC ATA AGA GAT TAT CTT AAA CCC GGA TCT      159
Pro Ser Asn Gln Gln Thr Thr Ile Arg Asp Tyr Leu Lys Pro Gly Ser
      15              20              25

ATT GTT GTG TTT GCC ATA ATT GTA ATA ATA ATT TCA TCT CAT TTC TCC      207
Ile Val Val Phe Ala Ile Ile Val Ile Ile Ile Ser Ser His Phe Ser
      30              35              40              45

AAC GCC TAT AAA ACC CTT ATC GCT TCT AAT AAA AAA CCA GTT TTA AGC      255
Asn Ala Tyr Lys Thr Leu Ile Ala Ser Asn Lys Lys Pro Val Leu Ser
              50              55              60

CAT TTA GAA ATT TGATTCTTA AACCTTTTTA TCAAAAATAC CGGTGTT      304
His Leu Glu Ile
              65

```

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

```

Met Asp Tyr Arg Leu Phe His Met Asp Ser Met Asp Leu Pro Ser Asn
  1              5              10              15
Gln Gln Thr Thr Ile Arg Asp Tyr Leu Lys Pro Gly Ser Ile Val Val
      20              25              30
Phe Ala Ile Ile Val Ile Ile Ile Ser Ser His Phe Ser Asn Ala Tyr
      35              40              45

```

Lys Thr Leu Ile Ala Ser Asn Lys Lys Pro Val Leu Ser His Leu Glu
 50 55 60
 Ile
 65

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...237
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

AGCTCACATT TTAGAAAAAT ATTTAAAGGG AGA ATG ATG CAA AAT AGC GTT AAA	54
Met Met Gln Asn Ser Val Lys	
1 5	
AAA TTA GAA TAT GAA GAG CGT TTC AAT GAC GCT CTT TTG AAA TTA CAA	102
Lys Leu Glu Tyr Glu Glu Arg Phe Asn Asp Ala Leu Leu Lys Leu Gln	
10 15 20	
GCA TGC CAA GAA GAA AAG CAG GTA ACG AGT TGT TTG AAA TGC GAG CAG	150
Ala Cys Gln Glu Glu Lys Gln Val Thr Ser Cys Leu Lys Cys Glu Gln	
25 30 35	
GTT TTG AAT TGC AAG ATC CGC AAC AGC TAT GTG GAT GCG GCT TAT GAG	198
Val Leu Asn Cys Lys Ile Arg Asn Ser Tyr Val Asp Ala Ala Tyr Glu	
40 45 50 55	
AGC ATG AGT TTA GGC GAA CGG GGC GGG TTT GAT TTC AAT TAAATGGGAT TA	249
Ser Met Ser Leu Gly Glu Arg Gly Gly Phe Asp Phe Asn	
60 65	
AAATGGCTAG TAATACTACC TT	271

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Met Met Gln Asn Ser Val Lys Lys Leu Glu Tyr Glu Glu Arg Phe Asn

1		5		10		15
Asp	Ala	Leu	Leu	Lys	Leu	Gln
		20		25		30
Ser	Cys	Leu	Lys	Cys	Glu	Gln
		35		40		45
Tyr	Val	Asp	Ala	Ala	Tyr	Glu
		50		55		60
Phe	Asp	Phe	Asn			
65						

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 27...524
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

AAAAGGCTTT TTAAAAGGAC ACACCA ATG AGC GAA CCA TTA GAA ACA TTA GAC	53
Met Ser Glu Pro Leu Glu Thr Leu Asp	
1 5	
AAG GAT AAA CAA GCT ATG AGT GAA GCA ATT AAA AAA GAT ATT GAA AAA	101
Lys Asp Lys Gln Ala Met Ser Glu Ala Ile Lys Lys Asp Ile Glu Lys	
10 15 20 25	
GAC AAA GAA AAC CTC GCA CGA GTC AAA GCA GAC AAA AAA GTC AAA GCC	149
Asp Lys Glu Asn Leu Ala Arg Val Lys Ala Asp Lys Lys Val Lys Ala	
30 35 40	
GAT GAA AGT GAA AAA GGC TAC GAA AAA GAC GAT GAC AAA AAA GCC GAG	197
Asp Glu Ser Glu Lys Gly Tyr Glu Lys Asp Asp Asp Lys Lys Ala Glu	
45 50 55	
AAT CTT GAC AAA GAA ATC GCT AAA GAC AAA GCT AGC CCT AAC GAT AAT	245
Asn Leu Asp Lys Glu Ile Ala Lys Asp Lys Ala Ser Pro Asn Asp Asn	
60 65 70	
GAG CTT TAT GAA GAG GAC GAT AGA GTT AAA CGA GAC AAA GAA AGA GAC	293
Glu Leu Tyr Glu Glu Asp Asp Arg Val Lys Arg Asp Lys Glu Arg Asp	
75 80 85	
GAT GCC TTG CGT GAT AAA GAA AAA GCC AAA GAT GAC GCA TGC ATG GTA	341
Asp Ala Leu Arg Asp Lys Glu Lys Ala Lys Asp Asp Ala Cys Met Val	
90 95 100 105	
AGA GCG GAC GAT GAC ACC ATA GAG GAC GAT GAG GAA TAT GGT GAT GAT	389
Arg Ala Asp Asp Asp Thr Ile Glu Asp Asp Glu Glu Tyr Gly Asp Asp	

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 82...2283

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

CAACAAGCTA	ACCAAAGCAT	TGAAGAAGCT	TTACAGAATG	TCCCGGGTCT	GCAAATTAGG	60
AATGCGACAG	GTGTAGGGGC	T ATG CCT ACT ATC CAA ATC CGT GGC TTT GGA	111			
		Met Pro Thr Ile Gln Ile Arg Gly Phe Gly				
		1 5 10				
GCT GGG GGT TCA GGG CAT AGC GAT GCG ACG CTG ATG TTA GTC AAT GGT	159					
Ala Gly Gly Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly						
	15 20 25					
ATT CCT GTT TAT ATG GCC CCC TAC GCT CAC ATT GAG CTA GAC ATT TTC	207					
Ile Pro Val Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe						
	30 35 40					
CCC GTT ACC TTT CAA GCC ATT GAT CGC ATT GAT GTG ATC AAG GGT GGA	255					
Pro Val Thr Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly						
	45 50 55					
GGC AGC GTG CAA TAC GGG CCT AAC ACT TAT GGG GGT ATT GTC AAT ATC	303					
Gly Ser Val Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile						
	60 65 70					
ATC ACT AAG CCT ATC CCT AAT CAA TGG GAA AAC CAA GCG GCT GAA AGG	351					
Ile Thr Lys Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg						
	75 80 85 90					
ATC ACT TAT TGG GCT AAG GCT AGA AAC GCT GGG TTT GCC GCT CCT CCT	399					
Ile Thr Tyr Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro Pro						
	95 100 105					
GAT AAA ACC GGC GAT CCT TCT TTC ATC AAG TCT TTA GGC AAC AAC CTC	447					
Asp Lys Thr Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu						
	110 115 120					
CTC TAT AAC ACT TAT GTG AGG AGT GGA GGG ATG ATC AAT AAG CAT GTG	495					
Leu Tyr Asn Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val						
	125 130 135					
GGT ATC CAA GCG CAA GCT AAC TGG GTT AGA GGA CAA GGC TTT AGG GAC	543					
Gly Ile Gln Ala Gln Ala Asn Trp Val Arg Gly Gln Gly Phe Arg Asp						
	140 145 150					
AAT AGC CCC TCT AAC ATT TCA AAC TAT TGG CTA GAT GGA GTC TAT GAC	591					
Asn Ser Pro Ser Asn Ile Ser Asn Tyr Trp Leu Asp Gly Val Tyr Asp						
	155 160 165 170					
ATC AAT GAA AAC AAT GGG ATT AAA GCC TAT TAC CAA TAC TAC GAT TTT	639					
Ile Asn Glu Asn Asn Gly Ile Lys Ala Tyr Tyr Gln Tyr Tyr Asp Phe						
	175 180 185					

415										420					425					
CAA	ATC	CCT	GAG	AAG	GAT	TTA	AGA	AAA	ATC	AAG	CAC	ATG	AAC	AAT	TGG	1407				
Gln	Ile	Pro	Glu	Lys	Asp	Leu	Arg	Lys	Ile	Lys	His	Met	Asn	Asn	Trp					
			430					435					440							
ATG	CCC	TCA	ACC	AAC	ATT	GGC	TTT	ATC	CCC	GTG	CAA	GGC	GAT	CAC	AAT	1455				
Met	Pro	Ser	Thr	Asn	Ile	Gly	Phe	Ile	Pro	Val	Gln	Gly	Asp	His	Asn					
			445				450					455								
GTG	CTT	ACC	TAC	TTT	AAC	TAC	CAA	CGC	TCT	TTC	GTC	CCG	CCT	CAA	TTA	1503				
Val	Leu	Thr	Tyr	Phe	Asn	Tyr	Gln	Arg	Ser	Phe	Val	Pro	Pro	Gln	Leu					
	460					465					470									
GAC	GTT	TTG	AGC	TAT	GGA	GGA	GCG	GAG	TAT	TTT	ACC	CAG	CAC	TTT	GAC	1551				
Asp	Val	Leu	Ser	Tyr	Gly	Gly	Ala	Glu	Tyr	Phe	Thr	Gln	His	Phe	Asp					
	475				480				485						490					
ACG	GTG	GAA	GCA	GGA	GCG	CGC	TAC	ACC	TAT	AAG	GAT	AAA	TTC	AGC	TTC	1599				
Thr	Val	Glu	Ala	Gly	Ala	Arg	Tyr	Thr	Tyr	Lys	Asp	Lys	Phe	Ser	Phe					
				495				500						505						
AAT	GCG	GAC	TAC	TTC	AGG	ATT	TGG	GCG	CGC	GAT	TTT	GCC	ACC	GGG	CAG	1647				
Asn	Ala	Asp	Tyr	Phe	Arg	Ile	Trp	Ala	Arg	Asp	Phe	Ala	Thr	Gly	Gln					
			510					515					520							
TAT	TCA	GTC	TAT	ACA	AGC	GGT	CCC	ATG	AAG	GGT	AAT	GTG	CGC	CCC	ATT	1695				
Tyr	Ser	Val	Tyr	Thr	Ser	Gly	Pro	Met	Lys	Gly	Asn	Val	Arg	Pro	Ile					
		525					530					535								
AAT	GGC	TAT	TCT	CAA	GGC	GTG	GAG	CTG	GAA	TTG	TAT	TAC	AGG	CCT	ATT	1743				
Asn	Gly	Tyr	Ser	Gln	Gly	Val	Glu	Leu	Glu	Leu	Tyr	Tyr	Arg	Pro	Ile					
	540					545			550											
AGA	GGG	TTG	CAA	TTC	CAT	GCC	GCT	TTC	AAC	TAC	ATT	GAC	ACT	CGT	GTA	1791				
Arg	Gly	Leu	Gln	Phe	His	Ala	Ala	Phe	Asn	Tyr	Ile	Asp	Thr	Arg	Val					
	555				560				565						570					
ACC	AGC	CAT	GGC	CCT	TTA	ACC	GAC	TTG	AAC	GGG	GAT	GTG	CTA	AAA	GGG	1839				
Thr	Ser	His	Gly	Pro	Leu	Thr	Asp	Leu	Asn	Gly	Asp	Val	Leu	Lys	Gly					
			575					580						585						
ACT	AGC	TAT	AAC	AAG	CAT	TTC	CCT	TTT	GTA	AGC	CCT	TTC	CAA	TTC	ATT	1887				
Thr	Ser	Tyr	Asn	Lys	His	Phe	Pro	Phe	Val	Ser	Pro	Phe	Gln	Phe	Ile					
			590					595					600							
CTT	GAC	GCT	CGT	TAC	AAT	TGG	CGT	AAA	ACC	ACC	ATC	GGT	ATT	TCT	AGC	1935				
Leu	Asp	Ala	Arg	Tyr	Asn	Trp	Arg	Lys	Thr	Thr	Ile	Gly	Ile	Ser	Ser					
		605					610					615								
TAT	TTT	TAC	AGC	CGT	GCT	TAT	AGC	GGG	ATT	AGC	AAC	AGT	GCA	GCA	GGA	1983				
Tyr	Phe	Tyr	Ser	Arg	Ala	Tyr	Ser	Gly	Ile	Ser	Asn	Ser	Ala	Ala	Gly					
	620					625					630									
GGC	TAT	TAT	GGG	ATG	CAA	TAT	TAT	AGT	GGG	GGG	AAC	AAC	TAT	GAA	AGC	2031				
Gly	Tyr	Tyr	Gly	Met	Gln	Tyr	Tyr	Ser	Gly	Gly	Asn	Asn	Tyr	Glu	Ser					
	635				640				645						650					

625		630		635		640									
Tyr	Tyr	Ser	Gly	Gly	Asn	Asn	Tyr	Glu	Ser	Val	Leu	Asn	Ser	Gly	Tyr
				645				650						655	
Gln	Cys	Glu	Ala	Trp	Cys	Met	Thr	Gln	His	Glu	Gly	Leu	Leu	Pro	Trp
			660					665					670		
Tyr	Trp	Val	Trp	Asn	Ile	Gln	Val	Ser	Gln	Ile	Phe	Trp	Glu	Asn	Gly
		675					680					685			
Arg	His	Arg	Val	Thr	Gly	Ser	Leu	Gln	Ile	Asn	Asn	Ile	Phe	Asn	Met
	690					695				700					
Lys	Tyr	Tyr	Phe	Thr	Gly	Ile	Gly	Ser	Ser	Pro	Ala	Gly	Leu	Gln	Pro
705					710					715					720
Ala	Pro	Gly	Arg	Ser	Val	Thr	Ala	Tyr	Leu	Asn	Tyr	Thr	Phe		
			725						730						

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...204
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

CATTGGAGAT	TGTGCCATTC	TTTGATTTTA	TCTAAA	ATG	TCT	TTA	GGG	GCA	GTG	54
				Met	Ser	Leu	Gly	Ala	Val	
				1				5		
ATT AAG CTT ATT TTT TGT TAT AAA TTA GAG GGG GTA ATA TTA GAT TTA	102									
Ile Lys Leu Ile Phe Cys Tyr Lys Leu Glu Gly Val Ile Leu Asp Leu										
	10	15	20							
AAG CGC ATC AAT TTC AAA TCC TAT TAT CCC AAT AAT AAA AAT GCA TTA	150									
Lys Arg Ile Asn Phe Lys Ser Tyr Tyr Pro Asn Asn Lys Asn Ala Leu										
	25	30	35							
TTT ATC AAC AAT AAA AAA ATC CAT TAT CTA GTG CCT CAA AGG TTC ATA	198									
Phe Ile Asn Asn Lys Lys Ile His Tyr Leu Val Pro Gln Arg Phe Ile										
	40	45	50							
TTG CTT TAACTTGCT ATGGACGATT AGAAATCG	232									
Leu Leu										
55										

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Met	Ser	Leu	Gly	Ala	Val	Ile	Lys	Leu	Ile	Phe	Cys	Tyr	Lys	Leu	Glu
1				5				10					15		
Gly	Val	Ile	Leu	Asp	Leu	Lys	Arg	Ile	Asn	Phe	Lys	Ser	Tyr	Tyr	Pro
			20				25					30			
Asn	Asn	Lys	Asn	Ala	Leu	Phe	Ile	Asn	Asn	Lys	Lys	Ile	His	Tyr	Leu
		35				40					45				
Val	Pro	Gln	Arg	Phe	Ile	Leu	Leu								
50					55										

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 24...1094
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

CTTTTAGAAT TAGGGCTTAA AGC ATG AAA GCT AGT ATT TAT GAT TTC ACT CTA	53
Met Lys Ala Ser Ile Tyr Asp Phe Thr Leu	
1 5 10	
AAG GAA TTG AGC CAG CTT TTA AAA CCA AGC TTT AGG GCT AAA CAG CTT	101
Lys Glu Leu Ser Gln Leu Leu Lys Pro Ser Phe Arg Ala Lys Gln Leu	
15 20 25	
TAT TTG TGG CTC TAT GCG AAG TAT AAA ACA AGC TTT AAG GAC ATG CAA	149
Tyr Leu Trp Leu Tyr Ala Lys Tyr Lys Thr Ser Phe Lys Asp Met Gln	
30 35 40	
AAT AAT TTT TCA AAA GAT TTT ATC GCT TAT TTG GAG CGA GAA TTT GCT	197
Asn Asn Phe Ser Lys Asp Phe Ile Ala Tyr Leu Glu Arg Glu Phe Ala	
45 50 55	
TTG CGC ACG ATA GAA ATC ACG CAT GTG AGG GAG AGC GTT GAT GGC TCT	245
Leu Arg Thr Ile Glu Ile Thr His Val Arg Glu Ser Val Asp Gly Ser	
60 65 70	
AAA AAA TAC CTT TTT AAA TCT TTA AGA GAC AAC CAC ACT TTT GAA GCG	293
Lys Lys Tyr Leu Phe Lys Ser Leu Arg Asp Asn His Thr Phe Glu Ala	
75 80 85 90	


```

Lys Asp Leu Asn Asp Ser Leu Asp Cys Ala Lys Lys Leu Leu Lys Leu
    275                280                285
Leu Asn Gly Ile Lys Ser Lys Val Asn Leu Ile Leu Phe Asn Pro His
    290                295                300
Glu Gly Ser Lys Phe Glu Arg Pro Ser Leu Glu Asn Ala Arg Met Phe
    305                310                315                320
Ala Asp Phe Leu Asn Ser Lys Gly Leu Leu Cys Thr Ile Arg Glu Ser
    325                330                335
Lys Ala Leu Asp Ile Glu Ala Ala Cys Gly Gln Leu Arg Glu Lys Lys
    340                345                350
Leu Ser Gln Gln Ile
    355

```

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...987
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```

ATG CCC ATT CTT TTT GAT TGT AAC GCT ATT GCT TCA CAA GTT TTA AAA      48
Met Pro Ile Leu Phe Asp Cys Asn Ala Ile Ala Ser Gln Val Leu Lys
  1                5                10                15

GAT GAA GCG AGC GCG CTT TTA GAA AGC GTT GGA CAA TTC CAA AAA CCC      96
Asp Glu Ala Ser Ala Leu Leu Glu Ser Val Gly Gln Phe Gln Lys Pro
    20                25                30

AAC GAT TTA GAA GCG ATT GTC AAA CTC ATT TTA AAA AGC CAA GAA AAT     144
Asn Asp Leu Glu Ala Ile Val Lys Leu Ile Leu Lys Ser Gln Glu Asn
    35                40                45

GGG GGT AAG CTT GTG ATA GTG GGT GTG GGT AAG AGC GCT TTA GTG GCG     192
Gly Gly Lys Leu Val Ile Val Gly Val Gly Lys Ser Ala Leu Val Ala
    50                55                60

CAA AAA ATC GTT GCT TCC ATG CTA AGC ACC GGT AAC AGG AGC GCG TTT     240
Gln Lys Ile Val Ala Ser Met Leu Ser Thr Gly Asn Arg Ser Ala Phe
    65                70                75                80

TTA CAC CCC ACA GAA GCC ATG CAT GGG GAT TTG GGC ATG GTG GAA AAA     288
Leu His Pro Thr Glu Ala Met His Gly Asp Leu Gly Met Val Glu Lys
    85                90                95

AAC GAT GTG GTT TTA ATG ATT AGC TAT GGG GGC GAG TCT TTA GAA TTA     336
Asn Asp Val Val Leu Met Ile Ser Tyr Gly Gly Glu Ser Leu Glu Leu
    100                105                110

```

TTG Leu	AAT Asn	CTG Leu 115	GTG Val	AGC Ser	CAT His	TTA Leu	AAA Lys 120	CGC Arg	TTG Leu	AGC Ser	CAT His	AAA Lys 125	ATC Ile	ATC Ile	ACT Thr	384
TTC Phe	ACT Thr 130	AAA Lys	AGC Ser	CCT Pro	AAT Asn	AGC Ser 135	TCG Ser	CTC Leu	TCT Ser	AAA Lys 140	CTC Leu	GGC Gly	GAT Asp	TAT Tyr	TAT Tyr	432
TTG Leu 145	AGC Ser	TTG Leu	AAA Lys	ATT Ile 150	CAA Gln	AAA Lys	GAA Glu	GCT Ala	TGC Cys	CCG Pro 155	ATT Ile	AAC Asn	ACC Thr	GCT Ala 160	CCA Pro	480
ACG Thr	ACT Thr	TCT Ser	ACC Thr 165	ACC Thr	CTA Leu	ACT Thr	CTA Leu	GCG Ala	TTA Leu 170	GGC Gly	GAT Asp	GTT Val	TTA Leu	ATG Met 175	GCA Ala	528
TGC Cys	TTG Leu	ATG Met	CGA Arg 180	GCG Ala	AAA Lys	AAC Asn	TTT Phe	AGC Ser 185	CAA Gln	GAA Glu	GAT Asp	TTT Phe 190	GCC Ala	TCC Ser	TTT Phe	576
CAT His	CCG Pro	GGC Gly 195	GGG Gly	CTT Leu	TTA Leu	GGC Gly 200	AAA Lys	AAA Lys	CTT Leu	TTT Phe	GTC Val	AAG Lys 205	GTT Val	AAA Lys	GAT Asp	624
TTA Leu 210	CTG Leu	CAA Gln	ACC Thr	ACG Thr	AAC Asn	CTC Leu 215	CCC Pro	CTA Leu	ATC Ile	GCT Ala 220	CCT Pro	AGC Ser	ACA Thr	AGT Ser	TTT Phe	672
AAA Lys 225	GAC Asp	GCG Ala	CTC Leu	ATA Ile 230	GAA Glu	ATG Met	AGT Ser	GAA Glu	AAA Lys	CGC Arg 235	TTA Leu	GGC Gly	AGC Ser	GCG Ala	ATT Ile 240	720
TTA Leu	GTC Val	AAT Asn	GAA Glu 245	GCT Ala	AAC Asn	GAG Glu	CTT Leu	GTG Val	GGG Gly 250	GTG Val	TTA Leu	AGC Ser	GAT Asp	GGC Gly 255	GAT Asp	768
GTC Val	CGT Arg	AGG Arg 260	GCG Ala	TTA Leu	TTA Leu	AAA Lys	GGG Gly 265	GTG Val	AGT Ser	TTA Leu	AAG Lys	AGC Ser	GAA Glu 270	GTG Val	AGG Arg	816
CAT His	TTT Phe 275	GCC Ala	ACT Thr	TTA Leu	AAA Lys	CCT Pro	AAA Lys 280	AGC Ser	TTT Phe	AAG Lys	AAT Asn 285	TTA Leu	GAC Asp	GCT Ala	CTT Leu	864
CTT Leu 290	TTA Leu	GAA Glu	GCG Ala	TTG Leu	GAA Glu	TTT Phe 295	TTA Leu	GAG Glu	CGC Arg	CAT His 300	AAG Lys	ATC Ile	CAG Gln	CTT Leu	TTA Leu	912
GTG Val 305	TGC Cys	GTA Val	GAT Asp	GAT Asp 310	CAT His	AAT Asn	AAG Lys	GTT Val	TTA Leu	GGG Gly 315	GTC Val	TTG Leu	CAC His	TTG Leu	CAC His 320	960
CAA Gln	CTT Leu	TTA Leu	GAA Glu 325	TTA Leu	GGG Gly	CTT Leu	AAA Lys	GCA Ala	TGA							990

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Met	Pro	Ile	Leu	Phe	Asp	Cys	Asn	Ala	Ile	Ala	Ser	Gln	Val	Leu	Lys
1				5					10					15	
Asp	Glu	Ala	Ser	Ala	Leu	Leu	Glu	Ser	Val	Gly	Gln	Phe	Gln	Lys	Pro
			20					25					30		
Asn	Asp	Leu	Glu	Ala	Ile	Val	Lys	Leu	Ile	Leu	Lys	Ser	Gln	Glu	Asn
		35					40					45			
Gly	Gly	Lys	Leu	Val	Ile	Val	Gly	Val	Gly	Lys	Ser	Ala	Leu	Val	Ala
	50					55				60					
Gln	Lys	Ile	Val	Ala	Ser	Met	Leu	Ser	Thr	Gly	Asn	Arg	Ser	Ala	Phe
65					70				75						80
Leu	His	Pro	Thr	Glu	Ala	Met	His	Gly	Asp	Leu	Gly	Met	Val	Glu	Lys
				85				90					95		
Asn	Asp	Val	Val	Leu	Met	Ile	Ser	Tyr	Gly	Gly	Glu	Ser	Leu	Glu	Leu
		100					105						110		
Leu	Asn	Leu	Val	Ser	His	Leu	Lys	Arg	Leu	Ser	His	Lys	Ile	Ile	Thr
		115					120					125			
Phe	Thr	Lys	Ser	Pro	Asn	Ser	Ser	Leu	Ser	Lys	Leu	Gly	Asp	Tyr	Tyr
	130					135					140				
Leu	Ser	Leu	Lys	Ile	Gln	Lys	Glu	Ala	Cys	Pro	Ile	Asn	Thr	Ala	Pro
145					150				155						160
Thr	Thr	Ser	Thr	Thr	Leu	Thr	Leu	Ala	Leu	Gly	Asp	Val	Leu	Met	Ala
				165				170					175		
Cys	Leu	Met	Arg	Ala	Lys	Asn	Phe	Ser	Gln	Glu	Asp	Phe	Ala	Ser	Phe
		180					185					190			
His	Pro	Gly	Gly	Leu	Leu	Gly	Lys	Lys	Leu	Phe	Val	Lys	Val	Lys	Asp
		195					200				205				
Leu	Leu	Gln	Thr	Thr	Asn	Leu	Pro	Leu	Ile	Ala	Pro	Ser	Thr	Ser	Phe
	210				215						220				
Lys	Asp	Ala	Leu	Ile	Glu	Met	Ser	Glu	Lys	Arg	Leu	Gly	Ser	Ala	Ile
225					230				235						240
Leu	Val	Asn	Glu	Ala	Asn	Glu	Leu	Val	Gly	Val	Leu	Ser	Asp	Gly	Asp
			245					250					255		
Val	Arg	Arg	Ala	Leu	Leu	Lys	Gly	Val	Ser	Leu	Lys	Ser	Glu	Val	Arg
			260				265						270		
His	Phe	Ala	Thr	Leu	Lys	Pro	Lys	Ser	Phe	Lys	Asn	Leu	Asp	Ala	Leu
		275					280					285			
Leu	Leu	Glu	Ala	Leu	Glu	Phe	Leu	Glu	Arg	His	Lys	Ile	Gln	Leu	Leu
	290				295						300				
Val	Cys	Val	Asp	Asp	His	Asn	Lys	Val	Leu	Gly	Val	Leu	His	Leu	His
305					310				315						320
Gln	Leu	Leu	Glu	Leu	Gly	Leu	Lys	Ala							
				325											

(2) INFORMATION FOR SEQ ID NO:353:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 991 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 64...939
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

TCCTTAAAC ATTTGAAGTA TAATACACTC TTATGGTCAA ATATTAAGTT TAGGAAAAGC	60
TGC ATG TGG AGT TTC ATT CAA AAA ATC TTT AAG GCT TTA ATC ATC GCA	108
Met Trp Ser Phe Ile Gln Lys Ile Phe Lys Ala Leu Ile Ile Ala	
1 5 10 15	
CCT TTA GAT TTT ATC ACG AAG TAT TTC AAG TCG TTT GTG CTG TTA CTC	156
Pro Leu Asp Phe Ile Thr Lys Tyr Phe Lys Ser Phe Val Leu Leu Leu	
20 25 30	
ATT GTA TTA GTC TTT TTT AGC GCT AAA GAA AGC GCG CCA AGC GCC CCG	204
Ile Val Leu Val Phe Phe Ser Ala Lys Glu Ser Ala Pro Ser Ala Pro	
35 40 45	
CCT AAT CTC GCT AAA CTC TAT TTA AAT GGG GCG ATT TTT AGC ACC GAG	252
Pro Asn Leu Ala Lys Leu Tyr Leu Asn Gly Ala Ile Phe Ser Thr Glu	
50 55 60	
GAT TTT GAC AAA GAA GTG GAT AAA ATC CTA AAA ACC CCT AGC ATT AAG	300
Asp Phe Asp Lys Glu Val Asp Lys Ile Leu Lys Thr Pro Ser Ile Lys	
65 70 75	
GGC GTT TTG CTT TTG ATT GAC TCT CCT GGT GGG GCG GTG TCA GCG AGC	348
Gly Val Leu Leu Leu Ile Asp Ser Pro Gly Gly Ala Val Ser Ala Ser	
80 85 90 95	
GTG GAA TTG AGC GAA AAA ATC GCT GAT TTG AAG CAA AAA ATG CCC GTT	396
Val Glu Leu Ser Glu Lys Ile Ala Asp Leu Lys Gln Lys Met Pro Val	
100 105 110	
TTA GCG TAT GCT AGG GGG GTT ATG GCG AGC GGG AGC TAT TAT GCG GGC	444
Leu Ala Tyr Ala Arg Gly Val Met Ala Ser Gly Ser Tyr Tyr Ala Gly	
115 120 125	
ATG CAA GCG AGC GAA GTT TAT GCC TCT AAA GCG AGT TTG ATA GGA TCC	492
Met Gln Ala Ser Glu Val Tyr Ala Ser Lys Ala Ser Leu Ile Gly Ser	
130 135 140	
ATT GGG GTG ATT TTT TCA GGT GCG AAT GTG GAA AAT TTG CTC AAT AAA	540
Ile Gly Val Ile Phe Ser Gly Ala Asn Val Glu Asn Leu Leu Asn Lys	
145 150 155	
GTC GGC GTA GCC ACT CAA GGC GTG CAT GCG GGC GAA TAC AAA GAA ATA	588
Val Gly Val Ala Thr Gln Gly Val His Ala Gly Glu Tyr Lys Glu Ile	
160 165 170 175	

GGC ACT TTC ACC AGA GCG TGG AAA CCC AAC GAA AAA GAT TTT TTG CAA	636
Gly Thr Phe Thr Arg Ala Trp Lys Pro Asn Glu Lys Asp Phe Leu Gln	
180 185 190	
AAT TTA GTC AAT GAG CAA TAC CAA ATG TTT GTG AAT GAT GTC GCA AAA	684
Asn Leu Val Asn Glu Gln Tyr Gln Met Phe Val Asn Asp Val Ala Lys	
195 200 205	
GCT AGG AAA TTA GAC GCT AAG GAT TAT AAG GAT TTT GCT GAA GGG AAG	732
Ala Arg Lys Leu Asp Ala Lys Asp Tyr Lys Asp Phe Ala Glu Gly Lys	
210 215 220	
GTC TTT AGC GCT CAA AAG GCT CTG AAA TTA AAA CTC ATT GAT AAA ATC	780
Val Phe Ser Ala Gln Lys Ala Leu Lys Leu Lys Leu Ile Asp Lys Ile	
225 230 235	
AGC ACG ATT AAG CAA GCG CAA GAT CGC TTA ATG GAA TTG AGT AAG GTT	828
Ser Thr Ile Lys Gln Ala Gln Asp Arg Leu Met Glu Leu Ser Lys Val	
240 245 250 255	
AAA AAA GCT TAT TGG CTA GAA AAA AGC CCT ATG GAG CGC TTC ATT GAA	876
Lys Lys Ala Tyr Trp Leu Glu Lys Ser Pro Met Glu Arg Phe Ile Glu	
260 265 270	
AAA GCC ACG CAA TCA GCC ACA AAC ATC ATC ACA CAA GCC TTT GGC TAT	924
Lys Ala Thr Gln Ser Ala Thr Asn Ile Ile Thr Gln Ala Phe Gly Tyr	
275 280 285	
CAA TTA TTA ATG AGA TAAAGATGTT AGAATTTATT TTAAAAATTC AAGCTAGAGA C	980
Gln Leu Leu Met Arg	
290	
TCTAAAGGCT T	991

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Met Trp Ser Phe Ile Gln Lys Ile Phe Lys Ala Leu Ile Ile Ala Pro	
1 5 10 15	
Leu Asp Phe Ile Thr Lys Tyr Phe Lys Ser Phe Val Leu Leu Ile	
20 25 30	
Val Leu Val Phe Phe Ser Ala Lys Glu Ser Ala Pro Ser Ala Pro Pro	
35 40 45	
Asn Leu Ala Lys Leu Tyr Leu Asn Gly Ala Ile Phe Ser Thr Glu Asp	
50 55 60	
Phe Asp Lys Glu Val Asp Lys Ile Leu Lys Thr Pro Ser Ile Lys Gly	
65 70 75 80	
Val Leu Leu Leu Ile Asp Ser Pro Gly Gly Ala Val Ser Ala Ser Val	
85 90 95	

Asn	Ser	Thr	Val	Lys	Ile	Ile	Ser	Lys	Thr	Asp	Asn	Ile	Glu	Ile	Gln	
40						45					50					
GAC	TTG	AAG	CTC	AAT	CGT	GGC	AAT	TGT	GAG	CAT	GAT	CAA	AAT	TTC	TTG	246
Asp	Leu	Lys	Leu	Asn	Arg	Gly	Asn	Cys	Glu	His	Asp	Gln	Asn	Phe	Leu	
55					60					65					70	
GTA	AAG	TTA	ATC	CAA	GAA	ACA	GCC	AAT	ACA	TAC	CTG	TTT	GCA	TCA	GAA	294
Val	Lys	Leu	Ile	Gln	Glu	Thr	Ala	Asn	Thr	Tyr	Leu	Phe	Ala	Ser	Glu	
				75					80					85		
AAA	GAA	AAA	GCG	ATC	AAA	AAC	CAC	CAA	GCA	AAA	ATC	GCA	AGA	CTT	CAA	342
Lys	Glu	Lys	Ala	Ile	Lys	Asn	His	Gln	Ala	Lys	Ile	Ala	Arg	Leu	Gln	
			90					95					100			
AAA	GAT	TTA	GAA	GAA	CTC	ACA	CAG	CAT	GTG	CAA	CAA	TCC	AAT	AAT	CTT	390
Lys	Asp	Leu	Glu	Glu	Leu	Thr	Gln	His	Val	Gln	Gln	Ser	Asn	Asn	Leu	
		105					110					115				
GAT	AAA	TTG	TTA	GAA	AAT	GGA	GGA	CTA	TTC	GTT	AGT	GGC	CAT	GAT	TAT	438
Asp	Lys	Leu	Leu	Glu	Asn	Gly	Gly	Leu	Phe	Val	Ser	Gly	His	Asp	Tyr	
	120					125					130					
AAA	TAT	ACA	AAA	GAT	GAT	AAC	CCA	ATA	TAT	GTT	GTT	AAG	AGG	ATG	CTT	486
Lys	Tyr	Thr	Lys	Asp	Asp	Asn	Pro	Ile	Tyr	Val	Val	Lys	Arg	Met	Leu	
	135				140					145					150	
GAT	AAC	CTT	GAT	AGC	TAT	AAA	TAT	GAA	TCA	GAC	GAC	GTG	CTA	GAC	GTG	534
Asp	Asn	Leu	Asp	Ser	Tyr	Lys	Tyr	Glu	Ser	Asp	Asp	Val	Leu	Asp	Val	
				155					160					165		
CCA	TAT	GAG	AAG	CTA	TTG	GAA	ATA	AGC	ATT	GCT	ATT	GAA	GAC	ACT	AAA	582
Pro	Tyr	Glu	Lys	Leu	Leu	Glu	Ile	Ser	Ile	Ala	Ile	Glu	Asp	Thr	Lys	
			170					175					180			
AAC	CCC	AAA	GAC	TAC	CCT	TAT	ATC	AAC	CTT	AAA	GAA	CTC	AAA	AAA	TTA	630
Asn	Pro	Lys	Asp	Tyr	Pro	Tyr	Ile	Asn	Leu	Lys	Glu	Leu	Lys	Lys	Leu	
		185					190					195				
ATA	GAT	AGT	ATT	ATT	GAT	GAT	CAT	GGT	TAT	ATG	GCC	GAT	GGC	TTT	TTG	678
Ile	Asp	Ser	Ile	Ile	Asp	Asp	His	Gly	Tyr	Met	Ala	Asp	Gly	Phe	Leu	
	200				205					210						
AAT	GAA	TAT	TCT	AAT	AGG	GTA	TCA	AAA	AAA	GGT	CTC	CAA	ATC	CTT	GCT	726
Asn	Glu	Tyr	Ser	Asn	Arg	Val	Ser	Lys	Lys	Gly	Leu	Gln	Ile	Leu	Ala	
	215				220					225					230	
AAA	CTA	AAA	TCC	ATG	TGG	CCT	AGC	GTA	GGG	AAA	TTT	TAT	TTC	GCC	TCT	774
Lys	Leu	Lys	Ser	Met	Trp	Pro	Ser	Val	Gly	Lys	Phe	Tyr	Phe	Ala	Ser	
				235					240					245		
TTG	AAA	GAG	GCT	ATC	CCA	AGG	CAT	GCC	AAA	GAA	GTT	ACT	GAC	AAG	ATG	822
Leu	Lys	Glu	Ala	Ile	Pro	Arg	His	Ala	Lys	Glu	Val	Thr	Asp	Lys	Met	
			250					255					260			
ATT	AGC	TCT	GAA	GAA	AAA	TCT	ATC	AAA	GCC	AAT	CAA	GTC	AAA	CTC	ACT	870
Ile	Ser	Ser	Glu	Glu	Lys	Ser	Ile	Lys	Ala	Asn	Gln	Val	Lys	Leu	Thr	
		265					270					275				

Gly	Leu	Gln	Ile	Leu	Ala	Lys	Leu	Lys	Ser	Met	Trp	Pro	Ser	Val	Gly
225					230					235					240
Lys	Phe	Tyr	Phe	Ala	Ser	Leu	Lys	Glu	Ala	Ile	Pro	Arg	His	Ala	Lys
				245					250					255	
Glu	Val	Thr	Asp	Lys	Met	Ile	Ser	Ser	Glu	Glu	Lys	Ser	Ile	Lys	Ala
			260					265					270		
Asn	Gln	Val	Lys	Leu	Thr	Glu	Ala	Lys	Gln	Asp	Ile	Asp	Lys	Met	Glu
		275					280					285			
Lys	Ile	Ile	Lys	Asp	Leu	Glu	Ser	Lys	Lys	Asn	Thr	Leu	Ser	Val	Tyr
	290					295					300				
Leu	Lys	Phe	Gly	Glu	Ser	Phe	Thr	Ala	His	Tyr	Lys	Cys	Gln	Asn	Leu
305					310					315					320
Ile	Glu	Val	Gly	Val	Lys	Thr	Asp	Lys	Gly	Ser	Trp	Thr	Phe	Asn	Phe
			325						330					335	

Asn Arg

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 94...807
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

GCCTTGACGC	ATGTTTTTGA	AGTTTATCCT	AAAGTCAATA	TTTTTTTAAA	AATCCTTCAC	60										
AAAGAAGGGG	CTTACCACAA	GCTTATTTCT	CGC	ATG	TGT	TTG	GTC	AAA	GAC	AAG	114					
			Met	Cys	Leu	Val	Lys	Asp	Lys							
			1						5							
CTC	AAA	GAC	ATT	ATC	AGC	GTC	AAA	AGC	GCG	CTT	TCT	TTT	TCG	TTA	AAA	162
Leu	Lys	Asp	Ile	Ile	Ser	Val	Lys	Ser	Ala	Leu	Ser	Phe	Ser	Leu	Lys	
		10					15					20				
GGG	GAT	TTT	GAC	TGC	CCT	TTA	GAA	GAA	AAC	TCG	CTC	TTT	AAA	GCC	CTC	210
Gly	Asp	Phe	Asp	Cys	Pro	Leu	Glu	Glu	Asn	Ser	Leu	Phe	Lys	Ala	Leu	
	25					30					35					
CAA	ATT	TTA	AAG	AAT	TTT	TTA	AAA	TCA	AAA	AAT	TTC	TCT	CAT	TCT	GTC	258
Gln	Ile	Leu	Lys	Asn	Phe	Leu	Lys	Ser	Lys	Asn	Phe	Ser	His	Ser	Val	
	40				45				50						55	
ATC	AAA	TCC	CTA	GAC	ACC	CTA	GCG	ATT	GAA	GTG	GAA	AAA	AAC	ATC	CCC	306
Ile	Lys	Ser	Leu	Asp	Thr	Leu	Ala	Ile	Glu	Val	Glu	Lys	Asn	Ile	Pro	
				60					65					70		
ACT	CAA	GCC	GGA	TTA	GGC	GGT	GGG	AGC	ACT	GAT	GCT	GGG	GGG	CTA	TTG	354
Thr	Gln	Ala	Gly	Leu	Gly	Gly	Gly	Ser	Thr	Asp	Ala	Gly	Gly	Leu	Leu	

ATG Met	TTA Leu	CAA Gln	CTC Leu	AGC Ser	GAA Glu	GGC Gly	TCG Ser	CCG Pro	GTC Val	TTG Leu	CAC His	TAC Tyr	GGG Gly	CAG Gln	GCT Ala	198
45																
TGT Cys	TTT Phe	GAA Glu	GGC Gly	TTG Leu	AAG Lys	GCT Ala	TAC Tyr	CGC Arg	TCT Ser	CAA Gln	AAG Lys	GGG Gly	AAA Lys	GCT Ala	TTA Leu	246
60																
CTC Leu	TTT Phe	CGC Arg	CCT Pro	TTA Leu	GAA Glu	AAC Asn	GCC Ala	AAA Lys	CGC Arg	TTG Leu	CAA Gln	ACT Thr	TCA Ser	TGC Cys	GAA Glu	294
75																
AGA Arg	CTG Leu	CTC Leu	ATG Met	CCC Pro	AAA Lys	GTG Val	AGC Ser	GAA Glu	GAG Glu	CTG Leu	TTT Phe	TTA Leu	AGG Arg	GCA Ala	TGC Cys	342
90																
GCT Ala	GAA Glu	GTG Val	GTG Val	AAA Lys	GCG Ala	AAT Asn	CAA Gln	AAA Lys	TGG Trp	CTC Leu	GCT Ala	CCT Pro	TAT Tyr	AAA Lys	AGC Ser	390
110																
GGG Gly	GCG Ala	AGT Ser	TTG Leu	TAT Tyr	TTG Leu	CGC Arg	CCT Pro	TTT Phe	GTC Val	ATA Ile	GGC Gly	GTA Val	GGG Gly	GAT Asp	AAT Asn	438
125																
TTG Leu	GGG Gly	GTG Val	AAG Lys	CCG Pro	GCT Ala	AAT Asn	GAA Glu	TAC Tyr	CTT Leu	TTT Phe	ATC Ile	GTG Val	TTT Phe	TGT Cys	GCG Ala	486
140																
CCT Pro	GTG Val	GGG Gly	GCG Ala	TAT Tyr	TTT Phe	AAG Lys	GGG Gly	GGT Gly	ATA Ile	GAA Glu	AAA Lys	GGG Gly	GGG Gly	GCT Ala	AGG Arg	534
155																
TTT Phe	ATC Ile	ACT Thr	ACG Thr	ATT Ile	TTT Phe	GAT Asp	AGG Arg	GCC Ala	GCG Ala	CCT Pro	AAA Lys	GGC Gly	ACC Thr	GGT Gly	GGG Gly	582
170																
GTG Val	AAA Lys	GTG Val	GGA Gly	GGG Gly	AAT Asn	TAC Tyr	GCT Ala	GCA Ala	AGC Ser	CTG Leu	TTA Leu	GCC Ala	CAT His	AAA Lys	ATG Met	630
190																
GCC Ala	ACA Thr	GAG Glu	CAA Gln	GGC Gly	TAT Tyr	GAT Asp	GAT Asp	TGC Cys	ATT Ile	TAT Tyr	TTA Leu	GAC Asp	CCT Pro	ACT Thr	ACG Thr	678
205																
CAC His	ACT Thr	AAA Lys	ATT Ile	GAA Glu	GAA Glu	GTG Val	GGG Gly	GCG Ala	GCG Ala	AAT Asn	TTT Phe	TTT Phe	GGC Gly	ATC Ile	ACG Thr	726
220																
CAT His	GAT Asp	GAT Asp	GCC Ala	TTT Phe	ATC Ile	ACC Thr	CCG Pro	CAT His	TCG Ser	CCA Pro	AGC Ser	ATT Ile	CTG Leu	CCA Pro	AGC Ser	774
235																
ATT Ile	ACC Thr	AAA Lys	AAA Lys	AGC Ser	TTG Leu	ATG Met	GTT Val	TTG Leu	GCT Ala	AAA Lys	GAA Glu	TAT Tyr	TTG Leu	AAC Asn	CTC Leu	822
250																
AAA Lys	GTA Val	GAA Glu	GAG Glu	AGG Arg	GAA Glu	ATC Ile	CTA Leu	ATG Met	GAT Asp	GAG Glu	TTG Leu	GAT Asp	GCG Ala	TTT Phe	AAA Lys	870

270	275	280	
GAA GCT GGA GCG TGC GGG ACA GCT GCG ATC ATT ACG CCC ATT AAA GAA			918
Glu Ala Gly Ala Cys Gly Thr Ala Ala Ile Ile Thr Pro Ile Lys Glu			
285	290	295	
ATC GTG CAC AAC AAC AAG TCT TAT TTT TTT GAA GCG CCG GGC CAT ATT			966
Ile Val His Asn Asn Lys Ser Tyr Phe Phe Glu Ala Pro Gly His Ile			
300	305	310	
ACT AAA CGA CTC TAT GAT TTG CTT TTA TCC ATC CAA CAA GGC GAA CAA			1014
Thr Lys Arg Leu Tyr Asp Leu Leu Leu Ser Ile Gln Gln Gly Glu Gln			
315	320	325	
GAA GCC CCC AAA GAT TGG ATT TTT GAA GTT GGC TAAAAGGTTA AAATTTATAG			1067
Glu Ala Pro Lys Asp Trp Ile Phe Glu Val Gly			
330	335	340	
CTGTATGCCG CATAAAATAA GGGCG			1092

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Met	Ala	Asn	Leu	Glu	Asn	Leu	Asp	Trp	Lys	Asn	Leu	Gly	Phe	Ser	Tyr
1				5					10					15	
Ile	Lys	Thr	Asp	Phe	Arg	Phe	Ile	Ala	Thr	Tyr	Lys	Asn	Gly	Ser	Trp
			20					25					30		
Ser	Gln	Gly	Gly	Leu	Val	Ser	Glu	Asn	Met	Leu	Gln	Leu	Ser	Glu	Gly
		35					40				45				
Ser	Pro	Val	Leu	His	Tyr	Gly	Gln	Ala	Cys	Phe	Glu	Gly	Leu	Lys	Ala
	50					55					60				
Tyr	Arg	Ser	Gln	Lys	Gly	Lys	Ala	Leu	Leu	Phe	Arg	Pro	Leu	Glu	Asn
65					70					75				80	
Ala	Lys	Arg	Leu	Gln	Thr	Ser	Cys	Glu	Arg	Leu	Leu	Met	Pro	Lys	Val
			85					90						95	
Ser	Glu	Glu	Leu	Phe	Leu	Arg	Ala	Cys	Ala	Glu	Val	Val	Lys	Ala	Asn
			100				105						110		
Gln	Lys	Trp	Leu	Ala	Pro	Tyr	Lys	Ser	Gly	Ala	Ser	Leu	Tyr	Leu	Arg
		115				120						125			
Pro	Phe	Val	Ile	Gly	Val	Gly	Asp	Asn	Leu	Gly	Val	Lys	Pro	Ala	Asn
		130				135					140				
Glu	Tyr	Leu	Phe	Ile	Val	Phe	Cys	Ala	Pro	Val	Gly	Ala	Tyr	Phe	Lys
145					150					155				160	
Gly	Gly	Ile	Glu	Lys	Gly	Gly	Ala	Arg	Phe	Ile	Thr	Thr	Ile	Phe	Asp
			165					170						175	
Arg	Ala	Ala	Pro	Lys	Gly	Thr	Gly	Gly	Val	Lys	Val	Gly	Gly	Asn	Tyr
			180				185						190		
Ala	Ala	Ser	Leu	Leu	Ala	His	Lys	Met	Ala	Thr	Glu	Gln	Gly	Tyr	Asp
		195				200						205			

```

Asp Cys Ile Tyr Leu Asp Pro Thr Thr His Thr Lys Ile Glu Glu Val
210                215                220
Gly Ala Ala Asn Phe Phe Gly Ile Thr His Asp Asp Ala Phe Ile Thr
225                230                235                240
Pro His Ser Pro Ser Ile Leu Pro Ser Ile Thr Lys Lys Ser Leu Met
                245                250                255
Val Leu Ala Lys Glu Tyr Leu Asn Leu Lys Val Glu Glu Arg Glu Ile
                260                265                270
Leu Met Asp Glu Leu Asp Ala Phe Lys Glu Ala Gly Ala Cys Gly Thr
                275                280                285
Ala Ala Ile Ile Thr Pro Ile Lys Glu Ile Val His Asn Asn Lys Ser
290                295                300
Tyr Phe Phe Glu Ala Pro Gly His Ile Thr Lys Arg Leu Tyr Asp Leu
305                310                315                320
Leu Leu Ser Ile Gln Gln Gly Glu Gln Glu Ala Pro Lys Asp Trp Ile
                325                330                335
Phe Glu Val Gly
                340

```

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...2067
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

GTTATAATTT TATTTTTTAA AAGGATACCC ATG AAT AAA GTT CAA TCT ATT GAT      54
                               Met Asn Lys Val Gln Ser Ile Asp
                               1                               5

CCT TTA ATC GCT GAT AAG TTC AAC AAC GAG TTA AGA AGT TAT AAC CTA      102
Pro Leu Ile Ala Asp Lys Phe Asn Asn Glu Leu Arg Ser Tyr Asn Leu
10                               15                               20

GAA TAC AAA CTA GAG CAA GAA AGC CTG AAT AAA GAA ATT GAT GAA GCT      150
Glu Tyr Lys Leu Glu Gln Glu Ser Leu Asn Lys Glu Ile Asp Glu Ala
25                               30                               35                               40

TTA AAA AAT TAC GCT TCT AAA AAT GGG GGT TTA GGG GGT AAC CGC CCT      198
Leu Lys Asn Tyr Ala Ser Lys Asn Gly Gly Leu Gly Gly Asn Arg Pro
45                               50                               55

GAT GTG AAA CTT TTA TTA AAC ACA CAA GAC CCC AAC AGA AGA GTC CCT      246
Asp Val Lys Leu Leu Leu Asn Thr Gln Asp Pro Asn Arg Arg Val Pro
60                               65                               70

ATT TTA ATA GAA TAC AAA GGG CTA AAA GAT AAG CTC ATT AAA TTA GAC      294

```

Ile	Leu	Ile	Glu	Tyr	Lys	Gly	Leu	Lys	Asp	Lys	Leu	Ile	Lys	Leu	Asp	
		75					80					85				
AAA	AAC	AAA	CTG	GTA	GAA	AAC	TTT	AAA	AAC	CAT	GAG	CCT	CAT	TAT	AAA	342
Lys	Asn	Lys	Leu	Val	Glu	Asn	Phe	Lys	Asn	His	Glu	Pro	His	Tyr	Lys	
		90					95					100				
AAC	ATT	AGA	GAA	TAC	GCC	CTA	AAT	GGG	GCT	TTG	CAT	TAC	GCT	AAT	GCG	390
Asn	Ile	Arg	Glu	Tyr	Ala	Leu	Asn	Gly	Ala	Leu	His	Tyr	Ala	Asn	Ala	
105					110					115					120	
ATT	TTA	CAC	CAC	ACG	AGC	TAC	ACT	GAA	TGC	ATC	GCC	ATA	GGC	ATT	ACA	438
Ile	Leu	His	His	Thr	Ser	Tyr	Thr	Glu	Cys	Ile	Ala	Ile	Gly	Ile	Thr	
				125					130					135		
GGC	TAT	AAA	GAC	AAT	AAG	GGC	GGC	ATA	TGC	TCT	CAA	ATC	GCT	GTC	TAT	486
Gly	Tyr	Lys	Asp	Asn	Lys	Gly	Gly	Ile	Cys	Ser	Gln	Ile	Ala	Val	Tyr	
			140					145					150			
TAT	GTG	AAT	AAA	AGC	AAT	CTA	GGC	ATG	GGG	ATA	GAT	GTT	TCA	AAA	GGC	534
Tyr	Val	Asn	Lys	Ser	Asn	Leu	Gly	Met	Gly	Ile	Asp	Val	Ser	Lys	Gly	
		155					160					165				
GAG	CAA	GGT	TAT	AGC	GAT	CTC	TCC	TTT	TTA	AGC	CGT	AAG	CAT	TTT	AAC	582
Glu	Gln	Gly	Tyr	Ser	Asp	Leu	Ser	Phe	Leu	Ser	Arg	Lys	His	Phe	Asn	
	170					175					180					
GAC	TTT	ATT	AAA	CGA	GTA	GAC	ACC	CTT	TCT	TTA	AGC	GAT	GAA	GAT	TTA	630
Asp	Phe	Ile	Lys	Arg	Val	Asp	Thr	Leu	Ser	Leu	Ser	Asp	Glu	Asp	Leu	
185					190					195					200	
GAG	CGC	ATT	AGA	GAA	AAG	AAA	AAC	CAA	GAA	ATA	GAA	GAC	TGC	TTA	ATG	678
Glu	Arg	Ile	Arg	Glu	Lys	Lys	Asn	Gln	Glu	Ile	Glu	Asp	Cys	Leu	Met	
				205					210				215			
CGG	CTC	AAC	AAC	AAT	ATT	TAC	AAC	AAA	GAA	AAG	AAT	TTT	TTA	AGC	GAA	726
Arg	Leu	Asn	Asn	Asn	Ile	Tyr	Asn	Lys	Glu	Lys	Asn	Phe	Leu	Ser	Glu	
			220					225					230			
CAC	AAT	CGG	GTA	TAT	TTA	GTG	ATT	GCG	AGC	ATT	ATC	GCT	AAT	TTA	GGC	774
His	Asn	Arg	Val	Tyr	Leu	Val	Ile	Ala	Ser	Ile	Ile	Ala	Asn	Leu	Gly	
		235				240						245				
ATC	CCT	AAT	TTG	GTA	ACC	CCC	CTA	AAC	AAA	GAA	GAT	CTA	AAA	TCC	AGC	822
Ile	Pro	Asn	Leu	Val	Thr	Pro	Leu	Asn	Lys	Glu	Asp	Leu	Lys	Ser	Ser	
	250					255					260					
GAT	GAG	GTC	CAT	CAA	AGA	GAT	GGC	GAC	ATC	ATG	CTC	AGA	AAA	ATC	CAA	870
Asp	Glu	Val	His	Gln	Arg	Asp	Gly	Asp	Ile	Met	Leu	Arg	Lys	Ile	Gln	
265					270					275					280	
TCC	TTT	TTA	GAG	AAT	AAG	GAT	TTG	TCT	CCA	GAG	AAA	AGG	CAA	AGC	ATT	918
Ser	Phe	Leu	Glu	Asn	Lys	Asp	Leu	Ser	Pro	Glu	Lys	Arg	Gln	Ser	Ile	
				285					290				295			
ATT	TCT	TCA	TTA	GAG	ACT	TTA	TTA	AGA	AAC	GAA	AAC	AAC	AAC	AAA	GCC	966
Ile	Ser	Ser	Leu	Glu	Thr	Leu	Leu	Arg	Asn	Glu	Asn	Asn	Asn	Lys	Ala	
			300					305					310			

ACT Thr	AAT Asn	GGC Gly 315	GAA Glu	AGC Ser	TGT Cys	TTG Leu	AAG Lys 320	CGT Arg	TGT Cys	TTT Phe	AGT Ser	GAG Glu 325	ATT Ile	GTG Val	GAT Asp	1014
AGT Ser	TTG Leu 330	GGC Gly	ATT Ile	TAT Tyr	TAT Tyr	AAA Lys 335	ATC Ile	GGT Gly	CTT Leu	AGC Ser	ACG Thr 340	GAT Asp	TTT Phe	ACC Thr	GGT Gly	1062
AAA Lys 345	TTG Leu	TTC Phe	AAT Asn	GAA Glu	ATG Met 350	TAT Tyr	CGC Arg	TGG Trp	CTG Leu	GGT Gly 355	TTC Phe	ACG Thr	AAA Lys	GAC Asp	CAA Gln 360	1110
TTA Leu	AAC Asn	GAT Asp	GTG Val	GTG Val 365	CTC Leu	ACA Thr	CCC Pro	CCT Pro	TAT Tyr 370	GTC Val	GCC Ala	ACG Thr	CTT Leu	TTA Leu 375	GCT Ala	1158
AGA Arg	CTT Leu	TCT Ser	AAA Lys 380	GTC Val	AAT Asn	AAG Lys	GAT Asp 385	AGT Ser	TTC Phe	GTG Val	TGG Trp	GAT Asp 390	TTT Phe	GCC Ala	ACC Thr	1206
GGA Gly	AGC Ser	GCT Ala 395	GGG Gly	CTA Leu	TTA Leu	GTC Val	GCA Ala 400	AGC Ser	ATG Met	AAT Asn	TTG Leu	ATG Met 405	ATA Ile	GAA Glu	GAC Asp	1254
GCT Ala	AAA Lys 410	AAG Lys	CGT Arg	ATC Ile	ACT Thr	AGT Ser 415	CCA Pro	GAG Glu	GAA Glu	TTA Leu	GAG Glu 420	CAA Gln	AAA Lys	ATC Ile	GCC Ala	1302
CAC His 425	ATT Ile	AAA Lys	GCC Ala	AAG Lys	CAA Gln 430	CTT Leu	TTA Leu	GGG Gly	ATA Ile	GAA Glu 435	ATC Ile	TTA Leu	TCG Ser	GAT Asp	ATC Ile 440	1350
CAT His	ACT Thr	TTA Leu	GCG Ala	GTG Val 445	TTA Leu	AAC Asn	ATG Met	ATT Ile	TTA Leu 450	ATG Met	GGC Gly	GAT Asp	GGG Gly	AGC Ser 455	AGT Ser	1398
CAA Gln	ATC Ile	TTA Leu	AAC Asn 460	CAA Gln	GAC Asp	GGC Gly	TTG Leu	AGC Ser 465	GGT Gly	TTT Phe	GAT Asp	GGC Gly 470	AAA Lys	GTC Val	AAT Asn	1446
AAC Asn	GAA Glu	GCG Ala 475	TTT Phe	AAG Lys	GCT Ala	AAT Asn	GCC Ala 480	TTT Phe	GTT Val	TTA Leu	AAC Asn	CCG Pro 485	CCT Pro	TAT Tyr	TCC Ser	1494
GCT Ala	AGC Ser 490	GGT Gly	AAT Asn	GGC Gly	ATG Met	GTG Val 495	TTT Phe	GTG Val	GAG Glu	CAG Gln	GCT Ala 500	TTA Leu	GAA Glu	AAA Lys	ATG Met	1542
CAA Gln 505	AGC Ser	GGT Gly	TAT Tyr	GCG Ala	AGC Ser 510	GTG Val	ATC Ile	ATC Ile	CAA Gln	TCA Ser 515	AGC Ser	GCC Ala	GGC Gly	AGT Ser	GGT Gly 520	1590
AAA Lys	GCC Ala	AAA Lys	GAA Glu	TAC Tyr 525	AAT Asn	GTA Val	AGG Arg	ATT Ile	TTG Leu 530	GAA Glu	AAA Lys	CAC His	ACG Thr	CTT Leu 535	TTA Leu	1638
GCG Ala	AGC Ser	ATT Ile	AAA Lys	ATG Met	CCT Pro	TTA Leu	GAT Asp	TTA Leu	TTC Phe	ATC Ile	GGT Gly	AAA Lys	AGC Ser	AGC Ser	GTT Val	1686

540	545	550	
CAA ACC CAT ATC TAT GTT TTT AGG GTC AAT GAA AAG CAT GAC GCT AAG			1734
Gln Thr His Ile Tyr Val Phe Arg Val Asn Glu Lys His Asp Ala Lys			
555	560	565	
CAA AGG GTG AAA TTT ATT AAT TTC AGT AAC GAC GGC TAC GCT AGA GCG			1782
Gln Arg Val Lys Phe Ile Asn Phe Ser Asn Asp Gly Tyr Ala Arg Ala			
570	575	580	
AAT CGC AAA AAA GCC AAA GCC AGC CAC AAT TTA AAA GAC ACG CAT AAC			1830
Asn Arg Lys Lys Ala Lys Ala Ser His Asn Leu Lys Asp Thr His Asn			
585	590	595	600
GCC AAA GAG CGC TAC AAC GAA GTC GTG GAT TTA GTC CAT ATT GGC CAA			1878
Ala Lys Glu Arg Tyr Asn Glu Val Val Asp Leu Val His Ile Gly Gln			
605	610	615	
TCA TGT TTG AAA TTT CTA AGC GAA GAT GAC TAT TAT GAA AAC ACC ATA			1926
Ser Cys Leu Lys Phe Leu Ser Glu Asp Asp Tyr Tyr Glu Asn Thr Ile			
620	625	630	
GAT CCC AAA AAC GGG AGC GAT TGG AAC CAA AAC AAA CCC ACT GAC ACC			1974
Asp Pro Lys Asn Gly Ser Asp Trp Asn Gln Asn Lys Pro Thr Asp Thr			
635	640	645	
AAA CCC GAA TTA GAG GAT TTT AAA AGA ACG ATA GCC GAT TAC CTT TCT			2022
Lys Pro Glu Leu Glu Asp Phe Lys Arg Thr Ile Ala Asp Tyr Leu Ser			
650	655	660	
TAT GAA GTA AGC TTG ATT TTA AAA AAC CAA ATG CCC CCA AAG CGA TAGGC			2072
Tyr Glu Val Ser Leu Ile Leu Lys Asn Gln Met Pro Pro Lys Arg			
665	670	675	
CCCCCTTAATA GCCAACTCAA CGCTATTAAG TGGGGCGAG			2111

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Met	Asn	Lys	Val	Gln	Ser	Ile	Asp	Pro	Leu	Ile	Ala	Asp	Lys	Phe	Asn
1				5					10					15	
Asn	Glu	Leu	Arg	Ser	Tyr	Asn	Leu	Glu	Tyr	Lys	Leu	Glu	Gln	Glu	Ser
			20					25					30		
Leu	Asn	Lys	Glu	Ile	Asp	Glu	Ala	Leu	Lys	Asn	Tyr	Ala	Ser	Lys	Asn
			35				40					45			
Gly	Gly	Leu	Gly	Gly	Asn	Arg	Pro	Asp	Val	Lys	Leu	Leu	Leu	Asn	Thr
	50				55				60						
Gln	Asp	Pro	Asn	Arg	Arg	Val	Pro	Ile	Leu	Ile	Glu	Tyr	Lys	Gly	Leu
65					70				75					80	

Lys	Asp	Lys	Leu	Ile	Lys	Leu	Asp	Lys	Asn	Lys	Leu	Val	Glu	Asn	Phe
				85					90					95	
Lys	Asn	His	Glu	Pro	His	Tyr	Lys	Asn	Ile	Arg	Glu	Tyr	Ala	Leu	Asn
			100					105					110		
Gly	Ala	Leu	His	Tyr	Ala	Asn	Ala	Ile	Leu	His	His	Thr	Ser	Tyr	Thr
			115				120					125			
Glu	Cys	Ile	Ala	Ile	Gly	Ile	Thr	Gly	Tyr	Lys	Asp	Asn	Lys	Gly	Gly
	130					135					140				
Ile	Cys	Ser	Gln	Ile	Ala	Val	Tyr	Tyr	Val	Asn	Lys	Ser	Asn	Leu	Gly
145					150					155					160
Met	Gly	Ile	Asp	Val	Ser	Lys	Gly	Glu	Gln	Gly	Tyr	Ser	Asp	Leu	Ser
				165					170					175	
Phe	Leu	Ser	Arg	Lys	His	Phe	Asn	Asp	Phe	Ile	Lys	Arg	Val	Asp	Thr
			180					185					190		
Leu	Ser	Leu	Ser	Asp	Glu	Asp	Leu	Glu	Arg	Ile	Arg	Glu	Lys	Lys	Asn
			195				200					205			
Gln	Glu	Ile	Glu	Asp	Cys	Leu	Met	Arg	Leu	Asn	Asn	Asn	Ile	Tyr	Asn
	210					215					220				
Lys	Glu	Lys	Asn	Phe	Leu	Ser	Glu	His	Asn	Arg	Val	Tyr	Leu	Val	Ile
225					230					235					240
Ala	Ser	Ile	Ile	Ala	Asn	Leu	Gly	Ile	Pro	Asn	Leu	Val	Thr	Pro	Leu
				245					250					255	
Asn	Lys	Glu	Asp	Leu	Lys	Ser	Ser	Asp	Glu	Val	His	Gln	Arg	Asp	Gly
			260					265					270		
Asp	Ile	Met	Leu	Arg	Lys	Ile	Gln	Ser	Phe	Leu	Glu	Asn	Lys	Asp	Leu
		275					280					285			
Ser	Pro	Glu	Lys	Arg	Gln	Ser	Ile	Ile	Ser	Ser	Leu	Glu	Thr	Leu	Leu
	290					295					300				
Arg	Asn	Glu	Asn	Asn	Asn	Lys	Ala	Thr	Asn	Gly	Glu	Ser	Cys	Leu	Lys
305					310					315					320
Arg	Cys	Phe	Ser	Glu	Ile	Val	Asp	Ser	Leu	Gly	Ile	Tyr	Tyr	Lys	Ile
				325					330					335	
Gly	Leu	Ser	Thr	Asp	Phe	Thr	Gly	Lys	Leu	Phe	Asn	Glu	Met	Tyr	Arg
			340					345					350		
Trp	Leu	Gly	Phe	Thr	Lys	Asp	Gln	Leu	Asn	Asp	Val	Val	Leu	Thr	Pro
		355					360					365			
Pro	Tyr	Val	Ala	Thr	Leu	Leu	Ala	Arg	Leu	Ser	Lys	Val	Asn	Lys	Asp
	370					375					380				
Ser	Phe	Val	Trp	Asp	Phe	Ala	Thr	Gly	Ser	Ala	Gly	Leu	Leu	Val	Ala
385					390					395					400
Ser	Met	Asn	Leu	Met	Ile	Glu	Asp	Ala	Lys	Lys	Arg	Ile	Thr	Ser	Pro
				405					410					415	
Glu	Glu	Leu	Glu	Gln	Lys	Ile	Ala	His	Ile	Lys	Ala	Lys	Gln	Leu	Leu
			420					425					430		
Gly															

Leu Phe Ile Gly Lys Ser Ser Val Gln Thr His Ile Tyr Val Phe Arg
 545 550 555 560
 Val Asn Glu Lys His Asp Ala Lys Gln Arg Val Lys Phe Ile Asn Phe
 565 570 575
 Ser Asn Asp Gly Tyr Ala Arg Ala Asn Arg Lys Lys Ala Lys Ala Ser
 580 585 590
 His Asn Leu Lys Asp Thr His Asn Ala Lys Glu Arg Tyr Asn Glu Val
 595 600 605
 Val Asp Leu Val His Ile Gly Gln Ser Cys Leu Lys Phe Leu Ser Glu
 610 615 620
 Asp Asp Tyr Tyr Glu Asn Thr Ile Asp Pro Lys Asn Gly Ser Asp Trp
 625 630 635 640
 Asn Gln Asn Lys Pro Thr Asp Thr Lys Pro Glu Leu Glu Asp Phe Lys
 645 650 655
 Arg Thr Ile Ala Asp Tyr Leu Ser Tyr Glu Val Ser Leu Ile Leu Lys
 660 665 670
 Asn Gln Met Pro Pro Lys Arg
 675

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...597
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

ATCCTTTGAT TTCAAAGGCT TAAA ATG TAT GTG GTG TTA GAA GGC GTT GAT	51
Met Tyr Val Val Leu Glu Gly Val Asp	
1 5	
GGC GCG GGC AAA AGC ACT CAA GTA GAA TTA TTA AAA GAC CGG TTT AAA	99
Gly Ala Gly Lys Ser Thr Gln Val Glu Leu Leu Lys Asp Arg Phe Lys	
10 15 20 25	
AAC GCC CTT TTT ACC AAA GAG CCA GGG GGG ACG AGA ATG GGC GAG AGT	147
Asn Ala Leu Phe Thr Lys Glu Pro Gly Gly Thr Arg Met Gly Glu Ser	
30 35 40	
TTA AGG CGT ATC GCT TTG AAT GAA AAC ATT AGC GAA TTG GCT AGA GCG	195
Leu Arg Arg Ile Ala Leu Asn Glu Asn Ile Ser Glu Leu Ala Arg Ala	
45 50 55	
TTT TTA TTC TTA AGC GAT AGG GCT GAG CAT ACA GAA AGC GTG ATA AAA	243
Phe Leu Phe Leu Ser Asp Arg Ala Glu His Thr Glu Ser Val Ile Lys	
60 65 70	
CCG GCA TTG AAA GAA AAA AAG CTC ATC ATT AGC GAC AGG AGC TTG ATC	291

AGT GCG TCT GTG ATG CTT AAA GAA AAG CGC CCC TTA CTC ATT GCC CCT	388
Ser Ala Ser Val Met Leu Lys Glu Lys Arg Pro Leu Leu Ile Ala Pro	
110 115 120	
AGA GAA ATG CCT TTA AGC GCT ATC ATG TTA GAA AAT TTG CTC AAA CTC	436
Arg Glu Met Pro Leu Ser Ala Ile Met Leu Glu Asn Leu Leu Lys Leu	
125 130 135	
TCC CAT TCT AAT GCA ATC ATT GCG CCG CCG ATG ATG ACT TAT TAC ACC	484
Ser His Ser Asn Ala Ile Ile Ala Pro Pro Met Met Thr Tyr Tyr Thr	
140 145 150	
CAG AGC AAG ACT TTA GAA GCG ATG CAA GAT TTT TTA GTG GGG AAG TGG	532
Gln Ser Lys Thr Leu Glu Ala Met Gln Asp Phe Leu Val Gly Lys Trp	
155 160 165 170	
TTT GAC AGC TTA GGG ATA GAA AAT GAC TTA TAC CCA CGA TGG GGA ATG	580
Phe Asp Ser Leu Gly Ile Glu Asn Asp Leu Tyr Pro Arg Trp Gly Met	
175 180 185	
AAC TGATGCAAAA AATCGGCATT TACCCGGGCA CTTTGA	620
Asn	

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Met	Lys	Leu	Val	Leu	Gly	Ile	Ser	Gly	Ala	Ser	Gly	Ile	Pro	Leu	Ala
1				5					10					15	
Leu	Arg	Phe	Leu	Glu	Lys	Leu	Pro	Lys	Glu	Ile	Glu	Val	Phe	Val	Val
			20					25					30		
Ala	Ser	Lys	Asn	Ala	His	Val	Val	Ala	Leu	Glu	Glu	Ser	Asn	Ile	Asn
		35				40						45			
Leu	Lys	Asn	Ala	Met	Lys	Asp	Leu	Arg	Pro	Ser	Gly	Thr	Phe	Phe	Asn
	50				55						60				
Glu	Gln	Asp	Ile	His	Ala	Ser	Ile	Ala	Ser	Gly	Ser	Tyr	Gly	Ile	His
65				70					75					80	
Lys	Met	Ala	Ile	Ile	Pro	Ala	Ser	Met	Asp	Met	Val	Ala	Lys	Ile	Ala
			85					90						95	
His	Gly	Phe	Gly	Gly	Asp	Leu	Ile	Ser	Arg	Ser	Ala	Ser	Val	Met	Leu
			100				105						110		
Lys	Glu	Lys	Arg	Pro	Leu	Leu	Ile	Ala	Pro	Arg	Glu	Met	Pro	Leu	Ser
		115				120						125			
Ala	Ile	Met	Leu	Glu	Asn	Leu	Leu	Lys	Leu	Ser	His	Ser	Asn	Ala	Ile
	130					135					140				
Ile	Ala	Pro	Pro	Met	Met	Thr	Tyr	Tyr	Thr	Gln	Ser	Lys	Thr	Leu	Glu
145				150						155				160	
Ala	Met	Gln	Asp	Phe	Leu	Val	Gly	Lys	Trp	Phe	Asp	Ser	Leu	Gly	Ile

165 170 175
 Glu Asn Asp Leu Tyr Pro Arg Trp Gly Met Asn
 180 185

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...309
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

CTCCCTGAAG CG ATG CTC GCA TGG ATG TCT TGC TCG TTG AAA AAA GTA CCA	51
Met Leu Ala Trp Met Ser Cys Ser Leu Lys Lys Val Pro	
1 5 10	
CTA GGC CGT AAA TCT TTC ATG GCG TTT TTA AGG TTA ATA TTA GAT TCT	99
Leu Gly Arg Lys Ser Phe Met Ala Phe Leu Arg Leu Ile Leu Asp Ser	
15 20 25	
TCT AAC GCC ACG ACA TGC GCG TTT TTA GAC GCC ACG ACA AAA ACT TCA	147
Ser Asn Ala Thr Thr Cys Ala Phe Leu Asp Ala Thr Thr Lys Thr Ser	
30 35 40 45	
ATT TCT TTG GGT AAT TTT TCT AAA AAC CGC AAG GCT AGG GGT ATC CCG	195
Ile Ser Leu Gly Asn Phe Ser Lys Asn Arg Lys Ala Arg Gly Ile Pro	
50 55 60	
CTC GCT CCA CTG ATG CCT AAA ACC AAT TTC ATG AAT GTC CTT TAT AAG	243
Leu Ala Pro Leu Met Pro Lys Thr Asn Phe Met Asn Val Leu Tyr Lys	
65 70 75	
ATT TGC GCT TTA GAG CTG CTC AAC ACT TTT GCT TTG AGT ATT TTA TTG	291
Ile Cys Ala Leu Glu Leu Leu Asn Thr Phe Ala Leu Ser Ile Leu Leu	
80 85 90	
CTT TCT AAA TTT TTC GCT TGAATGATTT GATTAAGCGC GCCATTTTCT AG	341
Leu Ser Lys Phe Phe Ala	
95	

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

```
Met Leu Ala Trp Met Ser Cys Ser Leu Lys Lys Val Pro Leu Gly Arg
 1           5           10          15
Lys Ser Phe Met Ala Phe Leu Arg Leu Ile Leu Asp Ser Ser Asn Ala
 20          25          30
Thr Thr Cys Ala Phe Leu Asp Ala Thr Thr Lys Thr Ser Ile Ser Leu
 35          40          45
Gly Asn Phe Ser Lys Asn Arg Lys Ala Arg Gly Ile Pro Leu Ala Pro
 50          55          60
Leu Met Pro Lys Thr Asn Phe Met Asn Val Leu Tyr Lys Ile Cys Ala
 65          70          75          80
Leu Glu Leu Leu Asn Thr Phe Ala Leu Ser Ile Leu Leu Leu Ser Lys
 85          90          95
Phe Phe Ala
```

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 85...822
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```
GGCGCCAACG ATTTTAATGA TCCTCATTGT GATTTTAGTG GTTGTCAAGC CTTTTTAAAG      60
ACAAGCCATG AAAAAAGAAA AGTC ATG AAA AAA GAA AAG CAT CTC AAG CAA      111
              Met Lys Lys Glu Lys His Leu Lys Gln
                1           5

GAA AAA ATC ATC AAC ATG TTT GAT GAT ATA GCC AGC TCT TAC GAT CAA      159
Glu Lys Ile Ile Asn Met Phe Asp Asp Ile Ala Ser Ser Tyr Asp Gln
10          15          20          25

GCC AAC CGC TTG ATG AGT TTT GGC TTA GAC GTT AAA TGG CGA GAA AGG      207
Ala Asn Arg Leu Met Ser Phe Gly Leu Asp Val Lys Trp Arg Glu Arg
          30          35          40

GCT TGC GAG CAT GCG TTT TTA TTT TTA GAA AAC AAG AAA GCG TTA AGG      255
Ala Cys Glu His Ala Phe Leu Phe Leu Glu Asn Lys Lys Ala Leu Arg
          45          50          55

CTT GTG GAT GTG GCA TGC GGG ACG GGG GAT ATG CTT GTG GCT TGG CAA      303
Leu Val Asp Val Ala Cys Gly Thr Gly Asp Met Leu Val Ala Trp Gln
        60          65          70
```

AAA Lys	AGC Ser	GCT Ala	CTC Leu	AAT Asn	TGC Cys	GGT Gly	ATA Ile	GAG Glu	TTT Phe	AAG Lys	GAA Glu	TGT Cys	TTG Leu	GGG Gly	ATT Ile	351
758085																
GAC Asp	CCC Pro	TCT Ser	AAT Asn	AAC Asn	ATG Met	CTT Leu	GAA Glu	TTA Leu	GCC Ala	ATC Ile	AAA Lys	AAA Lys	TGT Cys	GAA Glu	GAG Glu	399
9095100105																
CTT Leu	GAA Glu	AAC Asn	AAA Lys	GCT Ala	TCT Ser	TTC Phe	ATC Ile	CAA Gln	GCT Ala	CAA Gln	GCC Ala	AAA Lys	GAT Asp	TTA Leu	AAA Lys	447
110115120																
GGC Gly	GTT Val	GAA Glu	AAT Asn	AAC Asn	AGC Ser	GTG Val	GAT Asp	ATC Ile	CTC Leu	TCT Ser	ATT Ile	GCG Ala	TAT Tyr	GGC Gly	TTG Leu	495
125130135																
CGT Arg	AAT Asn	GTC Val	GTG Val	GAA Glu	AGA Arg	CAA Gln	GAG Glu	GCC Ala	TTA Leu	AAA Lys	GAG Glu	TTT Phe	TTT Phe	AGG Arg	GTG Val	543
140145150																
TTA Leu	AAA Lys	CCC Pro	AGG Arg	GGC Gly	GTT Val	TTA Leu	GTG Val	ATT Ile	TTA Leu	GAA Glu	TTT Phe	TTA Leu	AAA Lys	AAA Lys	GAC Asp	591
155160165																
AAC Asn	CCC Pro	ACA Thr	TGG Trp	CTG Leu	GAT Asp	AAA Lys	ATC Ile	TCA Ser	GGG Gly	TTT Phe	TAC Tyr	ACG Thr	AAT Asn	AAG Lys	GTT Val	639
170175180185																
TTG Leu	CCT Pro	TTA Leu	GTG Val	GGA Gly	GGG Gly	GCT Ala	ATC Ile	AGT Ser	AAG Lys	AAT Asn	TAT Tyr	GGT Gly	GCT Ala	TAT Tyr	TCT Ser	687
190195200																
TAT Tyr	TTA Leu	CCG Pro	CAA Gln	TCC Ser	ATT Ile	GAG Glu	GGG Gly	TTT Phe	TTG Leu	AGT Ser	TTA Leu	GAG Glu	GGT Gly	TTG Leu	AAG Lys	735
205210215																
CAT His	GAA Glu	TTA Leu	AGA Arg	AAC Asn	GCA Ala	GGG Gly	TTT Phe	GAG Glu	ATT Ile	TTA Leu	AGG Arg	ACT Thr	GAA Glu	GAT Asp	TCT Ser	783
220225230																
ATC Ile	GCT Ala	CAA Gln	ATT Ile	TCA Ser	ACG Thr	ACC Thr	ATG Met	CTT Leu	GTT Val	AAA Lys	AAA Lys	AAC Asn	TAAAGGAATG		TT	834
235240245																
ATGCAAGATG AATTATTTGA AACCG																
858																

TTG ATG GTT GCT TTT TTA TTG GTG CTG TTG AAC GCT TTT TTT GTG CTT	155
Leu Met Val Ala Phe Leu Leu Val Leu Leu Asn Ala Phe Phe Val Leu	
20 25 30	
TCA GAG TTT GCC CTT GTG AAA GTG CGT AAA ACC CGC TTA GAA GAG CTG	203
Ser Glu Phe Ala Leu Val Lys Val Arg Lys Thr Arg Leu Glu Glu Leu	
35 40 45	
GTT AAA ATC GGT AAT TCC AAC GCT AAA CTC GCT TTA AAG ATG AGT CAA	251
Val Lys Ile Gly Asn Ser Asn Ala Lys Leu Ala Leu Lys Met Ser Gln	
50 55 60 65	
AGA CTA GAC ACT TAT TTG AGC GCG ACG CAG TTA GGC ATC ACC CTT TCT	299
Arg Leu Asp Thr Tyr Leu Ser Ala Thr Gln Leu Gly Ile Thr Leu Ser	
70 75 80	
TCA TTA GCT TTA GGC TGG GTG GGT GAG CCC GCT ATC GCA AAA TTG TTA	347
Ser Leu Ala Leu Gly Trp Val Gly Glu Pro Ala Ile Ala Lys Leu Leu	
85 90 95	
GCC GCG CTG TTT GAG TCT ATG GAT TTG AGA GAA AAT CCT ATT TTT ATC	395
Ala Ala Leu Phe Glu Ser Met Asp Leu Arg Glu Asn Pro Ile Phe Ile	
100 105 110	
CAT TCA ATG AGC GTG GTC ATA GCG TTT TTA AGC ATC ACT TTT TTG CAT	443
His Ser Met Ser Val Val Ile Ala Phe Leu Ser Ile Thr Phe Leu His	
115 120 125	
GTC GTG TTG GGC GAG ATT GTG CCT AAA TCT TTA GCG ATC GCT AAA TCT	491
Val Val Leu Gly Glu Ile Val Pro Lys Ser Leu Ala Ile Ala Lys Ser	
130 135 140 145	
GAA AAA GCC ACC CTT TTT GCC GCA CGC CCT TTG CAT GTG TTT TGG GTG	539
Glu Lys Ala Thr Leu Phe Ala Ala Arg Pro Leu His Val Phe Trp Val	
150 155 160	
GTG TTT TAT CCG GTG GTG CGT TTG TTT GAT GTG ATC GCT CAT TTT TTT	587
Val Phe Tyr Pro Val Val Arg Leu Phe Asp Val Ile Ala His Phe Phe	
165 170 175	
TTG AAA AAG ATG GGC ATC AAT CCT AAA GAG CAT GAC GGC ACG CAT TCT	635
Leu Lys Lys Met Gly Ile Asn Pro Lys Glu His Asp Gly Thr His Ser	
180 185 190	
GAA GAA GAG TTA AAA ATC ATT GTG GGC GAG AGT TTG AGA GAG GGC ATT	683
Glu Glu Glu Leu Lys Ile Ile Val Gly Glu Ser Leu Arg Glu Gly Ile	
195 200 205	
ATT GAT TCA GTG GAG GGC GAA ATC ATT AAA AAC GCA GTG GAT TTT TCT	731
Ile Asp Ser Val Glu Gly Glu Ile Ile Lys Asn Ala Val Asp Phe Ser	
210 215 220 225	
GAC ACG AGC GCT AAA GAA ATC ATG ACC CCA CGA AAA GAC ATG GTG TGT	779
Asp Thr Ser Ala Lys Glu Ile Met Thr Pro Arg Lys Asp Met Val Cys	
230 235 240	
TTG GAT GAA GAA AAC AGC TAT GAA GAA AAT ATA GAC ATT GTT TTA AAA	827
Leu Asp Glu Glu Asn Ser Tyr Glu Glu Asn Ile Asp Ile Val Leu Lys	

245										250										255										
GGC	CAT	TTC	ACG	CGC	TAC	CCT	TAT	TGC	AAG	GGT	TCT	AAG	GAT	AAC	ATT	875														
Gly	His	Phe	Thr	Arg	Tyr	Pro	Tyr	Cys	Lys	Gly	Ser	Lys	Asp	Asn	Ile															
260										270																				
ATC	GGC	ATG	GTG	CAT	ATT	AGG	GAT	TTG	CTT	TCG	CGC	TCT	ATT	TTT	ACC	923														
Ile	Gly	Met	Val	His	Ile	Arg	Asp	Leu	Leu	Ser	Arg	Ser	Ile	Phe	Thr															
275										285																				
CCC	AAA	ATG	CAT	GAT	TTC	AAT	CAA	ATC	GTT	AGG	AAA	ATG	ATC	ATC	GTC	971														
Pro	Lys	Met	His	Asp	Phe	Asn	Gln	Ile	Val	Arg	Lys	Met	Ile	Ile	Val															
290										305																				
CCC	GAA	AGC	GCT	TCC	ATT	TCT	CAA	ATC	CTT	ATT	AAA	ATG	AAA	AAA	GAG	1019														
Pro	Glu	Ser	Ala	Ser	Ile	Ser	Gln	Ile	Leu	Ile	Lys	Met	Lys	Lys	Glu															
310										320																				
CAA	ATC	CAT	ACC	GCT	TTG	GTG	ATT	GAT	GAA	TAC	GGC	GGC	ACA	GCC	GGG	1067														
Gln	Ile	His	Thr	Ala	Leu	Val	Ile	Asp	Glu	Tyr	Gly	Gly	Thr	Ala	Gly															
325										335																				
TTG	CTC	ACT	ATG	GAA	GAC	ATC	ATT	GAA	GAG	ATC	ATG	GGC	GAG	ATT	AGC	1115														
Leu	Leu	Thr	Met	Glu	Asp	Ile	Ile	Glu	Glu	Ile	Met	Gly	Glu	Ile	Ser															
340										350																				
GAC	GAA	TAC	GAC	TTA	AAA	CAA	GAG	GGC	ATA	AAC	AAG	CTT	GAA	GAG	GGC	1163														
Asp	Glu	Tyr	Asp	Leu	Lys	Gln	Glu	Gly	Ile	Asn	Lys	Leu	Glu	Glu	Gly															
355										365																				
GTG	TTT	GAA	TTA	GAG	GGC	ATG	CTG	GAT	TTA	GAG	AGC	GTA	GAA	GAA	GCG	1211														
Val	Phe	Glu	Leu	Glu	Gly	Met	Leu	Asp	Leu	Glu	Ser	Val	Glu	Glu	Ala															
370										385																				
CTT	CAC	ATT	GAA	TTT	GAT	AAA	GAA	TGC	GAG	CAG	GTA	ACG	CTT	GGG	GGC	1259														
Leu	His	Ile	Glu	Phe	Asp	Lys	Glu	Cys	Glu	Gln	Val	Thr	Leu	Gly	Gly															
390										400																				
TAT	GTT	TTT	AGC	TTG	TTA	GAG	CGC	ATG	CCT	ATG	GAG	GGA	GAT	ACA	ATC	1307														
Tyr	Val	Phe	Ser	Leu	Leu	Glu	Arg	Met	Pro	Met	Glu	Gly	Asp	Thr	Ile															
405										415																				
GTT	TCG	CAT	GGG	TAT	TCT	TTT	GAA	GTC	TTA	AGC	GTG	GAT	GGG	GCT	AGG	1355														
Val	Ser	His	Gly	Tyr	Ser	Phe	Glu	Val	Leu	Ser	Val	Asp	Gly	Ala	Arg															
420										430																				
ATA	AAA	CGC	TTA	AAA	GCG	GTT	AAA	CAA	GAT	CAG	GGA	GAA	AAT	GAA	GCA	T	1404													
Ile	Lys	Arg	Leu	Lys	Ala	Val	Lys	Gln	Asp	Gln	Gly	Glu	Asn	Glu	Ala															
435										445																				
GAAAAAACA ACCCTCTTTG TATTGGGCTT ATTATTTAA																1443														

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 449 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Met Gly Arg Asn Gln Gly Ala Tyr Leu Asp Pro Ser Glu Ser Ile Leu
1 5 10 15
Met Leu Met Val Ala Phe Leu Leu Val Leu Leu Asn Ala Phe Phe Val
20 25 30
Leu Ser Glu Phe Ala Leu Val Lys Val Arg Lys Thr Arg Leu Glu Glu
35 40 45
Leu Val Lys Ile Gly Asn Ser Asn Ala Lys Leu Ala Leu Lys Met Ser
50 55 60
Gln Arg Leu Asp Thr Tyr Leu Ser Ala Thr Gln Leu Gly Ile Thr Leu
65 70 75 80
Ser Ser Leu Ala Leu Gly Trp Val Gly Glu Pro Ala Ile Ala Lys Leu
85 90 95
Leu Ala Ala Leu Phe Glu Ser Met Asp Leu Arg Glu Asn Pro Ile Phe
100 105 110
Ile His Ser Met Ser Val Val Ile Ala Phe Leu Ser Ile Thr Phe Leu
115 120 125
His Val Val Leu Gly Glu Ile Val Pro Lys Ser Leu Ala Ile Ala Lys
130 135 140
Ser Glu Lys Ala Thr Leu Phe Ala Ala Arg Pro Leu His Val Phe Trp
145 150 155 160
Val Val Phe Tyr Pro Val Val Arg Leu Phe Asp Val Ile Ala His Phe
165 170 175
Phe Leu Lys Lys Met Gly Ile Asn Pro Lys Glu His Asp Gly Thr His
180 185 190
Ser Glu Glu Glu Leu Lys Ile Ile Val Gly Glu Ser Leu Arg Glu Gly
195 200 205
Ile Ile Asp Ser Val Glu Gly Glu Ile Ile Lys Asn Ala Val Asp Phe
210 215 220
Ser Asp Thr Ser Ala Lys Glu Ile Met Thr Pro Arg Lys Asp Met Val
225 230 235 240
Cys Leu Asp Glu Glu Asn Ser Tyr Glu Glu Asn Ile Asp Ile Val Leu
245 250 255
Lys Gly His Phe Thr Arg Tyr Pro Tyr Cys Lys Gly Ser Lys Asp Asn
260 265 270
Ile Ile Gly Met Val His Ile Arg Asp Leu Leu Ser Arg Ser Ile Phe
275 280 285
Thr Pro Lys Met His Asp Phe Asn Gln Ile Val Arg Lys Met Ile Ile
290 295 300
Val Pro Glu Ser Ala Ser Ile Ser Gln Ile Leu Ile Lys Met Lys Lys
305 310 315 320
Glu Gln Ile His Thr Ala Leu Val Ile Asp Glu Tyr Gly Gly Thr Ala
325 330 335
Gly Leu Leu Thr Met Glu Asp Ile Ile Glu Glu Ile Met Gly Glu Ile
340 345 350
Ser Asp Glu Tyr Asp Leu Lys Gln Glu Gly Ile Asn Lys Leu Glu Glu
355 360 365
Gly Val Phe Glu Leu Glu Gly Met Leu Asp Leu Glu Ser Val Glu Glu
370 375 380
Ala Leu His Ile Glu Phe Asp Lys Glu Cys Glu Gln Val Thr Leu Gly
385 390 395 400
Gly Tyr Val Phe Ser Leu Leu Glu Arg Met Pro Met Glu Gly Asp Thr
405 410 415

Ile	Val	Ser	His	Gly	Tyr	Ser	Phe	Glu	Val	Leu	Ser	Val	Asp	Gly	Ala
			420					425					430		
Arg	Ile	Lys	Arg	Leu	Lys	Ala	Val	Lys	Gln	Asp	Gln	Gly	Glu	Asn	Glu
		435				440						445			
Ala															

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 47...367
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

AGAAACCGGC	ACGGTTACCA	ACCAAGCGGT	AACAATCTTT	TTTAAA	ATG	GAG	CGT		55							
					Met	Glu	Arg									
					1											
TTG	ATC	ACT	TCT	TCT	TTA	TAC	ACT	TTT	TTA	AGC	GAC	TTT	TTT	TCT	TTC	103
Leu	Ile	Thr	Ser	Ser	Leu	Tyr	Thr	Phe	Leu	Ser	Asp	Phe	Phe	Ser	Phe	
	5					10				15						
TTT	TTC	AAT	TCC	AAA	GCG	ATG	GCG	GTG	TTC	TTG	CTT	TTT	TTT	AAG	CTC	151
Phe	Phe	Asn	Ser	Lys	Ala	Met	Ala	Val	Phe	Leu	Leu	Phe	Phe	Lys	Leu	
20					25				30					35		
TCT	AGC	ATG	AGC	GAT	TTT	TCT	TTC	AAA	TTG	GCT	TTA	TCA	AAG	CGC	TCT	199
Ser	Ser	Met	Ser	Asp	Phe	Ser	Phe	Lys	Leu	Ala	Leu	Ser	Lys	Arg	Ser	
			40					45					50			
AAA	AAG	CCT	TCA	ATT	TCT	TCT	AAA	TCT	TCC	CCA	AAG	TGC	GCG	GCT	ACA	247
Lys	Lys	Pro	Ser	Ile	Ser	Ser	Lys	Ser	Ser	Pro	Lys	Cys	Ala	Ala	Thr	
		55					60					65				
ATG	TTG	TCT	CTG	ATT	CTA	GCA	AAA	CGC	CTT	CTT	GAT	TGC	TCT	CTT	AAG	295
Met	Leu	Ser	Leu	Ile	Leu	Ala	Lys	Arg	Leu	Leu	Asp	Cys	Ser	Leu	Lys	
	70					75					80					
CGC	TCC	CTT	AAA	AAG	CCC	ACC	CCA	AAC	ACC	GCG	CCC	ACC	ACA	ATA	TGC	343
Arg	Ser	Leu	Lys	Lys	Pro	Thr	Pro	Asn	Thr	Ala	Pro	Thr	Thr	Ile	Cys	
	85					90					95					
GTA	GAG	CTT	ACG	GGC	AAG	CCT	AAT	TGAGAGGCTA	AAAGCACGGT	GATGACT						394
Val	Glu	Leu	Thr	Gly	Lys	Pro	Asn									
100					105											

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Met Glu Arg Leu Ile Thr Ser Ser Leu Tyr Thr Phe Leu Ser Asp Phe
1 5 10 15
Phe Ser Phe Phe Phe Asn Ser Lys Ala Met Ala Val Phe Leu Leu Phe
20 25 30
Phe Lys Leu Ser Ser Met Ser Asp Phe Ser Phe Lys Leu Ala Leu Ser
35 40 45
Lys Arg Ser Lys Lys Pro Ser Ile Ser Ser Lys Ser Ser Pro Lys Cys
50 55 60
Ala Ala Thr Met Leu Ser Leu Ile Leu Ala Lys Arg Leu Leu Asp Cys
65 70 75 80
Ser Leu Lys Arg Ser Leu Lys Lys Pro Thr Pro Asn Thr Ala Pro Thr
85 90 95
Thr Ile Cys Val Glu Leu Thr Gly Lys Pro Asn
100 105

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...321
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

TCAAATCTCTT CATAA ATG ATT TTT TCT TTT AAA AGG ACT TCT TTT TGC GTG	51
Met Ile Phe Ser Phe Lys Arg Thr Ser Phe Cys Val	
1 5 10	
AGC GTG CCG GTT TTG TCT ATA AAG ATT TTT TTC ACT TTA GCC AGA GTT	99
Ser Val Pro Val Leu Ser Ile Lys Ile Phe Phe Thr Leu Ala Arg Val	
15 20 25	
TCT AAA AAC AAC GCT TCT TTA AAC ACG ATC AAA GGG TTT TTA AAC ACC	147
Ser Lys Asn Asn Ala Ser Leu Asn Thr Ile Lys Gly Phe Leu Asn Thr	
30 35 40	
CCT ATC ACT AAC GCA ATG GGC GTA GCC AGA GCG AAC GCG CAA GGG CAG	195
Pro Ile Thr Asn Ala Met Gly Val Ala Arg Ala Asn Ala Gln Gly Gln	
45 50 55 60	
CTG ATG ACT AGC ACG CTA ATA CAC ACC ATT AAG GCT TTT TCA AAA TTA	243
Leu Met Thr Ser Thr Leu Ile His Thr Ile Lys Ala Phe Ser Lys Leu	
65 70 75	
CCC CCC AAA CCA AAT TGC CAT AAC AAA AAG CTT ACA AAG GCT AAA AAC	291
Pro Pro Lys Pro Asn Cys His Asn Lys Lys Leu Thr Lys Ala Lys Asn	
80 85 90	
AAC ACC GCT TTA GAA AAA ATA TCC GCA ATT TGATTCGCGC TACTCTCAAT T	342
Asn Thr Ala Leu Glu Lys Ile Ser Ala Ile	
95 100	

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Met Ile Phe Ser Phe Lys Arg Thr Ser Phe Cys Val Ser Val Pro Val	
1 5 10 15	
Leu Ser Ile Lys Ile Phe Phe Thr Leu Ala Arg Val Ser Lys Asn Asn	
20 25 30	
Ala Ser Leu Asn Thr Ile Lys Gly Phe Leu Asn Thr Pro Ile Thr Asn	
35 40 45	
Ala Met Gly Val Ala Arg Ala Asn Ala Gln Gly Gln Leu Met Thr Ser	
50 55 60	
Thr Leu Ile His Thr Ile Lys Ala Phe Ser Lys Leu Pro Pro Lys Pro	
65 70 75 80	
Asn Cys His Asn Lys Lys Leu Thr Lys Ala Lys Asn Asn Thr Ala Leu	
85 90 95	
Glu Lys Ile Ser Ala Ile	
100	

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...1062
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

AGGCTTTTGTG CTCTTGCCTT TTTTCCCATC	ATG AGA CTT TAT GAG AGT TTA TTA	54
	Met Arg Leu Tyr Glu Ser Leu Leu	
	1 5	
GAA ATG TGC TTG AAT AAG GCA TGG GAG CAT CAA ACC CTA GCC TTA GAA		102
Glu Met Cys Leu Asn Lys Ala Trp Glu His Gln Thr Leu Ala Leu Glu		
10 15 20		
AAC CCA AGC GTA GCT TGC ATG GTG TTG GAT AAA AAC CAT GAG ATC TTG		150
Asn Pro Ser Val Ala Cys Met Val Leu Asp Lys Asn His Glu Ile Leu		
25 30 35 40		
AGT TTA GAA ACC CAC AAA AAA GCC AAA ACC CCG CAT GCA GAA GTC TTA		198
Ser Leu Glu Thr His Lys Lys Ala Lys Thr Pro His Ala Glu Val Leu		
45 50 55		
GCC GCC CAA TCA GCG CTA AAG ATT TTA CGC CCC AGT TTG AAA AAC GAT		246
Ala Ala Gln Ser Ala Leu Lys Ile Leu Arg Pro Ser Leu Lys Asn Asp		
60 65 70		
TTA GAA AAG TTA GAA GAC CCT AAA ACT TTA AGC GAT TTT TTA AAA ACG		294
Leu Glu Lys Leu Glu Asp Pro Lys Thr Leu Ser Asp Phe Leu Lys Thr		
75 80 85		
CAC CAC GAT AAC GCT TTT ACA GAC TGC GTT TTT TTA ATC ACC TTA GAG		342
His His Asp Asn Ala Phe Thr Asp Cys Val Phe Leu Ile Thr Leu Glu		
90 95 100		
CCA TGC AAT TCT TAT GGC AAA ACC CCG GCT TGT AGC GAA TTG TTA GAA		390
Pro Cys Asn Ser Tyr Gly Lys Thr Pro Ala Cys Ser Glu Leu Leu Glu		
105 110 115 120		
ATT TTA AAG CCT AAA AGA GTG GTC ATT GCC ACA GAA GAA AAC GAA GCT		438
Ile Leu Lys Pro Lys Arg Val Val Ile Ala Thr Glu Glu Asn Glu Ala		
125 130 135		
AAA AAA GGG GGT TTA GCA AGG CTA CAA AAG GCT CGT ATT GAA ACA ATA		486
Lys Lys Gly Gly Leu Ala Arg Leu Gln Lys Ala Arg Ile Glu Thr Ile		
140 145 150		

ATT TGC CAC AAT TTA GAA AAC AAA GCT AAA GAC TTG CTC TTG CCT TTT	534
Ile Cys His Asn Leu Glu Asn Lys Ala Lys Asp Leu Leu Leu Pro Phe	
155 160 165	
AGG GTA ATG GAA CAA AAG GGG CGT TTT AAT TTG TTC AAA CTC GCT TTA	582
Arg Val Met Glu Gln Lys Gly Arg Phe Asn Leu Phe Lys Leu Ala Leu	
170 175 180	
AGA ATG AAT GGG GAT TAC CAT CAT GGC AAG ATC ACC GGG CAA AAA AGC	630
Arg Met Asn Gly Asp Tyr His His Gly Lys Ile Thr Gly Gln Lys Ser	
185 190 195 200	
GTT ATT TTC ACG CAC AAC CAG CGA GCA ATA TGC GAC ACG CTT ATT GTT	678
Val Ile Phe Thr His Asn Gln Arg Ala Ile Cys Asp Thr Leu Ile Val	
205 210 215	
TCT GGG AAA ACC ATA AGA ACG GAC AAC CCC TTA TTG GAC GCT CGC TTT	726
Ser Gly Lys Thr Ile Arg Thr Asp Asn Pro Leu Leu Asp Ala Arg Phe	
220 225 230	
TGC GAC AGC TTT TAT CAA AAT AAA AAC CCC AAT ATC GCT ATT TTA TCC	774
Cys Asp Ser Phe Tyr Gln Asn Lys Asn Pro Asn Ile Ala Ile Leu Ser	
235 240 245	
AAG CGC TCA ATT GAC CCT AAT TCA AAA GTT TTT TCT GCG CCT AAT CGT	822
Lys Arg Ser Ile Asp Pro Asn Ser Lys Val Phe Ser Ala Pro Asn Arg	
250 255 260	
TTA GTT AAC ACT TTC CAT GAC CCC AAA GAT TTA CCC CTA GAG AAG GGG	870
Leu Val Asn Thr Phe His Asp Pro Lys Asp Leu Pro Leu Glu Lys Gly	
265 270 275 280	
TTT AAT TTC ATT GAA GGG GGG TGG GAA TTG TTT GAG AGC TTG AGG GAT	918
Phe Asn Phe Ile Glu Gly Gly Trp Glu Leu Phe Glu Ser Leu Arg Asp	
285 290 295	
AAA ATA GAC GCG TTG CTT TTG CAT TCG CAT GCG TCT ATG ATT GGC GAA	966
Lys Ile Asp Ala Leu Leu Leu His Ser His Ala Ser Met Ile Gly Glu	
300 305 310	
GCG TTT AAG GCA CTC GCT CTA AAA ACC CCT TTT AAA GGA CGG TTG TTG	1014
Ala Phe Lys Ala Leu Ala Leu Lys Thr Pro Phe Lys Gly Arg Leu Leu	
315 320 325	
CAT GCG CAA ATC TTA GAA AAT GAA GCC CTT TTA TGG ATA GAA AAC TCT T	1063
His Ala Gln Ile Leu Glu Asn Glu Ala Leu Leu Trp Ile Glu Asn Ser	
330 335 340	
AAGATTATAC CAGCCTTTGA ACGCTTATTC TTACAACAGC GATTC	1108

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Met Arg Leu Tyr Glu Ser Leu Leu Glu Met Cys Leu Asn Lys Ala Trp
1 5 10 15
Glu His Gln Thr Leu Ala Leu Glu Asn Pro Ser Val Ala Cys Met Val
20 25 30
Leu Asp Lys Asn His Glu Ile Leu Ser Leu Glu Thr His Lys Lys Ala
35 40 45
Lys Thr Pro His Ala Glu Val Leu Ala Ala Gln Ser Ala Leu Lys Ile
50 55 60
Leu Arg Pro Ser Leu Lys Asn Asp Leu Glu Lys Leu Glu Asp Pro Lys
65 70 75 80
Thr Leu Ser Asp Phe Leu Lys Thr His His Asp Asn Ala Phe Thr Asp
85 90 95
Cys Val Phe Leu Ile Thr Leu Glu Pro Cys Asn Ser Tyr Gly Lys Thr
100 105 110
Pro Ala Cys Ser Glu Leu Leu Glu Ile Leu Lys Pro Lys Arg Val Val
115 120 125
Ile Ala Thr Glu Glu Asn Glu Ala Lys Lys Gly Gly Leu Ala Arg Leu
130 135 140
Gln Lys Ala Arg Ile Glu Thr Ile Ile Cys His Asn Leu Glu Asn Lys
145 150 155 160
Ala Lys Asp Leu Leu Leu Pro Phe Arg Val Met Glu Gln Lys Gly Arg
165 170 175
Phe Asn Leu Phe Lys Leu Ala Leu Arg Met Asn Gly Asp Tyr His His
180 185 190
Gly Lys Ile Thr Gly Gln Lys Ser Val Ile Phe Thr His Asn Gln Arg
195 200 205
Ala Ile Cys Asp Thr Leu Ile Val Ser Gly Lys Thr Ile Arg Thr Asp
210 215 220
Asn Pro Leu Leu Asp Ala Arg Phe Cys Asp Ser Phe Tyr Gln Asn Lys
225 230 235 240
Asn Pro Asn Ile Ala Ile Leu Ser Lys Arg Ser Ile Asp Pro Asn Ser
245 250 255
Lys Val Phe Ser Ala Pro Asn Arg Leu Val Asn Thr Phe His Asp Pro
260 265 270
Lys Asp Leu Pro Leu Glu Lys Gly Phe Asn Phe Ile Glu Gly Gly Trp
275 280 285
Glu Leu Phe Glu Ser Leu Arg Asp Lys Ile Asp Ala Leu Leu Leu His
290 295 300
Ser His Ala Ser Met Ile Gly Glu Ala Phe Lys Ala Leu Ala Leu Lys
305 310 315 320
Thr Pro Phe Lys Gly Arg Leu Leu His Ala Gln Ile Leu Glu Asn Glu
325 330 335
Ala Leu Leu Trp Ile Glu Asn Ser
340

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 14...799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

ACGATTTTAA	AAA	ATG	GCT	AGA	AGT	TTC	AAG	CAT	TCT	CAA	TAT	CCT	AAA		49	
	Met	Ala	Arg	Ser	Phe	Lys	His	Ser	Gln	Tyr	Pro	Lys				
	1				5					10						
ATT	TTT	AAG	CCA	CTA	TAC	CCT	AAC	AAC	TTA	ACG	CTT	TCA	CTT	AAA	AAG	97
Ile	Phe	Lys	Pro	Leu	Tyr	Pro	Asn	Asn	Leu	Thr	Leu	Ser	Leu	Lys	Lys	
	15					20					25					
CAA	CAT	GTT	ATA	ATG	ATC	GCT	ATT	TTA	TTT	GAA	AGG	GTA	TTT	ATG	GAA	145
Gln	His	Val	Ile	Met	Ile	Ala	Ile	Leu	Phe	Glu	Arg	Val	Phe	Met	Glu	
	30					35					40					
AGC	GTT	TTA	AAT	TTC	CTA	ACC	AAT	ATC	AAT	GTG	ATT	TTC	ACC	CTT	TTG	193
Ser	Val	Leu	Asn	Phe	Leu	Thr	Asn	Ile	Asn	Val	Ile	Phe	Thr	Leu	Leu	
45					50				55						60	
GGC	TAT	TTG	ATT	GGG	GGG	ATT	CCT	TTT	GGC	TAT	GCG	TTA	ATG	AAA	ATC	241
Gly	Tyr	Leu	Ile	Gly	Gly	Ile	Pro	Phe	Gly	Tyr	Ala	Leu	Met	Lys	Ile	
				65					70					75		
TTT	TAC	GGC	ATG	GAT	ATT	ACT	AAA	ATC	GGA	TCG	GGG	GGC	ATT	GGC	GCA	289
Phe	Tyr	Gly	Met	Asp	Ile	Thr	Lys	Ile	Gly	Ser	Gly	Gly	Ile	Gly	Ala	
			80					85					90			
ACG	AAT	GTC	TTG	CGT	GCT	TTA	CAA	AGT	AAG	GGC	GTG	AGT	AAC	GCT	AAA	337
Thr	Asn	Val	Leu	Arg	Ala	Leu	Gln	Ser	Lys	Gly	Val	Ser	Asn	Ala	Lys	
		95					100					105				
CAA	ATG	GCC	CTA	TTA	GTT	TTA	ATC	TTG	GAT	CTC	TTC	AAA	GGC	ATG	TTT	385
Gln	Met	Ala	Leu	Leu	Val	Leu	Ile	Leu	Asp	Leu	Phe	Lys	Gly	Met	Phe	
	110					115					120					
GCA	GTA	TTT	TTG	AGC	AAA	TTG	TTT	GGG	TTG	GAT	TAT	AGT	TTG	CAA	TGG	433
Ala	Val	Phe	Leu	Ser	Lys	Leu	Phe	Gly	Leu	Asp	Tyr	Ser	Leu	Gln	Trp	
125					130				135						140	
ATG	GTC	GCT	ATC	GCT	AGC	ATT	TTA	GGG	CAT	TGC	TAT	TCG	CCT	TTT	TTG	481
Met	Val	Ala	Ile	Ala	Ser	Ile	Leu	Gly	His	Cys	Tyr	Ser	Pro	Phe	Leu	
				145					150					155		
AAT	TTC	AAT	GGA	GGT	AAG	GGC	GTT	TCT	ACG	ATC	ATG	GGC	TCT	GTG	GTG	529
Asn	Phe	Asn	Gly	Lys	Gly	Val	Ser	Thr	Ile	Met	Gly	Ser	Val	Val		
		160					165					170				
TTG	CTC	ATC	CCT	ATT	GAA	AGT	CTC	ATC	GGC	TTA	ACG	GTG	TGG	TTT	TTT	577
Leu	Leu	Ile	Pro	Ile	Glu	Ser	Leu	Ile	Gly	Leu	Thr	Val	Trp	Phe	Phe	
		175					180					185				
GTG	GGT	AAG	GTG	CTT	AAA	ATC	TCT	TCA	CTC	GCT	AGC	ATT	CTA	GGG	GTA	625

Val Gly Lys Val Leu Lys Ile Ser Ser Leu Ala Ser Ile Leu Gly Val
190 195 200

GGC ACA GCG ACT GTT CTT ATC TTT TTT GTG CCT TAT ATG CAT ATC CCA 673
Gly Thr Ala Thr Val Leu Ile Phe Phe Val Pro Tyr Met His Ile Pro
205 210 215 220

GAC AGC GTC AAT ATC CTT AAA GAA GTC GGC ACG CAA ACG CCG ATG GTG 721
Asp Ser Val Asn Ile Leu Lys Glu Val Gly Thr Gln Thr Pro Met Val
225 230 235

CTT ATT TTT ATT TTC ACC CTT ATC AAG CAT GCG GGT AAT ATT TTT AAT 769
Leu Ile Phe Ile Phe Thr Leu Ile Lys His Ala Gly Asn Ile Phe Asn
240 245 250

TTA TTG GCC GGC AAG GAA AAG AAA GTC TTA TGAAAACTAA ACAAGGCGTT CAT 822
Leu Leu Ala Gly Lys Glu Lys Lys Val Leu
255 260

A 823

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Met Ala Arg Ser Phe Lys His Ser Gln Tyr Pro Lys Ile Phe Lys Pro
1 5 10 15
Leu Tyr Pro Asn Asn Leu Thr Leu Ser Leu Lys Lys Gln His Val Ile
20 25 30
Met Ile Ala Ile Leu Phe Glu Arg Val Phe Met Glu Ser Val Leu Asn
35 40 45
Phe Leu Thr Asn Ile Asn Val Ile Phe Thr Leu Leu Gly Tyr Leu Ile
50 55 60
Gly Gly Ile Pro Phe Gly Tyr Ala Leu Met Lys Ile Phe Tyr Gly Met
65 70 75 80
Asp Ile Thr Lys Ile Gly Ser Gly Gly Ile Gly Ala Thr Asn Val Leu
85 90 95
Arg Ala Leu Gln Ser Lys Gly Val Ser Asn Ala Lys Gln Met Ala Leu
100 105 110
Leu Val Leu Ile Leu Asp Leu Phe Lys Gly Met Phe Ala Val Phe Leu
115 120 125
Ser Lys Leu Phe Gly Leu Asp Tyr Ser Leu Gln Trp Met Val Ala Ile
130 135 140
Ala Ser Ile Leu Gly His Cys Tyr Ser Pro Phe Leu Asn Phe Asn Gly
145 150 155 160
Gly Lys Gly Val Ser Thr Ile Met Gly Ser Val Val Leu Leu Ile Pro
165 170 175
Ile Glu Ser Leu Ile Gly Leu Thr Val Trp Phe Phe Val Gly Lys Val
180 185 190
Leu Lys Ile Ser Ser Leu Ala Ser Ile Leu Gly Val Gly Thr Ala Thr

	195		200		205	
Val	Leu	Ile	Phe	Phe	Val	Pro
	210		215		220	
Ile	Leu	Lys	Glu	Val	Gly	Thr
	225		230		235	
Phe	Thr	Leu	Ile	Lys	His	Ala
		245		250		255
Lys	Glu	Lys	Lys	Val	Leu	
	260					

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...381
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

TTTATTGGCC	GGCAAGGAAA	AGAAAGTCTT	ATG AAA ACT AAA CAA GGC GTT CAT	54
			Met Lys Thr Lys Gln Gly Val His	
			1 5	
ATC CAT AAC TTG GTG TTT GAG GCG ATT TTG GGG ATT TTA GAA TTT GAA	102			
Ile His Asn Leu Val Phe Glu Ala Ile Leu Gly Ile Leu Glu Phe Glu				
10 15 20				
CGC TTA AAA CCC CAA AAA ATA AGC GTG AAT TTG GAT CTT TTC TAC ACG	150			
Arg Leu Lys Pro Gln Lys Ile Ser Val Asn Leu Asp Leu Phe Tyr Thr				
25 30 35 40				
CAA TTA CCC AAT AAG GTT TAT TTA GAC TAC ATG GAA ATT CAA GAG CTT	198			
Gln Leu Pro Asn Lys Val Tyr Leu Asp Tyr Met Glu Ile Gln Glu Leu				
45 50 55				
ATT CAA AAG ATG ATG CAA GAA AAC CAA TAC CTT CTC ATT GAA GAC GCC	246			
Ile Gln Lys Met Met Gln Glu Asn Gln Tyr Leu Leu Ile Glu Asp Ala				
60 65 70				
CTG AAA GAT TTG AGC CAT GCT TTA AAA ACG CGC TAC AAG GAG ATC ACT	294			
Leu Lys Asp Leu Ser His Ala Leu Lys Thr Arg Tyr Lys Glu Ile Thr				
75 80 85				
GAA CTT TAT TTA AAA ATC AGC AAG TTA GAG ATT TCT CCC AAT TCT CAA	342			
Glu Leu Tyr Leu Lys Ile Ser Lys Leu Glu Ile Ser Pro Asn Ser Gln				
90 95 100				
GTG GGA GCG AGC GTG AAA ATC CGC TAT GAA AGC AAT CTT TAGCCTCTTT TT	393			
Val Gly Ala Ser Val Lys Ile Arg Tyr Glu Ser Asn Leu				

CCTTCTTATT G

404

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

[illegible]

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 52...1209
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

TAAAATAACG CTTATTTTAA ACTCTCAAAA AAGGAATCAA ACGCACTCAT C ATG GCT
Met Ala
1

57

AAA GAA ACG CTT GAA ATA ACC CCG GAT CTT TTG AAA AAC CCT TAT CAA
Lys Glu Thr Leu Glu Ile Thr Pro Asp Leu Leu Lys Asn Pro Tyr Gln

105

AAA Lys	ATC Ile	ATC Ile	AAT Asn	GCG Ala	AGC Ser	GCG Ala	AGC Ser	GTT Val	TTT Phe	GAT Asp	GAA Glu	AAG Lys	CAT His	GGG Gly	CGA Arg	153
202530																
TCG Ser	TTT Phe	TTT Phe	AGC Ser	ACG Thr	CAA Gln	TTT Phe	TAT Tyr	GAA Glu	AAA Lys	ATT Ile	GAA Glu	CCT Pro	TAT Tyr	TTA Leu	AAA Lys	201
354045																
GAA Glu	GTT Val	TTA Leu	ACC Thr	CAT His	CCC Pro	ATT Ile	GAT Asp	TTA Leu	GAA Glu	TGC Cys	GAT Asp	CTA Leu	AAC Asn	ACC Thr	GCT Ala	249
556065																
AAA Lys	AAA Lys	AAG Lys	AAC Asn	CGC Arg	TTA Leu	ACC Thr	CCT Pro	TTA Leu	AAA Lys	CAG Gln	CTT Leu	TTT Phe	AAA Lys	GCG Ala	TGT Cys	297
707580																
TTT Phe	AAC Asn	ACC Thr	GAA Glu	GAA Glu	ATT Ile	TTG Leu	ATT Ile	GTG Val	AAT Asn	AAT Asn	AAC Asn	ACC Thr	AGC Ser	GCG Ala	ATT Ile	345
859095																
TTC Phe	CTC Leu	ATC Ile	GCT Ala	AAC Asn	GCT Ala	TTA Leu	GCG Ala	CAA Gln	GAA Glu	AAA Lys	GAA Glu	ATC Ile	ATT Ile	GTT Val	TCT Ser	393
100105110																
TAT Tyr	GGC Gly	GAA Glu	TTA Leu	GTG Val	GGG Gly	GGG Gly	GAT Asp	TTT Phe	AAC Asn	CTT Leu	AAA Lys	GAT Asp	ATT Ile	TTA Leu	TTA Leu	441
115120125130																
AAT Asn	AGT Ser	GGG Gly	GCT Ala	AGG Arg	CTG Leu	CAT His	TTA Leu	GTG Val	GGG Gly	AAT Asn	ATT Ile	AAT Asn	CGC Arg	GCT Ala	TAT Tyr	489
135140145																
TTA Leu	AGG Arg	GAT Asp	TAC Tyr	CGC Arg	TTA Leu	GCC Ala	TTG Leu	AAT Asn	GAA Glu	AAC Asn	AGC Ser	AAA Lys	ATA Ile	CTC Leu	TTT Phe	537
150155160																
AAA Lys	ACC Thr	CAC His	AAC Asn	CCC Pro	CAT His	TTT Phe	AAA Lys	AAA Lys	GAC Asp	ACG Thr	CCC Pro	TTT Phe	AAA Lys	GAT Asp	TTA Leu	585
165170175																
CAA Gln	ACT Thr	CTT Leu	GCT Ala	AAA Lys	GAG Glu	CAT His	GAT Asp	CTC Leu	ATT Ile	GAT Asp	TAT Tyr	TAC Tyr	AAT Asn	TTA Leu	GGG Gly	633
180185190																
GAT Asp	GTG Val	GAT Asp	TTG Leu	TCA Ser	AAC Asn	AGA Arg	GTG Val	GCT Ala	TTG Leu	GAA Glu	GAA Glu	ATT Ile	TTA Leu	GCC Ala	CTA Leu	681
195200205210																
AAA Lys	CCA Pro	TCG Ser	CTT Leu	TTA Leu	AGC Ser	TTT Phe	AGC Ser	GCG Ala	GAT Asp	AAA Lys	TTC Phe	TTT Phe	AAC Asn	AGT Ser	GCG Ala	729
220225																
CAA Gln	GCG Ala	GGC Gly	ATT Ile	ATT Ile	ATG Met	GGG Gly	CAA Gln	AAA Lys	GAA Glu	CGG Arg	GTT Val	GAA Glu	GCG Ala	TTA Leu	AAA Lys	777
230235240																
AAC Asn	CAC His	CCC Pro	CTT Leu	TAT Tyr	AGA Arg	GTT Val	TTA Leu	AGG Arg	GTG Val	GGT Gly	AAA Lys	ATC Ile	ACG Thr	CTC Leu	ACC Thr	825

245					250					255										
TTG Leu	CTT Leu	TTT Phe	TGC Cys	AGC Ser	CTA Leu	AAA Lys	GCA Ala	TGG Trp	ATA Ile	AAT Asn	CAT His	CAA Gln	GAA Glu	GAC Asp	ATT Ile		873			
260					265					270										
ACA Thr	ATC Ile	CAT His	GCG Ala	TTA Leu	TTG Leu	AAC Asn	CAA Gln	ACT Thr	AAA Lys	GAC Asp	GCA Ala	TTA Leu	TTG Leu	CAA Gln	AAA Lys		921			
275					280					285					290					
GCC Ala	CTC Leu	AAA Lys	CTC Leu	TAC Tyr	GCT Ala	CTT Leu	TTA Leu	AAG Lys	CCT Pro	TTA Leu	GAA Glu	TTG Leu	AAT Asn	GTG Val	AGC Ser		969			
295					300					305										
ATA Ile	GCC Ala	TCT Ser	AGC Ser	TTT Phe	TCT Ser	AAA Lys	ATA Ile	GGG Gly	AAT Asn	TTG Leu	TTT Phe	GGT Gly	AGG Arg	GAA Glu	TTA Leu		1017			
310					315					320										
GAA Glu	TCC Ser	TTT Phe	TGC Cys	GTG Val	AAA Lys	ATC Ile	CAG Gln	CCC Pro	AAA Lys	AAC Asn	ACC Thr	CGT Arg	GCT Ala	TTA Leu	AAT Asn		1065			
325					330					335										
AGT Ser	GAG Glu	AAA Lys	CTT Leu	TAT Tyr	TTA Leu	AAG Lys	CTT Leu	TTC Phe	CAA Gln	AAA Lys	GGC Gly	GTT Val	ATC Ile	GCA Ala	AGG Arg		1113			
340					345					350										
ATT Ile	TCA Ser	TGC Cys	GAA Glu	TTC Phe	GTG Val	TGC Cys	TTT Phe	GAA Glu	GTC Val	TTT Phe	AGC Ser	TTG Leu	AAT Asn	GAA Glu	AAA Lys		1161			
355					360					365					370					
GAT Asp	TTT Phe	GAA Glu	AAA Lys	ATC Ile	GCT Ala	CTG Leu	GTT Val	TTA Leu	GAA Glu	GAA Glu	ATT Ile	CTT Leu	AAT Asn	AAA Lys	GCT Ala	T	1210			
375					380					385										
AAAAATTTCGC TATAATA																	1227			

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Met	Ala	Lys	Glu	Thr	Leu	Glu	Ile	Thr	Pro	Asp	Leu	Leu	Lys	Asn	Pro
1				5					10					15	
Tyr	Gln	Lys	Ile	Ile	Asn	Ala	Ser	Ala	Ser	Val	Phe	Asp	Glu	Lys	His
			20					25					30		
Gly	Arg	Ser	Phe	Phe	Ser	Thr	Gln	Phe	Tyr	Glu	Lys	Ile	Glu	Pro	Tyr
		35					40					45			
Leu	Lys	Glu	Val	Leu	Thr	His	Pro	Ile	Asp	Leu	Glu	Cys	Asp	Leu	Asn
	50					55					60				
Thr	Ala	Lys	Lys	Lys	Asn	Arg	Leu	Thr	Pro	Leu	Lys	Gln	Leu	Phe	Lys
65					70					75					80

AGGAACTTAA	GA	ATG	GAA	AAA	ATC	AGC	GAT	CTT	ATA	GAA	TGC	ATT	GCG	TAT	51	
	Met	Glu	Lys	Ile		Ser	Asp	Leu	Ile	Glu	Cys	Ile	Ala	Tyr		
	1					5					10					
GAA	AAA	AAT	TTG	CCT	AAA	GAG	ATG	ATT	TCA	AAA	GTG	ATT	CAA	GGC	TGT	99
Glu	Lys	Asn	Leu	Pro	Lys	Glu	Met	Ile	Ser	Lys	Val	Ile	Gln	Gly	Cys	
	15					20					25					
TTG	TTA	AAA	ATG	GCG	CAA	AAT	GAG	TTA	GAC	CCC	CTA	GCA	CGC	TAC	TTG	147
Leu	Leu	Lys	Met	Ala	Gln	Asn	Glu	Leu	Asp	Pro	Leu	Ala	Arg	Tyr	Leu	
30					35					40					45	
GTG	GTT	GAA	GAA	AAC	AAG	CAG	CTC	CAG	CTT	ATC	CAG	TTG	GTA	GAA	GTT	195
Val	Val	Glu	Glu	Asn	Lys	Gln	Leu	Gln	Leu	Ile	Gln	Leu	Val	Glu	Val	
				50				55						60		
TTA	GAA	GAT	GGT	GAT	GAA	AGA	TTG	GTT	AAC	GAC	CCT	TCT	AAA	TAC	ATC	243
Leu	Glu	Asp	Gly	Asp	Glu	Arg	Leu	Val	Asn	Asp	Pro	Ser	Lys	Tyr	Ile	
			65				70						75			
AGC	CTG	TCT	AAA	GCC	AAA	GAA	ATG	GAT	CCA	AGC	GTT	AAG	ATT	AAA	GAC	291
Ser	Leu	Ser	Lys	Ala	Lys	Glu	Met	Asp	Pro	Ser	Val	Lys	Ile	Lys	Asp	
	80						85					90				
GAA	TTG	TCC	TAT	AGC	TTG	AGT	TTG	GAG	AGC	ATG	AAA	CAA	GGA	GCG	ATC	339
Glu	Leu	Ser	Tyr	Ser	Leu	Ser	Leu	Glu	Ser	Met	Lys	Gln	Gly	Ala	Ile	
	95					100					105					
AAC	CGC	CTT	TTT	AAA	GAT	TTG	CAA	TAC	CAG	TTA	GAA	AAA	GCG	TTA	GAA	387
Asn	Arg	Leu	Phe	Lys	Asp	Leu	Gln	Tyr	Gln	Leu	Glu	Lys	Ala	Leu	Glu	
110					115					120					125	
GAC	AGC	CAC	TTT	GAA	GCG	TTT	CAA	AAG	CGT	CTT	AAC	AGC	GTT	TTA	ATG	435
Asp	Ser	His	Phe	Glu	Ala	Phe	Gln	Lys	Arg	Leu	Asn	Ser	Val	Leu	Met	
				130					135					140		
GGG	CAA	GTG	ATT	TTA	GTG	GAT	CAC	AAC	CAA	AAC	ACC	TTT	ATT	GAG	ATT	483
Gly	Gln	Val	Ile	Leu	Val	Asp	His	Asn	Gln	Asn	Thr	Phe	Ile	Glu	Ile	
			145				150						155			
GAG	CAG	CAA	TTT	CAG	GGC	GTT	CTT	TCC	ATG	CGC	CAT	CGC	ATC	AAG	GGC	531
Glu	Gln	Gln	Phe	Gln	Gly	Val	Leu	Ser	Met	Arg	His	Arg	Ile	Lys	Gly	
		160					165					170				
GAG	AGT	TTT	AAA	GTG	GGC	GAT	AGC	ATT	AAA	GCG	GTT	TTA	ACG	CAA	GTC	579
Glu	Ser	Phe	Lys	Val	Gly	Asp	Ser	Ile	Lys	Ala	Val	Leu	Thr	Gln	Val	
	175					180					185					
AAA	CGC	ACG	AAA	AAA	GGC	TTA	TTA	TTA	GAG	CTG	AGC	CGC	ACC	ACC	CCT	627
Lys	Arg	Thr	Lys	Lys	Gly	Leu	Leu	Leu	Glu	Leu	Ser	Arg	Thr	Thr	Pro	
190					195					200					205	
AAA	ATG	CTT	GAA	GCT	TTG	TTG	GAA	TTG								

	225						230						235						
AAA Lys	GTG Val	AGC Ser	TTT Phe	TTT Phe	TCC Ser	CAT His	AAC Asn	GCT Ala	AGG Arg	ATT Ile	GAC Asp	CCC Pro	ATA Ile	GGC Gly	GCG Ala	771			
		240					245					250							
GCT Ala	GTG Val	GGG Gly	GTT Val	AAG Lys	GGC Gly	GTG Val	CGC Arg	ATT Ile	AAT Asn	GCG Ala	ATC Ile	AGT Ser	AAC Asn	GAA Glu	TTG Leu	819			
		255				260					265								
AAT Asn	AAA Lys	GAA Glu	AAC Asn	ATT Ile	GAT Asp	TGC Cys	ATA Ile	GAA Glu	TAT Tyr	TCT Ser	AAT Asn	GTG Val	CCT Pro	GAA Glu	ATT Ile	867			
					275					280					285				
TAC Tyr	ATC Ile	ACT Thr	CTC Leu	GCA Ala	CTC Leu	GCT Ala	CCA Pro	GCC Ala	AAA Lys	ATT Ile	TTA Leu	AGC Ser	GTT Val	GAA Glu	ATC Ile	915			
				290					295					300					
AAA Lys	AAA Lys	ATC Ile	CCT Pro	ATA Ile	GAA Glu	GAA Glu	TTG Leu	AAT Asn	GCT Ala	GAA Glu	GAA Glu	AAA Lys	GAA Glu	TCC Ser	ATT Ile	963			
			305					310					315						
CAA Gln	GAG Glu	CGT Arg	TTT Phe	ATC Ile	GTC Val	AAT Asn	AAC Asn	CAT His	TTG Leu	CAA Gln	AAG Lys	GCT Ala	AAA Lys	GTG Val	CGT Arg	1011			
		320					325					330							
TTA Leu	TTG Leu	GAC Asp	ATT Ile	GAA Glu	AAA Lys	TCT Ser	AAG Lys	GCT Ala	ATC Ile	GGT Gly	AAG Lys	GGC Gly	GGG Gly	GTG Val	AAT Asn	1059			
		335				340					345								
GTG Val	TGC Cys	TTA Leu	GCG Ala	TCC Ser	ATG Met	CTT Leu	ACA Thr	GGC Gly	TAT Tyr	CAC His	ATA Ile	GAG Glu	TTT Phe	GAA Glu	ACC Thr	1107			
					355					360					365				
ATT Ile	CCT Pro	AGC Ser	GTG Val	AAA Lys	GAA Glu	AAC Asn	GCA Ala	GAA Glu	AAT Asn	GAA Glu	AGC Ser	GAA Glu	AAA Lys	GAA Glu	ACG Thr	1155			
				370					375					380					
CCA Pro	AAA Lys	GTG Val	GGG Gly	GTA Val	GAA Glu	GCT Ala	TTA Leu	GAG Glu	TCT Ser	TTG Leu	TTT Phe	AAG Lys	AAT Asn	TAAGGGTAT		1206			
			385					390					395						
CTAAAAATTCA ATCTCTAAAA AAGCTTTTAA CT																1238			

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Met Glu Lys Ile Ser Asp Leu Ile Glu Cys Ile Ala Tyr Glu Lys Asn
1 5 10 15

Leu	Pro	Lys	Glu	Met	Ile	Ser	Lys	Val	Ile	Gln	Gly	Cys	Leu	Leu	Lys
			20					25					30		
Met	Ala	Gln	Asn	Glu	Leu	Asp	Pro	Leu	Ala	Arg	Tyr	Leu	Val	Val	Glu
		35					40					45			
Glu	Asn	Lys	Gln	Leu	Gln	Leu	Ile	Gln	Leu	Val	Glu	Val	Leu	Glu	Asp
	50					55					60				
Gly	Asp	Glu	Arg	Leu	Val	Asn	Asp	Pro	Ser	Lys	Tyr	Ile	Ser	Leu	Ser
65				70						75				80	
Lys	Ala	Lys	Glu	Met	Asp	Pro	Ser	Val	Lys	Ile	Lys	Asp	Glu	Leu	Ser
				85					90				95		
Tyr	Ser	Leu	Ser	Leu	Glu	Ser	Met	Lys	Gln	Gly	Ala	Ile	Asn	Arg	Leu
			100					105					110		
Phe	Lys	Asp	Leu	Gln	Tyr	Gln	Leu	Glu	Lys	Ala	Leu	Glu	Asp	Ser	His
		115					120					125			
Phe	Glu	Ala	Phe	Gln	Lys	Arg	Leu	Asn	Ser	Val	Leu	Met	Gly	Gln	Val
		130				135					140				
Ile	Leu	Val	Asp	His	Asn	Gln	Asn	Thr	Phe	Ile	Glu	Ile	Glu	Gln	Gln
145					150					155				160	
Phe	Gln	Gly	Val	Leu	Ser	Met	Arg	His	Arg	Ile	Lys	Gly	Glu	Ser	Phe
				165					170					175	
Lys	Val	Gly	Asp	Ser	Ile	Lys	Ala	Val	Leu	Thr	Gln	Val	Lys	Arg	Thr
			180					185					190		
Lys	Lys	Gly	Leu	Leu	Leu	Glu	Leu	Ser	Arg	Thr	Thr	Pro	Lys	Met	Leu
		195					200					205			
Glu	Ala	Leu	Leu	Glu	Leu	Glu	Val	Pro	Glu	Ile	Lys	Asp	Lys	Glu	Ile
		210				215					220				
Glu	Ile	Ile	His	Cys	Ala	Arg	Ile	Pro	Gly	Asn	Arg	Ala	Lys	Val	Ser
225					230					235				240	
Phe	Phe	Ser	His	Asn	Ala	Arg	Ile	Asp	Pro	Ile	Gly	Ala	Ala	Val	Gly
				245					250					255	
Val	Lys	Gly	Val	Arg	Ile	Asn	Ala	Ile	Ser	Asn	Glu	Leu	Asn	Lys	Glu
			260					265					270		
Asn	Ile	Asp	Cys	Ile	Glu	Tyr	Ser	Asn	Val	Pro	Glu	Ile	Tyr	Ile	Thr
		275					280					285			
Leu	Ala	Leu	Ala	Pro	Ala	Lys	Ile	Leu	Ser	Val	Glu	Ile	Lys	Lys	Ile
		290				295					300				
Pro	Ile	Glu	Glu	Leu	Asn	Ala	Glu	Glu	Lys	Glu	Ser	Ile	Gln	Glu	Arg
305					310					315				320	
Phe	Ile	Val	Asn	Asn	His	Leu	Gln	Lys	Ala	Lys	Val	Arg	Leu	Leu	Asp
				325					330					335	
Ile	Glu	Lys	Ser	Lys	Ala	Ile	Gly	Lys	Gly	Gly	Val	Asn	Val	Cys	Leu
			340					345					350		
Ala	Ser	Met	Leu	Thr	Gly	Tyr	His	Ile	Glu	Phe	Glu	Thr	Ile	Pro	Ser
		355					360					365			
Val	Lys	Glu	Asn	Ala	Glu	Asn	Glu	Ser	Glu	Lys	Glu	Thr	Pro	Lys	Val
		370				375					380				
Gly	Val	Glu	Ala	Leu	Glu	Ser	Leu	Phe	Lys	Asn					
385					390					395					

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 21...3857
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

AAGCGATGTA AGGAATTAAC	ATG GAT TAT AAA AAA TTA GAT TTA CCC AAC	50
	Met Asp Tyr Lys Lys Leu Asp Leu Pro Asn	
	1 5 10	
ACA AAC TAC CCA AAT CAA GAG CAA CTG AAA GCT TTT GAA ACC GCT TTT		98
Thr Asn Tyr Pro Asn Gln Glu Gln Leu Lys Ala Phe Glu Thr Ala Phe		
	15 20 25	
GAC GCC TTT TTA GAA ACC AAC CAA CAA GAA AAT GAA AAT CAC CAA AAC		146
Asp Ala Phe Leu Glu Thr Asn Gln Gln Glu Asn Glu Asn His Gln Asn		
	30 35 40	
GAC GCT TTT AAT GAT TTA TTG AAA GGC GTT TTT AAA TAC AAG GTT AAG		194
Asp Ala Phe Asn Asp Leu Leu Lys Gly Val Phe Lys Tyr Lys Val Lys		
	45 50 55	
CCC ACC AAA AAA ATA GAC AGC ACT ATT CTT AAT GAA AAT AAC GAA GTG		242
Pro Thr Lys Lys Ile Asp Ser Thr Ile Leu Asn Glu Asn Asn Glu Val		
	60 65 70	
GAG GTG ATC ATT GAA TTT AAA GCC CTT AAA AAC CCC AAC GAA TTT ATT		290
Glu Val Ile Ile Glu Phe Lys Ala Leu Lys Asn Pro Asn Glu Phe Ile		
	75 80 85 90	
AAA AAG GGC GAT TTG AAT GTT AAA GCC TTT CAT GAA AGC CTT TTG TCT		338
Lys Lys Gly Asp Leu Asn Val Lys Ala Phe His Glu Ser Leu Leu Ser		
	95 100 105	
TAT CTC ACA GAA AGA AAA GAG GGT AAT AAC AAC CTT AAG CAT CTT ATC		386
Tyr Leu Thr Glu Arg Lys Glu Gly Asn Asn Asn Leu Lys His Leu Ile		
	110 115 120	
TTA GCC ACT ATT AAA GAG CTT TAT ATC ATT GAT GCA AAC GAA TTT GAG		434
Leu Ala Thr Ile Lys Glu Leu Tyr Ile Ile Asp Ala Asn Glu Phe Glu		
	125 130 135	
GTT TTT AAT AAA GAT AAA GAA ATT GAA AAC GCC TTT AAA AAT TGC CAC		482
Val Phe Asn Lys Asp Lys Glu Ile Glu Asn Ala Phe Lys Asn Cys His		
	140 145 150	
GAT AGA AAG GGT AAC GAT ACA CGC ACA AAA GCG TTT TAT GAT GCT TGC		530
Asp Arg Lys Gly Asn Asp Thr Arg Thr Lys Ala Phe Tyr Asp Ala Cys		
	155 160 165 170	
CAA AAG CGC CTT AAT GAG TTT GAT CGT TCT TTG AAA TAC CAC TAT ATC		578
Gln Lys Arg Leu Asn Glu Phe Asp Arg Ser Leu Lys Tyr His Tyr Ile		
	175 180 185	
CCC CTC AAA AAA GAA AAT TTA GCC CTA ATC TAT CAA GCC CTA AGC CCT		626

Pro	Leu	Lys	Lys	Glu	Asn	Leu	Ala	Leu	Ile	Tyr	Gln	Ala	Leu	Ser	Pro		
			190					195					200				
AAT	TTT	TTG	CTC	AAA	ATT	CCA	AAA	TAT	TCT	GAC	GCT	AAC	ACG	CTT	AAC	674	
Asn	Phe	Leu	Leu	Lys	Ile	Pro	Lys	Tyr	Ser	Asp	Ala	Asn	Thr	Leu	Asn		
		205					210					215					
AAA	GAT	TTT	TAT	GAA	GAA	TTG	CTT	TAC	ATT	TTA	GGG	TTA	GAA	GAG	CAA	722	
Lys	Asp	Phe	Tyr	Glu	Glu	Leu	Leu	Tyr	Ile	Leu	Gly	Leu	Glu	Glu	Gln		
	220					225					230						
AAT	GAC	AAA	GGG	AAA	ATT	TTA	ATC	AAG	CCC	AGC	CGC	ACC	CAA	AAT	TCC	770	
Asn	Asp	Lys	Gly	Lys	Ile	Leu	Ile	Lys	Pro	Ser	Arg	Thr	Gln	Asn	Ser		
235					240				245						250		
CTA	AGC	GAT	GCT	TTA	AAA	AAG	GAA	TAC	AAA	AAT	TTA	GAC	GAT	GAA	GAA	818	
Leu	Ser	Asp	Ala	Leu	Lys	Lys	Glu	Tyr	Lys	Asn	Leu	Asp	Asp	Glu	Glu		
				255					260					265			
GTC	ATG	GCG	TTG	CTC	ATC	GCT	TGG	AAT	AAC	CGC	ATC	TTG	TTT	TTA	CGG	866	
Val	Met	Ala	Leu	Leu	Ile	Ala	Trp	Asn	Asn	Arg	Ile	Leu	Phe	Leu	Arg		
			270					275					280				
CTT	TTA	GAA	AGC	CTT	TTA	ATT	TCT	TTT	AAG	CAT	TTT	GAA	AAT	CCT	TTC	914	
Leu	Leu	Glu	Ser	Leu	Leu	Ile	Ser	Phe	Lys	His	Phe	Glu	Asn	Pro	Phe		
		285					290					295					
TTA	ACC	ACA	GAA	AAC	TTT	GAA	AAT	TTC	AAC	GAT	TTA	AAC	ACG	CTC	TTT	962	
Leu	Thr	Thr	Glu	Asn	Phe	Glu	Asn	Phe	Asn	Asp	Leu	Asn	Thr	Leu	Phe		
	300					305					310						
TTT	GAA	GTC	CTA	GCC	AAG	AAA	AAC	AGC	GAG	CGC	TTA	CCA	GAA	ATT	AAA	1010	
Phe	Glu	Val	Leu	Ala	Lys	Lys	Asn	Ser	Glu	Arg	Leu	Pro	Glu	Ile	Lys		
315					320				325						330		
GAA	GAC	AAG	ATT	TTA	GAA	AAA	ATC	CCT	TAT	TTG	AAT	TCC	AGT	TTG	TTT	1058	
Glu	Asp	Lys	Ile	Leu	Glu	Lys	Ile	Pro	Tyr	Leu	Asn	Ser	Ser	Leu	Phe		
				335				340						345			
GAT	AAA	ACG	CCT	TTA	GAA	TTA	AAG	GGG	CAT	GAA	ATC	AAG	CTT	TTA	GAC	1106	
Asp	Lys	Thr	Pro	Leu	Glu	Leu	Lys	Gly	His	Glu	Ile	Lys	Leu	Leu	Asp		
			350					355					360				
AAT	AAA	AAG	CTA	GAA	ATC	TAT	AAA	AAT	TCC	GTT	CTC	AAA	AAA	CAT	AAA	1154	
Asn	Lys	Lys	Leu	Glu	Ile	Tyr	Lys	Asn	Ser	Val	Leu	Lys	Lys	His	Lys		
		365					370					375					
GAT	TAT	CAA	AAA	GAA	AAA	CCT	TTG	CCC	TTG	CTA	AAA	TAC	CTT	TTT	AAA	1202	
Asp	Tyr	Gln	Lys	Glu	Lys	Pro	Leu	Pro	Leu	Leu	Lys	Tyr	Leu	Phe	Lys		
	380					385					390						
TTT	TTG	CGT	CTT	TAT	AAA	TTC	ACC	ACC	ACC	CCT	AAA	GAC	ATT	AAA	GAT	1250	
Phe	Leu	Arg	Leu	Tyr	Lys	Phe	Thr	Thr	Thr	Pro	Lys	Asp	Ile	Lys	Asp		
395					400					405					410		
AAT	ACC	GAT	ACC	AGC	GAA	AGC	CGT	TTG	ATT	AAC	CCT	AGC	GTT	TTA	GGG	1298	
Asn	Thr	Asp	Thr	Ser	Glu	Ser	Arg	Leu	Ile	Asn	Pro	Ser	Val	Leu	Gly		
				415				420						425			

CTT Leu	GTT Val	TTT Phe	GAA Glu 430	AAA Lys	CTC Leu	AAC Asn	GGC Gly	TAT Tyr 435	AAA Lys	GAG Glu	GGG Gly	AGC Ser	TTT Phe 440	TAT Tyr	ACC Thr	1346
CCA Pro	AGC Ser	TTT Phe 445	ATC Ile	ACA Thr	AGC Ser	TAC Tyr	ATG Met 450	TGC Cys	AAA Lys	GAG Glu	AGC Ser	ATC Ile 455	ACG Thr	CCC Pro	ATC Ile	1394
GTG Val 460	TTG Leu	GAT Asp	AAA Lys	TTC Phe	AAC Asn	GCC Ala 465	ATT Ile	TAT Tyr	CAG Gln	TGG Trp	GAC Asp 470	TGC Cys	GAA Glu	AAT Asn	CTA Leu	1442
AAA Lys 475	GCG Ala	TTG Leu	CGA Arg	GGA Gly	GAA Glu 480	ATA Ile	GAC Asp	AGA Arg	AAT Asn	TTT Phe 485	TCA Ser	AAT Asn	GAA Glu	AAA Lys	GCT Ala 490	1490
AAA Lys	GAA Glu	TAC Tyr	CTA Leu	AAC Asn 495	ACG Thr	CTT Leu	TTA Leu	ACC Thr 500	TTG Leu	CGT Arg	ATT Ile	TGC Cys	GAT Asp 505	CCG Pro	GCG Ala	1538
GTG Val	GGG Gly	AGC Ser	GGG Gly 510	CAT His	TTC Phe	TTG Leu	GTT Val	TCA Ser 515	GCG Ala	CTC Leu	AAT Asn	GAA Glu 520	ATG Met	GTG Val	CGG Arg	1586
GTT Val	GCT Ala	TAT Tyr 525	GAG Glu	CTA Leu	GGA Gly	CTT Leu	ATT Ile 530	GCT Ala	TCC Ser	TTG Leu	TAT Tyr	CGC Arg 535	TAC Tyr	GAT Asp	CTT Leu	1634
AAA Lys	TTA Leu 540	GAA Glu	AAC Asn	GAT Asp	GAA Glu	ATC Ile 545	ATC Ile	ATT Ile	CAC His	CAC His	ACG Thr 550	CCA Pro	ACG Thr	GGT Gly	GAA Glu	1682
ATC Ile 555	TTT Phe	AAC Asn	TAC Tyr	ATA Ile	AAA Lys 560	CCA Pro	GAT Asp	AGC Ser	GAA Glu	AAC Asn 565	GAC Asp	CCC Pro	CAC His	CAC His	CAC His 570	1730
ATC Ile	CAA Gln	AAA Lys	GAA Glu	CTT Leu 575	TTT Phe	AAT Asn	CTT Leu	AAA Lys 580	AAA Lys	TCC Ser	ATT Ile	ATT Ile	GAA Glu	AAC Asn 585	TGC Cys	1778
CTT Leu	TTT Phe	GGC Gly	GTG Val 590	GAT Asp	ATT Ile	AAC Asn	CCC Pro	AAT Asn 595	TCT Ser	TGC Cys	GAA Glu	ATC Ile	ACC Thr 600	AAG Lys	CTC Leu	1826
AGG Arg	CTA Leu	TGG Trp 605	ATA Ile	GAG Glu	CTT Leu	TTA Leu	AAA Lys 610	TAC Tyr	AGC Ser	TAT Tyr	TAT Tyr	ATT Ile 615	TTT Phe	GAA Glu	AAG Lys	1874
GGC Gly	AAG Lys 620	AAC Asn	ACT Thr	AAC Asn	GCG Ala	CTT Leu 625	GAA Glu	ACC Thr	CTC Leu	CCC Pro	AAC Asn 630	ATT Ile	GAT Asp	ATT Ile	AAC Asn	1922
ATT Ile 635	AAG Lys	TGC Cys	GCT Ala	AAT Asn	TCG Ser 640	CTC Leu	ATT Ile	TCT Ser	AGG Arg	TTT Phe 645	GCC Ala	CTC Leu	AAA Lys	GAT Asp	AAA Lys 650	1970
GCC Ala	TTG Leu	TTA Leu	AAA Lys	AGC Ser	GAA Glu	AAA Lys	AAT Asn	AAA Lys	AAC Asn	CTA Leu	GAA Glu	TAC Tyr	TCT Ser	ATC Ile	GCT Ala	2018

				655				660				665					
GAA Glu	TAC Tyr	AAA Lys	GAA Glu	CTC Leu	GTT Val	AAA Lys	ATC Ile	TAT Tyr	AAA Lys	GAC Asp	CCT Pro	AAA Lys	ATC Ile	TTA Leu	GAA Glu	2066	
			670					675						680			
ACC Thr	CTA Leu	ACG Thr	CAC His	CCC Pro	ATA Ile	AAA Lys	GAC Asp	TCT Ser	AAC Asn	GCC Ala	GTT Val	AGA Arg	AAA Lys	TAC Tyr	GCT Ala	2114	
			685					690					695				
AAA Lys	GAA Glu	CGC Arg	CTT Leu	TAT Tyr	CAA Gln	GAA Glu	CTA Leu	AAA Lys	CAA Gln	AAT Asn	CCT Pro	AAC Asn	AAA Lys	GAT Asp	TTT Phe	2162	
			700				705					710					
AAA Lys	AAG Lys	GCT Ala	CTC Leu	AAT Asn	GAT Asp	AGG Arg	ATA Ile	GAG Glu	AAA Lys	ATT Ile	AAA Lys	AAA Lys	GCT Ala	TTT Phe	AAA Lys	2210	
						720					725				730		
CTC Leu	ACT Thr	TTA Leu	AAC Asn	CCC Pro	CCT Pro	CCA Pro	AAA Lys	GAA Glu	TTA Leu	AAA Lys	TTT Phe	AAA Lys	AAA Lys	TTT Phe	TTA Leu	2258	
					735				740						745		
AAA Lys	GAG Glu	CAT His	TTA Leu	GAA Glu	CTC Leu	TAT Tyr	GGC Gly	AAG Lys	AGT Ser	ATC Ile	TTA Leu	GAA Glu	GAG Glu	GCA Ala	AAC Asn	2306	
					750				755					760			
TAC Tyr	AAC Asn	GGC Gly	TTA Leu	GAA Glu	TTG Leu	GAA Glu	GCC Ala	CTA Leu	GCA Ala	TTA Leu	GAA Glu	AAG Lys	CAA Gln	ATG Met	GCG Ala	2354	
					765			770					775				
AAT Asn	CTT Leu	TTT Phe	TTT Phe	GAT Asp	TAT Tyr	AGA Arg	CCC Pro	TAC Tyr	CCC Pro	AAA Lys	CTA Leu	GAC Asp	AAA Lys	TCG Ser	GAT Asp	2402	
							785					790					
AAA Lys	GTA Val	GTA Val	GGA Gly	CTA Leu	GAA Glu	CAT His	TTT Phe	AAC Asn	CGC Arg	TAT Tyr	GTC Val	CTA Leu	ACA Thr	TCT Ser	TAT Tyr	2450	
						800					805				810		
AAA Lys	GAT Asp	TTA Leu	CAA Gln	GAT Asp	GAA Glu	AAC Asn	GAA Glu	CGC Arg	TAC Tyr	GCT Ala	AAC Asn	GCT Ala	CTT Leu	GAA Glu	TGG Trp	2498	
					815				820						825		
CGC Arg	TTT Phe	GAA Glu	TTC Phe	CCT Pro	GAA Glu	GTT Val	TTA Leu	GAT Asp	GAT Asp	GAG Glu	GGG Gly	GAT Asp	TTT Phe	TCA Ser	GGC Gly	2546	
					830				835					840			
TTT Phe	GAT Asp	TGC Cys	ATC Ile	ATT Ile	GGG Gly	AAT Asn	CCA Pro	CCT Pro	TAT Tyr	ATC Ile	CGC Arg	CAA Gln	GAA Glu	CAC His	ATC Ile	2594	
					845			850					855				
AAA Lys	GAC Asp	TTA Leu	AAG Lys	CCT Pro	TTA Leu	TTA Leu	GAA Glu	AAG Lys	CAA Gln	TAC Tyr	CAA Gln	GAT Asp	TTC Phe	TAT Tyr	AAC Asn	2642	
							865					870					
AGC Ser	ACC Thr	GCT Ala	GAC Asp	ATT Ile	TAC Tyr	ACC Thr	TAC Tyr	TTT Phe	TTT Phe	GCC Ala	CTG Leu	GCT Ala	TTC Phe	CAC His	CTT Leu	2690	
						880					885				890		

TTA Leu	AAA Lys	GAA Glu	AAG Lys	GGG Gly 895	TTT Phe	AGC Ser	GCT Ala	TTC Phe	ATC Ile 900	ACT Thr	TCT Ser	AAC Asn	AAA Lys	TAT Tyr 905	ACG Thr	2738
CGA Arg	GCC Ala	AAA Lys	TAC Tyr 910	GGC Gly	GCT Ala	AAA Lys	TTG Leu	AGG Arg 915	GAA Glu	TGG Trp	CTG Leu	CTC Leu	AAA Lys 920	AAA Lys	ACC Thr	2786
ACC Thr	ATC Ile	GTC Val 925	AGC Ser	TAC Tyr	ATG Met	GAA Glu 930	CTA Leu	AAC Asn	GCC Ala	TTA Leu	AAA Lys 935	GTC Val	TTT Phe	GAG Glu	AGC Ser	2834
GCT Ala	GCA Ala 940	GTG Val	GAT Asp	ACC Thr	AGC Ser	ATC Ile 945	ATT Ile	CAT His	TTC Phe	ATC Ile	AAA Lys 950	CAA Gln	ACG Thr	CCC Pro	TCT Ser	2882
AAA Lys 955	GAG Glu	AGC Ser	GAA Glu	TTT Phe 960	AAA Lys	TAT Tyr	TAC Tyr	GAA Glu	CCC Pro 965	ACC Thr	CCA Pro	AAC Asn	GAT Asp	AAA Lys	GAC Asp 970	2930
GAT Asp	TTG Leu	AAA Lys	AGC Ser 975	ACC Thr	CCA Pro	CAC His	CTT Leu	TTG Leu 980	ATG Met	AAA Lys	CAA Gln	AAC Asn	GTG Val	CTT Leu 985	TCA Ser	2978
ACA Thr	GAA Glu	AGC Ser	TTT Phe 990	ATT Ile	TTT Phe	GCC Ala	AAC Asn	GCC Ala 995	ACG Thr	CTT Leu	TTA Leu	GAT Asp 1000	TTG Leu	AGG Arg	GAC Asp	3026
AAA Lys	ATA Ile 1005	GAG Glu	AGT Ser	GTT Val	GGC Gly	ACC Thr 1010	CCG Pro	CTT Leu 1010	AAA Lys	GAC Asp	TGG Trp 1015	GAC Asp	ATT Ile	CAA Gln	ATC Ile	3074
AAT Asn 1020	TAT Tyr	GGG Gly	ATA Ile	AAA Lys	ACC Thr 1025	GGC Gly	GCG Ala	AAC Asn	GAA Glu	GCC Ala 1030	TTT Phe	ATC Ile	ATT Ile	CCC Pro	ACT Thr	3122
GAA Glu 1035	AAA Lys	AGA Arg	GAA Glu	GAG Glu 1040	ATC Ile	TTA Leu	AAC Asn	GCT Ala	TGC Cys 1045	AAG Lys	ACG Thr	CAA Gln	GAA Glu	GAA Glu 1050	AGG Arg	3170
GAG Glu	CGC Arg	ACA Thr	GAG Glu 1055	AGG Arg	CTT Leu	ATT Ile	AAG Lys	CCT Pro 1060	ATT Ile	TTA Leu	AGA Arg	GGG Gly	AAA Lys 1065	GAC Asp	ATT Ile	3218
AAA Lys	AGG Arg	TAT Tyr 1070	TCT Ser	TAT Tyr	GAG Glu	TGG Trp	GCG Ala 1075	CAT His	TTG Leu	TGG Trp	GTT Val	ATC Ile 1080	AAC Asn	ACC Thr	CAT His	3266
AAC Asn	GGC Gly 1085	TAC Tyr	ACT Thr	TCT Ser	TCT Ser	CTC Leu	AAA Lys 1090	TCC Ser	AAA Lys	ATC Ile	CCT Pro	CCC Pro 1095	ATT Ile	GAT Asp	ATA Ile	3314
GAA Glu 1100	AAA Lys	TAC Tyr	CCC Pro	GCA Ala	ATT Ile 1105	AAA Lys	GCG Ala	CAT His	TTA Leu	GAC Asp 1110	GCT Ala	CAT His	TAC Tyr	GAC Asp	ACT Thr	3362
ATT Ile	GCA Ala	ACA Thr	CGA Arg	TGC Cys	GAT Asp	CAA Gln	GGA Gly	GAC Asp	ACC Thr	CCC Pro	TAT Tyr	CAC His	TTA Leu	AGG Arg	AAT Asn	3410

Glu	Gln	Leu	Lys	Ala	Phe	Glu	Thr	Ala	Phe	Asp	Ala	Phe	Leu	Glu	Thr
			20					25					30		
Asn	Gln	Gln	Glu	Asn	Glu	Asn	His	Gln	Asn	Asp	Ala	Phe	Asn	Asp	Leu
		35					40					45			
Leu	Lys	Gly	Val	Phe	Lys	Tyr	Lys	Val	Lys	Pro	Thr	Lys	Lys	Ile	Asp
	50					55					60				
Ser	Thr	Ile	Leu	Asn	Glu	Asn	Asn	Glu	Val	Glu	Val	Ile	Ile	Glu	Phe
65					70					75					80
Lys	Ala	Leu	Lys	Asn	Pro	Asn	Glu	Phe	Ile	Lys	Lys	Gly	Asp	Leu	Asn
				85					90					95	
Val	Lys	Ala	Phe	His	Glu	Ser	Leu	Leu	Ser	Tyr	Leu	Thr	Glu	Arg	Lys
			100					105					110		
Glu	Gly	Asn	Asn	Asn	Leu	Lys	His	Leu	Ile	Leu	Ala	Thr	Ile	Lys	Glu
		115					120					125			
Leu	Tyr	Ile	Ile	Asp	Ala	Asn	Glu	Phe	Glu	Val	Phe	Asn	Lys	Asp	Lys
	130					135					140				
Glu	Ile	Glu	Asn	Ala	Phe	Lys	Asn	Cys	His	Asp	Arg	Lys	Gly	Asn	Asp
145					150					155					160
Thr	Arg	Thr	Lys	Ala	Phe	Tyr	Asp	Ala	Cys	Gln	Lys	Arg	Leu	Asn	Glu
				165					170					175	
Phe	Asp	Arg	Ser	Leu	Lys	Tyr	His	Tyr	Ile	Pro	Leu	Lys	Lys	Glu	Asn
			180					185					190		
Leu	Ala	Leu	Ile	Tyr	Gln	Ala	Leu	Ser	Pro	Asn	Phe	Leu	Leu	Lys	Ile
		195					200					205			
Pro	Lys	Tyr	Ser	Asp	Ala	Asn	Thr	Leu	Asn	Lys	Asp	Phe	Tyr	Glu	Glu
	210					215					220				
Leu	Leu	Tyr	Ile	Leu	Gly	Leu	Glu	Glu	Gln	Asn	Asp	Lys	Gly	Lys	Ile
225					230					235					240
Leu	Ile	Lys	Pro	Ser	Arg	Thr	Gln	Asn	Ser	Leu	Ser	Asp	Ala	Leu	Lys
				245					250					255	
Lys	Glu	Tyr	Lys	Asn	Leu	Asp	Asp	Glu	Glu	Val	Met	Ala	Leu	Leu	Ile
			260					265					270		
Ala	Trp	Asn	Asn	Arg	Ile	Leu	Phe	Leu	Arg	Leu	Leu	Glu	Ser	Leu	Leu
		275					280					285			
Ile	Ser	Phe	Lys	His	Phe	Glu	Asn	Pro	Phe	Leu	Thr	Thr	Glu	Asn	Phe
	290					295					300				
Glu	Asn	Phe	Asn	Asp	Leu	Asn	Thr	Leu	Phe	Phe	Glu	Val	Leu	Ala	Lys
305					310					315					320
Lys	Asn	Ser	Glu	Arg	Leu	Pro	Glu	Ile	Lys	Glu	Asp	Lys	Ile	Leu	Glu
				325					330					335	
Lys	Ile	Pro	Tyr	Leu	Asn	Ser	Ser	Leu	Phe	Asp	Lys	Thr	Pro	Leu	Glu
			340					345					350		
Leu	Lys	Gly	His	Glu	Ile	Lys	Leu	Leu	Asp	Asn	Lys	Lys	Leu	Glu	Ile
		355					360					365			
Tyr															

Ile	Asp	Arg	Asn	Phe	Ser	Asn	Glu	Lys	Ala	Lys	Glu	Tyr	Leu	Asn	Thr
				485					490					495	
Leu	Leu	Thr	Leu	Arg	Ile	Cys	Asp	Pro	Ala	Val	Gly	Ser	Gly	His	Phe
			500					505					510		
Leu	Val	Ser	Ala	Leu	Asn	Glu	Met	Val	Arg	Val	Ala	Tyr	Glu	Leu	Gly
		515					520					525			
Leu	Ile	Ala	Ser	Leu	Tyr	Arg	Tyr	Asp	Leu	Lys	Leu	Glu	Asn	Asp	Glu
	530					535					540				
Ile	Ile	Ile	His	His	Thr	Pro	Thr	Gly	Glu	Ile	Phe	Asn	Tyr	Ile	Lys
545					550					555					560
Pro	Asp	Ser	Glu	Asn	Asp	Pro	His	His	His	Ile	Gln	Lys	Glu	Leu	Phe
				565					570					575	
Asn	Leu	Lys	Lys	Ser	Ile	Ile	Glu	Asn	Cys	Leu	Phe	Gly	Val	Asp	Ile
			580					585					590		
Asn	Pro	Asn	Ser	Cys	Glu	Ile	Thr	Lys	Leu	Arg	Leu	Trp	Ile	Glu	Leu
		595					600					605			
Leu	Lys	Tyr	Ser	Tyr	Tyr	Ile	Phe	Glu	Lys	Gly	Lys	Asn	Thr	Asn	Ala
	610					615					620				
Leu	Glu	Thr	Leu	Pro	Asn	Ile	Asp	Ile	Asn	Ile	Lys	Cys	Ala	Asn	Ser
625					630					635					640
Leu	Ile	Ser	Arg	Phe	Ala	Leu	Lys	Asp	Lys	Ala	Leu	Leu	Lys	Ser	Glu
				645					650					655	
Lys	Asn	Lys	Asn	Leu	Glu	Tyr	Ser	Ile	Ala	Glu	Tyr	Lys	Glu	Leu	Val
			660					665					670		
Lys	Ile	Tyr	Lys	Asp	Pro	Lys	Ile	Leu	Glu	Thr	Leu	Thr	His	Pro	Ile
	675						680					685			
Lys	Asp	Ser	Asn	Ala	Val	Arg	Lys	Tyr	Ala	Lys	Glu	Arg	Leu	Tyr	Gln
	690					695					700				
Glu	Leu	Lys	Gln	Asn	Pro	Asn	Lys	Asp	Phe	Lys	Lys	Ala	Leu	Asn	Asp
705					710					715					720
Arg	Ile	Glu	Lys	Ile	Lys	Lys	Ala	Phe	Lys	Leu	Thr	Leu	Asn	Pro	Pro
				725					730					735	
Pro	Lys	Glu	Leu	Lys	Phe	Lys	Lys	Phe	Leu	Lys	Glu	His	Leu	Glu	Leu
			740					745					750		
Tyr	Gly	Lys	Ser	Ile	Leu	Glu	Glu	Ala	Asn	Tyr	Asn	Gly	Leu	Glu	Leu
	755						760					765			
Glu	Ala	Leu	Ala	Leu	Glu	Lys	Gln	Met	Ala	Asn	Leu	Phe	Phe	Asp	Tyr
	770					775					780				
Arg	Pro	Tyr	Pro	Lys	Leu	Asp	Lys	Ser	Asp	Lys	Val	Val	Gly	Leu	Glu
785					790					795					800
His	Phe	Asn	Arg	Tyr	Val	Leu	Thr	Ser	Tyr	Lys	Asp	Leu	Gln	Asp	Glu
				805					810					815	
Asn	Glu	Arg	Tyr	Ala	Asn	Ala	Leu	Glu	Trp	Arg	Phe	Glu	Phe	Pro	Glu
			820					825					830		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

TTTAAATCAT TTAAAAAAG GATAGAG ATG CAA AAT AAA GAA ATT GGT GAA GAA	54
Met Gln Asn Lys Glu Ile Gly Glu Glu	
1 5	
AAA AGC GTT AAT GAA AAA AAT GTA GAG GTT TTT AAT CGT TAT TTT CCC	102
Lys Ser Val Asn Glu Lys Asn Val Glu Val Phe Asn Arg Tyr Phe Pro	
10 15 20 25	
GGT TGC TTG AGT ATA GAA AAT GAT AAC AAG CTC ACG CTG GAT ACA GGA	150
Gly Cys Leu Ser Ile Glu Asn Asp Asn Lys Leu Thr Leu Asp Thr Gly	
30 35 40	
AAA TTA AAA GCG TTA CTA GGG GAT TTT AGC GAG ATA AAA GAA GAG GGC	198
Lys Leu Lys Ala Leu Leu Gly Asp Phe Ser Glu Ile Lys Glu Glu Gly	
45 50 55	
TAT GGG TTG GAT TTT GTG GGT AAG AAA ATC GCC TTA AAC CAA GCT TTT	246
Tyr Gly Leu Asp Phe Val Gly Lys Lys Ile Ala Leu Asn Gln Ala Phe	
60 65 70	
AAG AAA AAT CAT AAG ATT TTA AAG CCC TTA AAC GAA TCC ACT AGC AAG	294
Lys Lys Asn His Lys Ile Leu Lys Pro Leu Asn Glu Ser Thr Ser Lys	
75 80 85	
CAC GTT CTC ATC AAG GGC GAT AAT TTA GAC GCT CTC AAA ATC TTA AAA	342
His Val Leu Ile Lys Gly Asp Asn Leu Asp Ala Leu Lys Ile Leu Lys	
90 95 100 105	
CAA AGC TAT AGT GAA AAA ATC AAA ATG ATT TAC ATT GAC CCG CCT TAC	390
Gln Ser Tyr Ser Glu Lys Ile Lys Met Ile Tyr Ile Asp Pro Pro Tyr	
110 115 120	
AAC ACG AAA AAC GAG AAT TTT ATC TAT GGC GAT GAT TTC TCG CAA TCC	438
Asn Thr Lys Asn Glu Asn Phe Ile Tyr Gly Asp Asp Phe Ser Gln Ser	
125 130 135	
AAT GAA GAG GTT TTA AAA ACA TTG GAT TAT TCT AAA GAA AAA TTG GAT	486
Asn Glu Glu Val Leu Lys Thr Leu Asp Tyr Ser Lys Glu Lys Leu Asp	
140 145 150	
TAC ATC AAG AAC CTT TTT GGG TCA AAA TGC CAT AGC GGG TGG CTT AGT	534
Tyr Ile Lys Asn Leu Phe Gly Ser Lys Cys His Ser Gly Trp Leu Ser	
155 160 165	
TTC ATG TAT CCC AGA TTG TTG CTC GCT AAA GAT TTG CTC AAA CAA GAC	582
Phe Met Tyr Pro Arg Leu Leu Leu Ala Lys Asp Leu Leu Lys Gln Asp	
170 175 180 185	
GGC GTG ATT TTC ATT TCT ATT GAC GAT AAC GAA TGC GCT CAA CTC AAA	630
Gly Val Ile Phe Ile Ser Ile Asp Asp Asn Glu Cys Ala Gln Leu Lys	
190 195 200	
CTT TTA TGC GAT GAA ATT TTT GGG GAG GGG AAT TTT GTG GCG TGT TTA	678
Leu Leu Cys Asp Glu Ile Phe Gly Glu Gly Asn Phe Val Ala Cys Leu	
205 210 215	

[illegible]

TCATTCTCGT C

1415

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

```

Met Gln Asn Lys Glu Ile Gly Glu Glu Lys Ser Val Asn Glu Lys Asn
 1           5           10           15
Val Glu Val Phe Asn Arg Tyr Phe Pro Gly Cys Leu Ser Ile Glu Asn
 20           25           30
Asp Asn Lys Leu Thr Leu Asp Thr Gly Lys Leu Lys Ala Leu Leu Gly
 35           40           45
Asp Phe Ser Glu Ile Lys Glu Gly Tyr Gly Leu Asp Phe Val Gly
 50           55           60
Lys Lys Ile Ala Leu Asn Gln Ala Phe Lys Lys Asn His Lys Ile Leu
 65           70           75           80
Lys Pro Leu Asn Glu Ser Thr Ser Lys His Val Leu Ile Lys Gly Asp
 85           90           95
Asn Leu Asp Ala Leu Lys Ile Leu Lys Gln Ser Tyr Ser Glu Lys Ile
 100          105          110
Lys Met Ile Tyr Ile Asp Pro Pro Tyr Asn Thr Lys Asn Glu Asn Phe
 115          120          125
Ile Tyr Gly Asp Asp Phe Ser Gln Ser Asn Glu Glu Val Leu Lys Thr
 130          135          140
Leu Asp Tyr Ser Lys Glu Lys Leu Asp Tyr Ile Lys Asn Leu Phe Gly
 145          150          155          160
Ser Lys Cys His Ser Gly Trp Leu Ser Phe Met Tyr Pro Arg Leu Leu
 165          170          175
Leu Ala Lys Asp Leu Leu Lys Gln Asp Gly Val Ile Phe Ile Ser Ile
 180          185          190
Asp Asp Asn Glu Cys Ala Gln Leu Lys Leu Leu Cys Asp Glu Ile Phe
 195          200          205
Gly Glu Gly Asn Phe Val Ala Cys Leu Lys Trp Lys Lys Lys Lys Gln
 210          215          220
Pro Ser Phe Leu Ser Lys Val Ala Val Ile Leu Glu Tyr Ile Leu Val
 225          230          235
Tyr Ala Lys Asp Phe Ser Leu Ile Asp Lys Leu Gly Leu Asp Asn Val
 245          250          255
Ser Asp Ser Asp Lys Pro Ile Ile Asn Thr Ser Asn Asn Leu Ser Lys
 260          265          270
Arg Tyr Phe Lys Lys Gly Ile Arg Val Lys Ser Asp Leu Asn Phe Ile
 275          280          285
Lys Ser Gly Lys Tyr Gln Asn Lys Thr Met Thr Ile Glu Phe Met Asn
 290          295          300
Asp Ile Phe Ile Glu Asn Gly Arg Thr Lys Asn Asp Phe Glu Cys Ile
 305          310          315          320
Gly Lys Phe Arg Thr Gly Gln Glu Asn Ile Asn Glu Phe Ile Glu Lys
 325          330          335

```

Asp Leu Ile Phe Ile Thr Lys Asn Leu Gly Ile Arg Arg Asp Leu Leu
 340 345 350
 Glu Glu Glu Gln Ser Asn Lys Lys Thr Ile Thr Asp Leu Leu Thr Glu
 355 360 365
 Trp Gly Gln Asn Gln Asp Ala Thr Asn Glu Leu Asn Ile Leu Phe Asn
 370 375 380
 Asn Ser Ser Asp Glu Ser Ile Phe Ser Asn Pro Lys Pro Thr Lys Leu
 385 390 395 400
 Ile Asn Arg Leu Ile Glu Leu Ser Thr Asn Glu Gly Asp Ile Ile Leu
 405 410 415
 Asp Phe Phe Ala Gly Ser Gly Thr Thr Ala His Ala Val Leu Glu Ser
 420 425 430
 Asn Lys Ser Asp Tyr Gln Lys Leu Ser Glu Gly Gly Gly Gly Tyr Leu
 435 440 445
 Met Val
 450

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 55...1344
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GAAACGAATA AAAATTTTCC TTCACAACAT TTAAATGCAT TAAAATACAT TGAA ATG	57
Met	
1	
CTT TTT TAT ATG AAA AAT TTA GAG CGC AAA AAA TTG CAA TTT GGC GCT	105
Leu Phe Tyr Met Lys Asn Leu Glu Arg Lys Lys Leu Gln Phe Gly Ala	
5 10 15	
AAA ATC GCA TGC CCC AAT AAT AAC GAG CGC TTG AAA GCG TTT ATC GCT	153
Lys Ile Ala Cys Pro Asn Asn Asn Glu Arg Leu Lys Ala Phe Ile Ala	
20 25 30	
TCT TTA CCC TTT AAA CTC ACA CGC GAT CAA CAA AAC GCC ATT AAA GAA	201
Ser Leu Pro Phe Lys Leu Thr Arg Asp Gln Gln Asn Ala Ile Lys Glu	
35 40 45	
ATC CAA AAC GAT CTC ACT AGC TCC ATA GCG TGC AAG CGT TTG ATT ATA	249
Ile Gln Asn Asp Leu Thr Ser Ser Ile Ala Cys Lys Arg Leu Ile Ile	
50 55 60 65	
GGC GAT GTG GGG TGC GGG AAA ACG ATG GTG ATT TTA GCG AGC ATG GTA	297
Gly Asp Val Gly Cys Gly Lys Thr Met Val Ile Leu Ala Ser Met Val	
70 75 80	

TTA Leu	ACT Thr	TAC Tyr	CCA Pro 85	AAT Asn	AAA Lys	ACC Thr	CTT Leu	TTA Leu 90	ATG Met	GCG Ala	CCC Pro	ACT Thr	TCC Ser 95	ATT Ile	CTC Leu	345
GCT Ala	AAA Lys	CAG Gln 100	CTT Leu	TAT Tyr	AAC Asn	GAA Glu	GCC Ala 105	TTA Leu	AAA Lys	TTT Phe	TTA Leu	CCC Pro 110	CCT Pro	TAT Tyr	TTT Phe	393
GAA Glu	GTG Val 115	GAA Glu	TTG Leu	CTG Leu	CTC Leu	GGC Gly 120	GGG Gly	AGT Ser	TAC Tyr	AAG Lys	AAG Lys 125	CGA Arg	TCC Ser	AAT Asn	CAT His	441
TTG Leu 130	TTT Phe	GAA Glu	ACA Thr	ATC Ile	ACG Thr 135	CAT His	GTG Val	GTT Val	ATC Ile	GGC Gly 140	ACG Thr	CAA Gln	GCG Ala	TTG Leu	TTG Leu 145	489
TTT Phe	GAT Asp	AAG Lys	CGC Arg	GAT Asp 150	TTG Leu	AAT Asn	GAA Glu	TTC Phe	GCT Ala 155	CTA Leu	GTG Val	ATC Ile	ACT Thr	GAT Asp 160	GAA Glu	537
CAG Gln	CAC His	CGA Arg	TTT Phe 165	GGC Gly	ACC Thr	AAG Lys	CAG Gln	CGC Arg 170	TAC Tyr	CAA Gln	TTA Leu	GAA Glu	AAA Lys 175	ATG Met	GCA Ala	585
AGC Ser	AGT Ser	AAG Lys 180	GGT Gly	AAT Asn	AAA Lys	CCC Pro	CAT His 185	TCT Ser	TTG Leu	CAA Gln	TTT Phe	TCC Ser 190	GCT Ala	ACC Thr	CCC Pro	633
ATT Ile	CCT Pro 195	CGC Arg	ACG Thr	CTC Leu	GCC Ala	CTA Leu 200	GCC Ala	AAA Lys	AGC Ser	GCG Ala	TTT Phe 205	GTG Val	AAA Lys	ACG Thr	ACC Thr	681
ATG Met 210	ATT Ile	AGA Arg	GAA Glu	ATC Ile	CCT Pro 215	TAT Tyr	CCT Pro	AAA Lys	GAG Glu	ATT Ile 220	GAA Glu	ACT Thr	CTA Leu	GTC Val	TTG Leu 225	729
CAT His	AAA Lys	AGA Arg	GAT Asp	TTT Phe 230	AAA Lys	ATA Ile	GTG Val	ATG Met	GAG Glu 235	AAA Lys	ATC Ile	AGC Ser	GAA Glu	GAA Glu 240	ATC Ile	777
GCT Ala	AAA Lys	AAC Asn	CAT His 245	CAA Gln	GTC Val	ATT Ile	GTC Val	GTC Val 250	TAT Tyr	CCG Pro	CTG Leu	GTG Val	AAT Asn 255	GAG Glu	AGC Ser	825
GAA Glu	AAA Lys	ATC Ile 260	CCG Pro	TAT Tyr	TTA Leu	TCG Ser	CTC Leu 265	AGT Ser	GAG Glu	GGG Gly	GCG Ala	AGT Ser 270	TTT Phe	TGG Trp	CAA Gln	873
AAA Lys	CGC Arg 275	TTT Phe	AAA Lys	AAG Lys	GTT Val	TAT Tyr 280	ACC Thr	ACT Thr	TCA Ser	GGG Gly	CAA Gln 285	GAT Asp	AAA Lys	AAT Asn	AAA Lys	921
GAA Glu 290	GAA Glu	GTG Val	ATT Ile	GAA Glu	GAA Glu 295	TTT Phe	AGA Arg	GAA Glu	TCC Ser	GGG Gly 300	AGC Ser	ATT Ile	CTT Leu	TTA Leu	GCG Ala 305	969
ACT Thr	ACG Thr	CTC Leu	ATT Ile	GAG Glu	GTG Val	GGC Gly	ATT Ile	TCT Ser	TTA Leu	CCA Pro	CGA Arg	TTG Leu	AGC Ser	GTG Val	ATG Met	1017

310	315	320	
GTG ATT TTA GCG CCC GAA AGG TTA GGC TTA GCG ACT TTA CAC CAG TTA			1065
Val Ile Leu Ala Pro Glu Arg Leu Gly Leu Ala Thr Leu His Gln Leu			
325	330	335	
AGG GGG CGC GTT TCT CGT AAC GGC TTG AAA GGC TAT TGT TTT TTA TGC			1113
Arg Gly Arg Val Ser Arg Asn Gly Leu Lys Gly Tyr Cys Phe Leu Cys			
340	345	350	
ACG ATC CAA GAA GAA AAC GAA CGA TTA GAA AAG TTT GCT GAT GAA TTG			1161
Thr Ile Gln Glu Glu Asn Glu Arg Leu Glu Lys Phe Ala Asp Glu Leu			
355	360	365	
GAC GGC TTT AAA ATC GCT GAA TTG GAT TTA GAA TAC AGA AAA AGC GGG			1209
Asp Gly Phe Lys Ile Ala Glu Leu Asp Leu Glu Tyr Arg Lys Ser Gly			
370	375	380	385
GAT TTA CTC CAG GGA GGG GAG CAG AGC GGG AAT AGT TTT GAA TAC ATT			1257
Asp Leu Leu Gln Gly Gly Glu Gln Ser Gly Asn Ser Phe Glu Tyr Ile			
390	395	400	
GAC TTA GCC AAA GAT GAA AAC ATT ATC GCT GAA GTG AAA CGG GAT TTT			1305
Asp Leu Ala Lys Asp Glu Asn Ile Ile Ala Glu Val Lys Arg Asp Phe			
405	410	415	
TTA AAG GCC GCT AGC GTT TCA CGG GGA ACA TTT GAA AAT TGAAAATTAA GG			1356
Leu Lys Ala Ala Ser Val Ser Arg Gly Thr Phe Glu Asn			
420	425	430	
CAGAATTGGG TAATTTAAAT CATTTAAAAA AAG			1389

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Met	Leu	Phe	Tyr	Met	Lys	Asn	Leu	Glu	Arg	Lys	Lys	Leu	Gln	Phe	Gly
1				5				10					15		
Ala	Lys	Ile	Ala	Cys	Pro	Asn	Asn	Asn	Glu	Arg	Leu	Lys	Ala	Phe	Ile
			20					25					30		
Ala	Ser	Leu	Pro	Phe	Lys	Leu	Thr	Arg	Asp	Gln	Gln	Asn	Ala	Ile	Lys
		35					40					45			
Glu	Ile	Gln	Asn	Asp	Leu	Thr	Ser	Ser	Ile	Ala	Cys	Lys	Arg	Leu	Ile
	50					55				60					
Ile	Gly	Asp	Val	Gly	Cys	Gly	Lys	Thr	Met	Val	Ile	Leu	Ala	Ser	Met
65					70				75					80	
Val	Leu	Thr	Tyr	Pro	Asn	Lys	Thr	Leu	Leu	Met	Ala	Pro	Thr	Ser	Ile
				85				90					95		
Leu	Ala	Lys	Gln	Leu	Tyr	Asn	Glu	Ala	Leu	Lys	Phe	Leu	Pro	Pro	Tyr
			100					105					110		

TGTATTTCCT TTTTCATTCA CCACTTATTC ACGCTATAAT AACGCC ATG GAT ACC																55
Met Asp Thr																
1																
AAC Asn	AAC Asn	AAT Asn	ATT Ile	GAA Glu	AAA Lys	GAA Glu	ATC Ile	TTG Leu	GCG Ala	CTA Leu	GTC Val	AAA Lys	CAA Gln	AAT Asn	CCT Pro	103
5 10 15																
AAA Lys	GTT Val	AGT Ser	CTC Leu	ATA Ile	GAG Glu	TAT Tyr	GAA Glu	AAT Asn	TAC Tyr	TTT Phe	AGC Ser	CAA Gln	CTC Leu	AAA Lys	TAC Tyr	151
20 25 30 35																
AAC Asn	CCT Pro	AAC Asn	GCA Ala	AGC Ser	AAG Lys	AGC Ser	GAT Asp	ATT Ile	GCC Ala	TTT Phe	TTT Phe	TAT Tyr	GCC Ala	CCC Pro	AAC Asn	199
40 45 50																
CAA Gln	GTC Val	TTA Leu	TGC Cys	ACC Thr	ACG Thr	ATT Ile	ACA Thr	GCT Ala	AAA Lys	TAC Tyr	GGC Gly	GCG Ala	TTG Leu	CTT Leu	AAA Lys	247
55 60 65																
GAA Glu	ATT Ile	TTA Leu	AGC Ser	CAG Gln	AAT Asn	AAA Lys	GTC Val	GGC Gly	ATG Met	CAT His	TTA Leu	GCC Ala	CAC His	AGC Ser	GTG Val	295
70 75 80																
GAT Asp	GTG Val	CGT Arg	ATT Ile	GAA Glu	GTA Val	GCG Ala	CCT Pro	AAA Lys	ATC Ile	CAA Gln	ATT Ile	AAC Asn	GCC Ala	CAA Gln	TCT Ser	343
85 90 95																
AAT Asn	ATC Ile	AAT Asn	TAC Tyr	AAA Lys	GCC Ala	ATA Ile	AAA Lys	ACG Thr	AGC Ser	GTC Val	AAA Lys	GAC Asp	TCT Ser	TAC Tyr	ACT Thr	391
100 105 110 115																
TTT Phe	GAA Glu	AAT Asn	TTT Phe	GTC Val	GTA Val	GGC Gly	TCA Ser	TGC Cys	AAT Asn	AAC Asn	ACC Thr	GTT Val	TAT Tyr	GAA Glu	ATC Ile	439
120 125 130																
GCT Ala	AAA Lys	AAA Lys	GTC Val	GCC Ala	CAA Gln	AGC Ser	GAT Asp	ACC Thr	CCC Pro	CCT Pro	TAT Tyr	AAC Asn	CCG Pro	GTG Val	CTT Leu	487
135 140 145																
TTT Phe	TAT Tyr	GGC Gly	GGC Gly	ACA Thr	GGG Gly	TTA Leu	GGC Gly	AAA Lys	ACG Thr	CAC His	ATT Ile	TTA Leu	AAC Asn	GCT Ala	ATC Ile	535
150 155 160																
GGC Gly	AAC Asn	CAT His	GCC Ala	CTA Leu	GAA Glu	AAG Lys	CAT His	AAA Lys	AAA Lys	GTC Val	GTG Val	TTA Leu	GTC Val	ACT Thr	TCA Ser	583
165 170 175																
GAA Glu	GAC Asp	TTT Phe	TTG Leu	ACA Thr	GAC Asp	TTT Phe	TTA Leu	AAG Lys	CAT His	TTA Leu	GAC Asp	AAC Asn	AAA Lys	ACC Thr	ATG Met	631
180 185 190 195																
GAT Asp	TCT Ser	TTT Phe	AAA Lys	GCA Ala	AAA Lys	TAC Tyr	CGC Arg	CAT His	TGC Cys	GAC Asp	TTT Phe	TTC Phe	TTG Leu	TTA Leu	GAT Asp	679
200 205 210																
GAC Asp	GCT Ala	CAA Gln	TTT Phe	TTG Leu	CAA Gln	GGA Gly	AAA Lys	CCC Pro	AAG Lys	CTA Leu	GAA Glu	GAA Glu	GAA Glu	TTT Phe	TTC Phe	727

215						220						225						
CAC His	ACC Thr	TTT Phe 230	AAC Asn	GAA Glu	TTG Leu	CAC His	GCC Ala 235	AAC Asn	AGC Ser	AAA Lys	CAA Gln	ATC Ile 240	GTA Val	TTG Leu	ATT Ile	775		
TCA Ser	GAC Asp 245	CGA Arg	TCG Ser	CCT Pro	AAA Lys	AAC Asn 250	ATC Ile	GCC Ala	GGC Gly	TTA Leu	GAA Glu 255	GAT Asp	CGC Arg	TTA Leu	AAA Lys	823		
TCG Ser 260	CGC Arg	TTT Phe	GAA Glu	TGG Trp 265	GGG Gly	ATA Ile	ACC Thr	GCT Ala	AAA Lys	GTC Val 270	ATG Met	CCC Pro	CCT Pro	GAT Asp	TTA Leu 275	871		
GAA Glu	ACC Thr	AAA Lys	CTT Leu	TCC Ser 280	ATT Ile	GTC Val	AAA Lys	CAA Gln	AAA Lys 285	TGC Cys	CAG Gln	CTC Leu	AAT Asn	CAA Gln 290	ATC Ile	919		
ACT Thr	TTG Leu	CCT Pro	GAA Glu 295	GAG Glu	GTG Val	ATG Met	GAA Glu	TAC Tyr 300	ATC Ile	GCC Ala	CAA Gln	CAC His	ATC Ile 305	AGC Ser	GAC Asp	967		
AAT Asn	ATC Ile	CGC Arg 310	CAA Gln	ATG Met	GAA Glu	GGC Gly	GCG Ala 315	ATC Ile	ATT Ile	AAA Lys	ATC Ile	AGC Ser 320	GTG Val	AAC Asn	GCG Ala	1015		
AAC Asn	TTG Leu 325	ATG Met	AAC Asn	GCT Ala	TCC Ser	ATT Ile 330	GAT Asp	TTG Leu	AAC Asn	CTC Leu	GCT Ala 335	AAA Lys	ACC Thr	GTT Val	TTA Leu	1063		
GAA Glu 340	GAT Asp	TTG Leu	CAA Gln	AAA Lys	GAT Asp 345	CAT His	GCT Ala	GAA Glu	GGT Gly	TCA Ser 350	AGC Ser	TTG Leu	GAA Glu	AAT Asn	ATC Ile 355	1111		
CTA Leu	CTC Leu	GCT Ala	GTC Val	GCG Ala 360	CAA Gln	AGC Ser	CTG Leu	AAT Asn	CTC Leu 365	AAA Lys	TCC Ser	AGC Ser	GAA Glu	ATC Ile 370	AAA Lys	1159		
GTC Val	TCT Ser	TCG Ser	CGC Arg 375	CAA Gln	AAA Lys	AAT Asn	GTC Val	GCT Ala 380	TTG Leu	GCG Ala	AGG Arg	AAA Lys	TTA Leu 385	GTC Val	GTG Val	1207		
TAT Tyr	TTC Phe	GCC Ala 390	AGG Arg	CTT Leu	TAT Tyr	ACC Thr	CCT Pro 395	AAC Asn	CCC Pro	ACG Thr	CTC Leu	TCG Ser 400	CTC Leu	GCT Ala	CAA Gln	1255		
TTT Phe 405	TTG Leu	GAT Asp	TTA Leu	AAG Lys	GAT Asp	CAT His 410	TCA Ser	AGC Ser	ATT Ile	TCT Ser	AAA Lys 415	ATG Met	TAT Tyr	TCT Ser	GGC Gly	1303		
GTT Val 420	AAA Lys	AAA Lys	ATG Met	CTT Leu	GAA Glu 425	GAA Glu	GAA Glu	AAA Lys	AGC Ser	CCT Pro 430	TTT Phe	GTC Val	TTA Leu	AGC Ser	CTT Leu 435	1351		
AGA Arg	GAA Glu	GAA Glu	ATC Ile	AAA Lys 440	AAC Asn	CGC Arg	TTG Leu	AAC Asn	GAA Glu 445	TTG Leu	AAC Asn	GAC Asp	AAA Lys	AAA Lys	ACC Thr 450	1399		

GCT TTC AAT TCA AGT GAA TGAAAAAAGG CTTATGAAAA AGCGTTTCAT TCACTTCT 1455
 Ala Phe Asn Ser Ser Glu
 455

TTTCAAAT

1463

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Met	Asp	Thr	Asn	Asn	Asn	Ile	Glu	Lys	Glu	Ile	Leu	Ala	Leu	Val	Lys	1	5	10	15
Gln	Asn	Pro	Lys	Val	Ser	Leu	Ile	Glu	Tyr	Glu	Asn	Tyr	Phe	Ser	Gln	20	25	30	
Leu	Lys	Tyr	Asn	Pro	Asn	Ala	Ser	Lys	Ser	Asp	Ile	Ala	Phe	Phe	Tyr	35	40	45	
Ala	Pro	Asn	Gln	Val	Leu	Cys	Thr	Thr	Ile	Thr	Ala	Lys	Tyr	Gly	Ala	50	55	60	
Leu	Leu	Lys	Glu	Ile	Leu	Ser	Gln	Asn	Lys	Val	Gly	Met	His	Leu	Ala	65	70	75	80
His	Ser	Val	Asp	Val	Arg	Ile	Glu	Val	Ala	Pro	Lys	Ile	Gln	Ile	Asn	85	90	95	
Ala	Gln	Ser	Asn	Ile	Asn	Tyr	Lys	Ala	Ile	Lys	Thr	Ser	Val	Lys	Asp	100	105	110	
Ser	Tyr	Thr	Phe	Glu	Asn	Phe	Val	Val	Gly	Ser	Cys	Asn	Asn	Thr	Val	115	120	125	
Tyr	Glu	Ile	Ala	Lys	Lys	Val	Ala	Gln	Ser	Asp	Thr	Pro	Pro	Tyr	Asn	130	135	140	
Pro	Val	Leu	Phe	Tyr	Gly	Gly	Thr	Gly	Leu	Gly	Lys	Thr	His	Ile	Leu	145	150	155	160
Asn	Ala	Ile	Gly	Asn	His	Ala	Leu	Glu	Lys	His	Lys	Lys	Val	Val	Leu	165	170	175	
Val	Thr	Ser	Glu	Asp	Phe	Leu	Thr	Asp	Phe	Leu	Lys	His	Leu	Asp	Asn	180	185	190	
Lys	Thr	Met	Asp	Ser	Phe	Lys	Ala	Lys	Tyr	Arg	His	Cys	Asp	Phe	Phe	195	200	205	
Leu	Leu	Asp	Asp	Ala	Gln	Phe	Leu	Gln	Gly	Lys	Pro	Lys	Leu	Glu	Glu	210	215	220	
Glu	Phe	Phe	His	Thr	Phe	Asn	Glu	Leu	His	Ala	Asn	Ser	Lys	Gln	Ile	225	230	235	240
Val	Leu	Ile	Ser	Asp	Arg	Ser	Pro	Lys	Asn	Ile	Ala	Gly	Leu	Glu	Asp	245	250	255	
Arg	Leu	Lys	Ser	Arg	Phe	Glu	Trp	Gly	Ile	Thr	Ala	Lys	Val	Met	Pro	260	265	270	
Pro	Asp	Leu	Glu	Thr	Lys	Leu	Ser	Ile	Val	Lys	Gln	Lys	Cys	Gln	Leu	275	280	285	
Asn	Gln	Ile	Thr	Leu	Pro	Glu	Glu	Val	Met	Glu	Tyr	Ile	Ala	Gln	His	290	295	300	
Ile	Ser	Asp	Asn	Ile	Arg	Gln	Met	Glu	Gly	Ala	Ile	Ile	Lys	Ile	Ser	305	310	315	320

Asp	Ser	Val	Asn	Phe	Thr	Ile	Met	Gln	Glu	Val	Ala	Tyr	Gly	Trp	Leu	
75						80					85					
TGG	CGC	CAC	ATG	CAT	GCC	ACG	GCA	GCG	AGC	ATG	ATT	TTT	GTC	ATC	ATT	339
Trp	Arg	His	Met	His	Ala	Thr	Ala	Ala	Ser	Met	Ile	Phe	Val	Ile	Ile	
90					95				100						105	
TAT	ATC	CAC	ATG	TTT	GTT	GGC	ATC	TAT	TAT	GGC	TCT	TAC	AAA	AAG	GGT	387
Tyr	Ile	His	Met	Phe	Val	Gly	Ile	Tyr	Tyr	Gly	Ser	Tyr	Lys	Lys	Gly	
				110					115					120		
CGT	GAG	ATG	ATT	TGG	ATT	AGC	GGG	ATG	ATT	TTG	TTT	GTG	GTC	TTT	AGC	435
Arg	Glu	Met	Ile	Trp	Ile	Ser	Gly	Met	Ile	Leu	Phe	Val	Val	Phe	Ser	
			125					130					135			
GCG	GAA	GCC	TTT	AGC	GGG	TAT	ATG	CTG	CCT	TGG	GGG	CAG	ATG	AGT	TAT	483
Ala	Glu	Ala	Phe	Ser	Gly	Tyr	Met	Leu	Pro	Trp	Gly	Gln	Met	Ser	Tyr	
		140					145					150				
TGG	GCC	GCA	GCG	GTT	ATC	ACG	AAT	TTA	TTT	GGA	GGC	ATT	CCT	TTC	ATT	531
Trp	Ala	Ala	Ala	Val	Ile	Thr	Asn	Leu	Phe	Gly	Gly	Ile	Pro	Phe	Ile	
	155					160					165					
GGG	GCT	GAT	GTG	GTG	GAG	TGG	ATT	AGA	GGC	AAT	TAT	GTT	GTG	GCG	GAT	579
Gly	Ala	Asp	Val	Val	Glu	Trp	Ile	Arg	Gly	Asn	Tyr	Val	Val	Ala	Asp	
170					175					180					185	
TCC	ACT	TTA	ACG	CGC	TTT	TTC	ATG	CTC	CAT	GTG	TTT	TTA	CTG	CCC	ATT	627
Ser	Thr	Leu	Thr	Arg	Phe	Phe	Met	Leu	His	Val	Phe	Leu	Leu	Pro	Ile	
				190					195					200		
GCG	ATC	ATT	CTA	CTT	GTT	GGG	GTG	CAT	TTT	TAT	TCT	TTA	CGC	ATC	CCG	675
Ala	Ile	Ile	Leu	Leu	Val	Gly	Val	His	Phe	Tyr	Ser	Leu	Arg	Ile	Pro	
			205					210					215			
CAT	GTC	AAT	AAC	CAA	GAA	GGC	GAA	GAG	ATT	GAC	TTT	GAA	TTA	GAA	GAG	723
His	Val	Asn	Asn	Gln	Glu	Gly	Glu	Glu	Ile	Asp	Phe	Glu	Leu	Glu	Glu	
		220					225					230				
AAG	AAA	TTC	ATT	GAA	GGC	AAG	AAA	AAA	GAA	TCC	AAA	GTC	ATT	CCT	TTT	771
Lys	Lys	Phe	Ile	Glu	Gly	Lys	Lys	Lys	Glu	Ser	Lys	Val	Ile	Pro	Phe	
	235					240					245					
TGG	CCG	GTG	TTC	TTG	TCT	AAA	GAT	ATT	TTT	GTG	GTT	TGC	GCG	TTC	ATG	819
Trp	Pro	Val	Phe	Leu	Ser	Lys	Asp	Ile	Phe	Val	Val	Cys	Ala	Phe	Met	
250					255					260					265	
GTC	TTT	TTC	TTT	TAC	TTG	GTG	TGT	TAC	CAC	TAT	GAT	TTT	GCG	ATG	GAT	867
Val	Phe	Phe	Phe	Tyr	Leu	Val	Cys	Tyr	His	Tyr	Asp	Phe	Ala	Met	Asp	
				270					275					280		
CCT	ATC	AAC	TTT	GAA	AGG	GCT	AAC	AGC	CTT							

Ile Ser Ser Gln Glu Leu Val Val Glu Arg Lys Gly Ile Leu Ile Gly
100 105 110
Glu Thr Arg Pro Lys Asn Ile Gln Gly Gly Ala Leu Leu Ile Asn Glu
115 120 125
Gln Glu Lys Lys Ile Glu Asn Lys
130 135

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...348
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

TAAGGAGTTT	CT	ATG	GAT	TGG	GGT	CGG	GTC	GTT	CAT	GTG	CTG	TTC	AGC	CTT	51
	Met	Asp	Trp	Gly	Arg	Val	Val	His	Val	Leu	Phe	Ser	Leu		
	1				5					10					
ATT TCT TTA ACC ACC ATT GCA GGG TTT TTG TAT GAG CCT AAT ACG GTG	99														
Ile Ser Leu Thr Thr Ile Ala Gly Phe Leu Tyr Glu Pro Asn Thr Val															
15 20 25															
GTG TTG TTT GTA GCG TTA GCT TTA AAC CTT ATT TCT GTT ACG CTT AAA	147														
Val Leu Phe Val Ala Leu Ala Leu Asn Leu Ile Ser Val Thr Leu Lys															
30 35 40 45															
ATT GGG GTG ATC AAG CGT TTC GCT TCA GAG CTA TTG GCC AGC TCT TTA	195														
Ile Gly Val Ile Lys Arg Phe Ala Ser Glu Leu Leu Ala Ser Ser Leu															
50 55 60															
GCC ACC GTA TTG CAT CTC ATA CCG GCA TTT GTG TTT TTA CAG ATT TTA	243														
Ala Thr Val Leu His Leu Ile Pro Ala Phe Val Phe Leu Gln Ile Leu															
65 70 75															
AAT AAT TTG GTT ACC GCT TAC ATG CTC ATG ATC GGG GCG TTG ATT AGC	291														
Asn Asn Leu Val Thr Ala Tyr Met Leu Met Ile Gly Ala Leu Ile Ser															
80 85 90															
AAC GCT TTC AGT CTC ATC TTT TTG TTG ATT GAA AGC GTT GTA ACG AGC	339														
Asn Ala Phe Ser Leu Ile Phe Leu Leu Ile Glu Ser Val Val Thr Ser															
95 100 105															
GAA ACG GAT TAAGGGGTAG TGATGGATTT TATCAATATA GAAAAAAAT GGC	391														
Glu Thr Asp															
110															

[illegible]

- (A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Met	Asp	Trp	Gly	Arg	Val	Val	His	Val	Leu	Phe	Ser	Leu	Ile	Ser	Leu
1				5					10					15	
Thr	Thr	Ile	Ala	Gly	Phe	Leu	Tyr	Glu	Pro	Asn	Thr	Val	Val	Leu	Phe
			20					25					30		
Val	Ala	Leu	Ala	Leu	Asn	Leu	Ile	Ser	Val	Thr	Leu	Lys	Ile	Gly	Val
		35					40					45			
Ile	Lys	Arg	Phe	Ala	Ser	Glu	Leu	Leu	Ala	Ser	Ser	Leu	Ala	Thr	Val
	50					55					60				
Leu	His	Leu	Ile	Pro	Ala	Phe	Val	Phe	Leu	Gln	Ile	Leu	Asn	Asn	Leu
65					70					75					80
Val	Thr	Ala	Tyr	Met	Leu	Met	Ile	Gly	Ala	Leu	Ile	Ser	Asn	Ala	Phe
				85					90					95	
Ser	Leu	Ile	Phe	Leu	Leu	Ile	Glu	Ser	Val	Val	Thr	Ser	Glu	Thr	Asp
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 25...993
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GAATAAAAAGA	GCTTAGGAGG	TTTT	ATG	GAA	TTA	TTC	AAA	CGA	ACT	AGA	ATC		51			
			Met	Glu	Leu	Phe	Lys	Arg	Thr	Arg	Ile					
			1				5									
TTA	AGC	TTC	ATG	CGT	TAT	TCC	AAT	TAT	GGG	GTG	ATC	GTT	TCA	GCA	ATT	99
Leu	Ser	Phe	Met	Arg	Tyr	Ser	Asn	Tyr	Gly	Val	Ile	Val	Ser	Ala	Ile	
10					15					20					25	
TTA	GCG	CTT	CTA	GCG	TTG	GGG	CTT	TTG	TTT	TTC	AAA	GGG	TTT	TCT	TTA	147
Leu	Ala	Leu	Leu	Ala	Leu	Gly	Leu	Leu	Phe	Phe	Lys	Gly	Phe	Ser	Leu	
				30					35				40			
GGG	ATT	GAT	TTT	GCG	GGG	GGG	AGT	TTG	GTG	CAA	GTG	CGC	TAC	ACT	CAA	195

ATC GCC CCT AAA GTG GCG TTA TTG TTA GGC TTT GAT ATG GAT AAA TAT 915
 Ile Ala Pro Lys Val Ala Leu Leu Leu Gly Phe Asp Met Asp Lys Tyr
 285 290 295

TAT GAG AAT GAG ACT AGA AAA ATT AAA AAA GCT CAA GAG AAA GAA AAA 963
 Tyr Glu Asn Glu Thr Arg Lys Ile Lys Lys Ala Gln Glu Lys Glu Lys
 300 305 310

ATG CGC CGT TTG TAT GAG AGC GGT CAA GTT TAAGGAGTTT CTATGGATTG GGG 1016
 Met Arg Arg Leu Tyr Glu Ser Gly Gln Val
 315 320

TCGGGTCGTT CATGTGCTG 1035

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met	Glu	Leu	Phe	Lys	Arg	Thr	Arg	Ile	Leu	Ser	Phe	Met	Arg	Tyr	Ser	1	5	10	15
Asn	Tyr	Gly	Val	Ile	Val	Ser	Ala	Ile	Leu	Ala	Leu	Leu	Ala	Leu	Gly	20	25	30	
Leu	Leu	Phe	Phe	Lys	Gly	Phe	Ser	Leu	Gly	Ile	Asp	Phe	Ala	Gly	Gly	35	40	45	
Ser	Leu	Val	Gln	Val	Arg	Tyr	Thr	Gln	Asn	Ala	Pro	Ile	Lys	Glu	Val	50	55	60	
Arg	Asp	Leu	Phe	Glu	Lys	Glu	Ala	Arg	Phe	Lys	Gly	Val	Gln	Val	Ser	65	70	75	80
Glu	Phe	Gly	Ser	Lys	Glu	Glu	Ile	Leu	Ile	Lys	Phe	Pro	Phe	Val	Glu	85	90	95	
Thr	Ala	Glu	Asn	Glu	Asp	Leu	Asn	Ala	Ile	Val	Ala	Asn	Ile	Leu	Lys	100	105	110	
Pro	Ser	Gly	Asp	Phe	Glu	Ile	Arg	Lys	Phe	Asp	Thr	Val	Gly	Pro	Arg	115	120	125	
Val	Gly	Ser	Glu	Leu	Lys	Glu	Lys	Gly	Ile	Leu	Ser	Leu	Ile	Leu	Ala	130	135	140	
Leu	Ile	Ala	Ile	Met	Val	Tyr	Val	Ser	Phe	Arg	Tyr	Glu	Trp	Arg	Phe	145	150	155	160
Ala	Leu	Ala	Ser	Val	Ile	Ala	Leu	Val	His	Asp	Val	Ile	Leu	Val	Ala	165	170	175	
Ser	Ser	Val	Ile	Val	Phe	Lys	Ile	Asp	Met	Asn	Leu	Glu	Val	Ile	Ala	180	185	190	
Ala	Leu	Leu	Thr	Leu	Ile	Gly	Tyr	Ser	Ile	Asn	Asp	Thr	Ile	Ile	Ile	195	200	205	
Phe	Asp	Arg	Ile	Arg	Glu	Glu	Met	Xaa	Ser	Gln	Lys	Thr	Lys	Asn	Ala	210	215	220	
Thr	Gln	Ala	Ile	Asp	Glu	Ala	Ile	Ser	Ser	Thr	Leu	Thr	Arg	Thr	Leu	225	230	235	240
Leu	Thr	Ser	Leu	Thr	Val	Phe	Phe	Val	Val	Leu	Ile	Leu	Cys	Val	Phe	245	250	255	

Gly	Ser	Lys	Ile	Ile	Ile	Gly	Phe	Ser	Leu	Pro	Met	Leu	Ile	Gly	Thr
			260					265					270		
Ile	Val	Gly	Thr	Tyr	Ser	Ser	Ile	Phe	Ile	Ala	Pro	Lys	Val	Ala	Leu
		275					280					285			
Leu	Leu	Gly	Phe	Asp	Met	Asp	Lys	Tyr	Tyr	Glu	Asn	Glu	Thr	Arg	Lys
	290					295					300				
Ile	Lys	Lys	Ala	Gln	Glu	Lys	Glu	Lys	Met	Arg	Arg	Leu	Tyr	Glu	Ser
305				310					315						320
Gly	Gln	Val													

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 56...634
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

TAGCTATTTTC	TTTAAAGCCG	CTCTTTTGTC	TAGCGCAAAT	AAATACAAAG	CCCCT	ATG	58
					Met		
					1		
ATC CCA GAA ATC AAA GAT CCG AGT AAA ATC GCA ATT TTT GCC ACT TCC	106						
Ile Pro Glu Ile Lys Asp Pro Ser Lys Ile Ala Ile Phe Ala Thr Ser							
	5		10		15		
ATA GCG TCT TTA TGC TCG CTC GTG AAG GCC AGA TTA GAA ATA AAC ATA	154						
Ile Ala Ser Leu Cys Ser Leu Val Lys Ala Arg Leu Glu Ile Asn Ile							
	20		25		30		
GAC ATG GTA AAG CCA ATC CCT GCT AAA AGC CCA GCC CCT AAA ATA TGC	202						
Asp Met Val Lys Pro Ile Pro Ala Lys Ser Pro Ala Pro Lys Ile Cys							
	35		40		45		
CAC CAG CTG ATG CCT TTA GGG CGT GCG GTG ATT TTA AGC TTT TCG CTT	250						
His Gln Leu Met Pro Leu Gly Arg Ala Val Ile Leu Ser Phe Ser Leu							
	50		55		60		65
ATA AAA GTG ATT AAG AAA ATC CCT AAA GGT TTG CCC AAG CAA AGC CCT	298						
Ile Lys Val Ile Lys Lys Ile Pro Lys Gly Leu Pro Lys Gln Ser Pro							
	70		75		80		
AAA ATA ACC CCT AAA AGC ACC TTA TCC ACT TCT AAA TTG ATG CTA GAA	346						
Lys Ile Thr Pro Lys Ser Thr Leu Ser Thr Ser Lys Leu Met Leu Glu							
	85		90		95		
TCA ACG CTC ACC CCA GCG TTT GCA AAC GCG AAT AAG GGC ATG ATG AAA	394						

		165		170		175
Gly	Ile	Ile	Lys	Ala	Arg	Ile
				Thr	Ala	Ala
					Ile	Val
					Ala	Trp
						Ile
						Pro
		180		185		190
Leu						

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1365
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

AAGACTGCTT	GAAAAATT	ATG	GGT	CTG	AAA	TTA	AAA	ATT	TTA	AGG	TTG	TCT	51
		Met	Gly	Leu	Lys	Leu	Lys	Ile	Leu	Arg	Leu	Ser	
		1				5					10		
ATG	AAT	CTC	AAA	AAA	ACA	GAA	AAC	GCG	CTC	AGT	TTG	ACG	99
Met	Asn	Leu	Lys	Lys	Thr	Glu	Asn	Ala	Leu	Ser	Leu	Thr	
		15				20					25		
TTC	ATT	AAA	AGC	GAG	TCT	TTT	GGA	GGG	ATT	TTC	CTC	TTT	147
Phe	Ile	Lys	Ser	Glu	Ser	Phe	Gly	Gly	Ile	Phe	Leu	Phe	
		30				35					40		
GTT	TTA	GCG	ATG	GTG	GTG	GCT	AAT	TCG	TTT	TTA	AAA	GAA	195
Val	Leu	Ala	Met	Val	Val	Ala	Asn	Ser	Phe	Leu	Lys	Glu	
		45				50					55		
GCA	CTA	TGG	CAC	ACC	CCT	TTT	GGG	TTT	CAA	ATA	GGG	GAT	243
Ala	Leu	Trp	His	Thr	Pro	Phe	Gly	Phe	Gln	Ile	Gly	Asp	
		60			65				70				75
GGC	TTT	AGT	TTG	CAC	AAC	TGG	ATT	GAT	GAT	GTC	TTA	ATG	291
Gly	Phe	Ser	Leu	His	Asn	Trp	Ile	Asp	Asp	Val	Leu	Met	
				80				85				90	
TTT	TTA	ATG	ATA	GGC	TTA	GAA	ATC	AAA	CGA	GAA	TTG	TTG	339
Phe	Leu	Met	Ile	Gly	Leu	Glu	Ile	Lys	Arg	Glu	Leu	Leu	
		95						100				105	
TTA	TCC	AGT	TTC	AAA	AAA	GCT	TCT	TTT	CCT	GTG	ATT	GCG	387
Leu	Ser	Ser	Phe	Lys	Lys	Ala	Ser	Phe	Pro	Val	Ile	Ala	
		110				115						120	
GGC	ATG	ATA	GCC	CCA	GGA	TTG	ATT	TAT	TTT	TTT	CTT	AAC	435
Gly	Met	Ile	Ala	Pro	Gly	Leu	Ile	Tyr	Phe	Phe	Leu	Asn	
												Ala	Asn
												Thr	

125				130				135								
CCT Pro 140	TCC Ser	CAG Gln	CAT His	GGT Gly	TTT Phe 145	GGG Gly	ATC Ile	CCT Pro	ATG Met	GCG Ala 150	ACG Thr	GAT Asp	ATT Ile	GCG Ala	TTC Phe 155	483
GCT Ala	TTA Leu	GGC Gly	GTG Val	ATC Ile 160	ATG Met	CTT Leu	TTA Leu	GGC Gly	AAG Lys 165	AGG Arg	GTG Val	CCA Pro	ACC Thr	GCT Ala 170	TTA Leu	531
AAG Lys	GTT Val	TTT Phe 175	TTA Leu	ATC Ile	ACT Thr	CTA Leu	GCG Ala 180	GTG Val	GCT Ala	GAT Asp	GAC Asp	TTG Leu	GGG Gly 185	GCT Ala	ATT Ile	579
GTG Val	GTG Val	ATC Ile 190	GCG Ala	CTC Leu	TTT Phe	TAT Tyr	ACC Thr 195	ACG Thr	AAT Asn	TTA Leu	AAA Lys	TTC Phe 200	GCA Ala	TGG Trp	CTT Leu	627
TTA Leu	GGG Gly 205	GCT Ala	TTA Leu	GGG Gly	GTG Val 210	GTT Val	CTT Leu	GTT Val	TTA Leu	GCC Ala 215	GTA Val 215	TTA Leu	AAC Asn	CGC Arg	CTG Leu	675
AAT Asn 220	ATG Met	CGC Arg	TCG Ser	CTC Leu	ATC Ile 225	CCT Pro	TAC Tyr	TTG Leu	CTT Leu	TTA Leu 230	GGG Gly	GTG Val	TTG Leu	CTT Leu	TGG Trp 235	723
TTT Phe	TGC Cys	GTG Val	CAT His 240	CAA Gln	AGC Ser	GGT Gly	ATC Ile	CAT His 245	GCG Ala	ACG Thr	ATT Ile	GCT Ala	GCA Ala	GTG Val 250	ATT Ile	771
CTA Leu	GCT Ala	TTT Phe 255	ATG Met	ATA Ile	CCG Pro	GTG Val	AAG Lys 260	ATC Ile	CCT Pro	AAA Lys	GAT Asp	TCT Ser	AAA Lys 265	AAT Asn	GTA Val	819
GAG Glu	CTT Leu	TTG Leu 270	GAA Glu	CTA Leu	GGC Gly	AAA Lys 275	CGA Arg	TAC Tyr	GCA Ala	GAA Glu	ACG Thr	AGT Ser 280	TCA Ser	GGA Gly	GCG Ala	867
CTT Leu	TTG Leu 285	AGT Ser	AAA Lys	GAG Glu	CAG Gln	CAA Gln 290	GAA Glu	ATC Ile	TTG Leu	CAT His	TCT Ser 295	ATT Ile	GAA Glu	GAA Glu	AAA Lys	915
GCG Ala 300	AGC Ser	GCC Ala	TTA Leu	CAA Gln	AGC Ser 305	CCC Pro	TTA Leu	GAA Glu	AGA Arg	TTG Leu 310	GAG Glu	CAT His	TTT Phe	CTA Leu	GCC Ala 315	963
CCC Pro	ATT Ile	AGC Ser	GGG Gly	TAT Tyr 320	TTC Phe	ATC Ile	ATG Met	CCC Pro	TTA Leu 325	TTC Phe	GCG Ala	TTT Phe	GCA Ala	AAC Asn 330	GCT Ala	1011
GGG Gly	GTG Val	AGC Ser 335	GTT Val	GAT Asp	TCT Ser	AGC Ser	ATC Ile	AAT Asn 340	TTA Leu	GAA Glu	GTG Val	GAT Asp	AAG Lys 345	GTG Val	CTT Leu	1059
TTA Leu	GGG Gly 350	GTT Val	ATT Ile	TTA Leu	GGG Gly	CTT Leu 355	TGC Cys	TTG Leu 355	GGC Gly	AAA Lys	CCT Pro 360	TTA Leu 360	GGG Gly	ATT Ile	TTC Phe	1107

TTA ATC ACT TTT ATA AGC GAA AAG CTT AAA ATC ACC GCA CGC CCT AAA 1155
 Leu Ile Thr Phe Ile Ser Glu Lys Leu Lys Ile Thr Ala Arg Pro Lys
 365 370 375

GGC ATC AGC TGG TGG CAT ATT TTA GGG GCT GGG CTT TTA GCA GGG ATT 1203
 Gly Ile Ser Trp Trp His Ile Leu Gly Ala Gly Leu Leu Ala Gly Ile
 380 385 390 395

GGC TTT ACC ATG TCT ATG TTT ATT TCT AAT CTG GCC TTC ACG AGC GAG 1251
 Gly Phe Thr Met Ser Met Phe Ile Ser Asn Leu Ala Phe Thr Ser Glu
 400 405 410

CAT AAA GAC GCT ATG GAA GTG GCA AAA ATT GCG ATT TTA CTC GGA TCT 1299
 His Lys Asp Ala Met Glu Val Ala Lys Ile Ala Ile Leu Leu Gly Ser
 415 420 425

TTG ATT TCT GGG ATC ATA GGG GCT TTG TAT TTA TTT GCG CTA GAC AAA 1347
 Leu Ile Ser Gly Ile Ile Gly Ala Leu Tyr Leu Phe Ala Leu Asp Lys
 430 435 440

AGA GCG GCT TTA AAG AAA TAGCTAAAAA TGCTATAATT TGAGATTAAA ACATCTTT 1403
 Arg Ala Ala Leu Lys Lys
 445

TAAGGAAATT AAATGGGACA AATT 1427

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Met Gly Leu Lys Leu Lys Ile Leu Arg Leu Ser Met Asn Leu Lys Lys
 1 5 10 15
 Thr Glu Asn Ala Leu Ser Leu Thr Leu Lys Asn Phe Ile Lys Ser Glu
 20 25 30
 Ser Phe Gly Gly Ile Phe Leu Phe Leu Asn Ala Val Leu Ala Met Val
 35 40 45
 Val Ala Asn Ser Phe Leu Lys Glu Ser Tyr Phe Ala Leu Trp His Thr
 50 55 60
 Pro Phe Gly Phe Gln Ile Gly Asp Phe Phe Ile Gly Phe Ser Leu His
 65 70 75 80
 Asn Trp Ile Asp Asp Val Leu Met Ala Leu Phe Phe Leu Met Ile Gly
 85 90 95
 Leu Glu Ile Lys Arg Glu Leu Leu Phe Gly Glu Leu Ser Ser Phe Lys
 100 105 110
 Lys Ala Ser Phe Pro Val Ile Ala Ala Ile Gly Gly Met Ile Ala Pro
 115 120 125
 Gly Leu Ile Tyr Phe Phe Leu Asn Ala Asn Thr Pro Ser Gln His Gly
 130 135 140
 Phe Gly Ile Pro Met Ala Thr Asp Ile Ala Phe Ala Leu Gly Val Ile
 145 150 155 160

Met	Leu	Leu	Gly	Lys	Arg	Val	Pro	Thr	Ala	Leu	Lys	Val	Phe	Leu	Ile
				165					170					175	
Thr	Leu	Ala	Val	Ala	Asp	Asp	Leu	Gly	Ala	Ile	Val	Val	Ile	Ala	Leu
			180					185					190		
Phe	Tyr	Thr	Thr	Asn	Leu	Lys	Phe	Ala	Trp	Leu	Leu	Gly	Ala	Leu	Gly
		195				200						205			
Val	Val	Leu	Val	Leu	Ala	Val	Leu	Asn	Arg	Leu	Asn	Met	Arg	Ser	Leu
	210					215					220				
Ile	Pro	Tyr	Leu	Leu	Leu	Gly	Val	Leu	Leu	Trp	Phe	Cys	Val	His	Gln
225					230					235					240
Ser	Gly	Ile	His	Ala	Thr	Ile	Ala	Ala	Val	Ile	Leu	Ala	Phe	Met	Ile
				245					250					255	
Pro	Val	Lys	Ile	Pro	Lys	Asp	Ser	Lys	Asn	Val	Glu	Leu	Leu	Glu	Leu
			260					265						270	
Gly	Lys	Arg	Tyr	Ala	Glu	Thr	Ser	Ser	Gly	Ala	Leu	Leu	Ser	Lys	Glu
		275					280						285		
Gln	Gln	Glu	Ile	Leu	His	Ser	Ile	Glu	Glu	Lys	Ala	Ser	Ala	Leu	Gln
	290					295					300				
Ser	Pro	Leu	Glu	Arg	Leu	Glu	His	Phe	Leu	Ala	Pro	Ile	Ser	Gly	Tyr
305					310					315					320
Phe	Ile	Met	Pro	Leu	Phe	Ala	Phe	Ala	Asn	Ala	Gly	Val	Ser	Val	Asp
				325					330					335	
Ser	Ser	Ile	Asn	Leu	Glu	Val	Asp	Lys	Val	Leu	Leu	Gly	Val	Ile	Leu
			340					345					350		
Gly	Leu	Cys	Leu	Gly	Lys	Pro	Leu	Gly	Ile	Phe	Leu	Ile	Thr	Phe	Ile
		355					360					365			
Ser	Glu	Lys	Leu	Lys	Ile	Thr	Ala	Arg	Pro	Lys	Gly	Ile	Ser	Trp	Trp
	370					375					380				
His	Ile	Leu	Gly	Ala	Gly	Leu	Leu	Ala	Gly	Ile	Gly	Phe	Thr	Met	Ser
385					390					395					400
Met	Phe	Ile	Ser	Asn	Leu	Ala	Phe	Thr	Ser	Glu	His	Lys	Asp	Ala	Met
				405					410					415	
Glu	Val	Ala	Lys	Ile	Ala	Ile	Leu	Leu	Gly	Ser	Leu	Ile	Ser	Gly	Ile
			420					425					430		
Ile	Gly	Ala	Leu	Tyr	Leu	Phe	Ala	Leu	Asp	Lys	Arg	Ala	Ala	Leu	Lys
		435					440					445			
Lys															

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...1857
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

AAGTAAGTGC TT ATG GAT AAT AGG AAT ATT GAT CCT TAC TTC AAC CCA GAG 51

Met Asp Asn Arg Asn Ile Asp Pro Tyr Phe Asn Pro Glu																
		1				5				10						
CAA	TTT	TTA	GAA	ACC	CAA	AAA	TAC	AAA	GGC	ACG	GTT	ACA	GCA	TTA	ATC	99
Gln	Phe	Leu	Glu	Thr	Gln	Lys	Tyr	Lys	Gly	Thr	Val	Thr	Ala	Leu	Ile	
15						20				25						
TTT	TTA	TTG	CTT	TTT	TTT	ATT	TTT	TTA	ATG	GTG	GCT	TTT	AAA	AAA	GCT	147
Phe	Leu	Leu	Leu	Phe	Phe	Ile	Phe	Leu	Met	Val	Ala	Phe	Lys	Lys	Ala	
30						35				40				45		
TTT	TTT	GCC	CAA	GCC	AAC	ATG	CCT	AAT	CTA	GTG	ATG	AGC	AAA	CAA	GAC	195
Phe	Phe	Ala	Gln	Ala	Asn	Met	Pro	Asn	Leu	Val	Met	Ser	Lys	Gln	Asp	
				50				55						60		
ACT	GCG	GCT	AGG	GGG	ACT	ATC	TAT	AGT	CAA	GAC	AAC	TAC	AGC	CTA	GCC	243
Thr	Ala	Ala	Arg	Gly	Thr	Ile	Tyr	Ser	Gln	Asp	Asn	Tyr	Ser	Leu	Ala	
				65				70						75		
ACT	TCA	CAA	ACC	CTT	TTC	AAA	CTG	GGC	TTT	GAT	ACA	AGG	TTT	TTA	AAC	291
Thr	Ser	Gln	Thr	Leu	Phe	Lys	Leu	Gly	Phe	Asp	Thr	Arg	Phe	Leu	Asn	
		80				85						90				
CCG	GAT	AAA	GAA	GAT	TTT	TTC	ATT	GAT	TTC	CTT	TCT	ATT	TAT	AGC	AAT	339
Pro	Asp	Lys	Glu	Asp	Phe	Phe	Ile	Asp	Phe	Leu	Ser	Ile	Tyr	Ser	Asn	
95						100				105						
ATC	CCT	AAA	AAG	TCC	TTA	AAA	GAC	GCC	ATC	AAT	ACA	AAA	GGC	TAT	ATC	387
Ile	Pro	Lys	Lys	Ser	Leu	Lys	Asp	Ala	Ile	Asn	Thr	Lys	Gly	Tyr	Ile	
110				115				120						125		
ATT	CTA	GCC	TAT	GAT	CTC	ACG	CCC	AAT	ATG	GCT	GCT	AAT	ATT	AGA	GAC	435
Ile	Leu	Ala	Tyr	Asp	Leu	Thr	Pro	Asn	Met	Ala	Ala	Asn	Ile	Arg	Asp	
				130				135						140		
TTA	AAT	AAG	AAA	TTT	TTA	GCC	TTT	GGG	GTT	TTT	CAA	AAT	TTC	AAA	GAC	483
Leu	Asn	Lys	Lys	Phe	Leu	Ala	Phe	Gly	Val	Phe	Gln	Asn	Phe	Lys	Asp	
		145				150				155						
GCG	CAC	GAT	AAG	GTG	TGG	CAA	AAG	CAA	GGG	CTA	AAC	ATT	GAA	GTG	AGC	531
Ala	His	Asp	Lys	Val	Trp	Gln	Lys	Gln	Gly	Leu	Asn	Ile	Glu	Val	Ser	
		160				165				170						
GGC	GTT	TCT	AGG	CAT	TAC	CCT	TAT	CAA	AAT	AGC	CTA	GAG	CCA	ATC	ATT	579
Gly	Val	Ser	Arg	His	Tyr	Pro	Tyr	Gln	Asn	Ser	Leu	Glu	Pro	Ile	Ile	
175						180				185						
GGC	TAT	GTG	CAA	AAA	CAA	GAA	GAA	GAC	AAG	CTC	ACT	TTA	ACT	ACC	GGT	627
Gly	Tyr	Val	Gln	Lys	Gln	Glu	Glu	Asp	Lys	Leu	Thr	Leu	Thr	Thr	Gly	
190				195				200						205		
AAA	AAA	GGC	GTT	GAA	AAA	TCT	CAA	GAT	CAC	TTG	CTT	AAA	GCC	CAA	CAA	675
Lys	Lys	Gly	Val	Glu	Lys	Ser	Gln	Asp	His	Leu	Leu	Lys	Ala	Gln	Gln	
				210				215						220		
AAT	GGC	ATA	AGA	ACA	GGC	AAA	AGA	GAC	GTG	AGT	TTT	AAC	TTT	ATC	CAA	723
Asn	Gly	Ile	Arg	Thr	Gly	Lys	Arg	Asp	Val	Ser	Phe	Asn	Phe	Ile	Gln	
		225				230				235						

AAC Asn	CAC His	TCT Ser 240	TAT Tyr	ACA Thr	GAG Glu	GTT Val	GAA Glu 245	CGC Arg	CTT Leu	GAT Asp	GGC Gly	TAT Tyr 250	GAG Glu	GTG Val	TAT Tyr	771
TTG Leu	AGC Ser 255	GTT Val	CCT Pro	TTA Leu	AAA Lys	CTC Leu 260	CAA Gln	AGA Arg	GAA Glu	ATT Ile	GAA Glu 265	ACC Thr	CTA Leu	TTG Leu	GAT Asp	819
AAA Lys 270	ACT Thr	AAA Lys	GAC Asp	AAA Lys	CTC Leu 275	AAG Lys	GCT Ala	AAA Lys	GAA Glu	ATC Ile 280	CTA Leu	GTG Val	GGT Gly	ATC Ile	ATT Ile 285	867
AAC Asn	CCT Pro	AAA Lys	AGC Ser	GGG Gly 290	GAA Glu	ATT Ile	TTA Leu	TCG Ser	CTA Leu 295	GCT Ala	TCA Ser	AGC Ser	AAG Lys	CGC Arg 300	TTC Phe	915
AAT Asn	CCT Pro	AAT Asn	GCG Ala 305	ATT Ile	AAA Lys	ACC Thr	AGC Ser	GAT Asp 310	TAT Tyr	GAA Glu	AGC Ser	TTG Leu 315	AAT Asn	TTG Leu	AGC Ser	963
GTT Val	GCT Ala 320	GAA Glu	AAG Lys	GTT Val	TTT Phe	GAG Glu	CCA Pro 325	GGC Gly	AGC Ser	ACG Thr	ATC Ile 330	AAA Lys	CCC Pro	ATT Ile	GTT Val	1011
TAT Tyr	TCC Ser 335	TTG Leu	CTG Leu	TTA Leu	GAC Asp	AAG Lys 340	AAT Asn	TTG Leu	ATC Ile	AAC Asn	CCC Pro 345	AAA Lys	GAA Glu	CGC Arg	ATT Ile	1059
GAT Asp 350	TTA Leu	AAC Asn	CAT His	GGC Gly	TAT Tyr 355	TAC Tyr	CAA Gln	TTA Leu	GGA Gly	AAA Lys 360	TAC Tyr	ACC Thr	ATT Ile	AAA Lys	GAC Asp 365	1107
GAC Asp	TTT Phe	ATC Ile	CCC Pro	AGT Ser 370	AAA Lys	AAA Lys	GCC Ala	GTT Val	GTG Val 375	GAA Glu	GAC Asp	ATT Ile	TTG Leu	ATC Ile 380	CAA Gln	1155
TCT Ser	AGC Ser	AAT Asn 385	GTG Val	GGC Gly	ATG Met	ATA Ile	AAA Lys	ATC Ile 390	AGT Ser	AAA Lys	AAC Asn	TTA Leu 395	AAC Asn	CCA Pro	AAG Lys	1203
GAT Asp	TTC Phe	TAT Tyr 400	AAT Asn	GGG Gly	CTT Leu	TTA Leu	GGC Gly 405	TAT Tyr	GGA Gly	TTT Phe	TCT Ser	CAA Gln 410	AAA Lys	ACC Thr	GGC Gly	1251
ATT Ile	GAT Asp 415	TTA Leu	TCT Ser	CTA Leu	GAA Glu	GCC Ala 420	ACA Thr	GGA Gly	AAG Lys	ATC Ile	CCT Pro 425	CCT Pro	TTG Leu	TCC Ser	GCT Ala	1299
TTC Phe 430	AAG Lys	CGT Arg	GAA Glu	GTG Val	TTA Leu 435	AAG Lys	GGG Gly	AGC Ser	GTT Val	TCT Ser 440	TAT Tyr	GGC Gly	TAT Tyr	GGG Gly	CTG Leu 445	1347
AAC Asn	GCG Ala	ACT Thr	TTT Phe	TTG Leu 450	CAG Gln	CTT Leu	TTA Leu	AGG Arg	GCT Ala 455	TAT Tyr	GCG Ala	GTG Val	TTT Phe	TCT Ser 460	AAT Asn	1395
GAA Glu	GGC Gly	AAA Lys	TTG Leu	ACT Thr	ACC Thr	CCC Pro	TAT Tyr	TTA Leu	GTG Val	CAA Gln	CGA Arg	GAA Glu	ACC Thr	GCC Ala	CCT Pro	1443

Gln	Ala	Asn	Met	Pro	Asn	Leu	Val	Met	Ser	Lys	Gln	Asp	Thr	Ala	Ala
50						55					60				
Arg	Gly	Thr	Ile	Tyr	Ser	Gln	Asp	Asn	Tyr	Ser	Leu	Ala	Thr	Ser	Gln
65					70					75					80
Thr	Leu	Phe	Lys	Leu	Gly	Phe	Asp	Thr	Arg	Phe	Leu	Asn	Pro	Asp	Lys
				85					90					95	
Glu	Asp	Phe	Phe	Ile	Asp	Phe	Leu	Ser	Ile	Tyr	Ser	Asn	Ile	Pro	Lys
			100					105					110		
Lys	Ser	Leu	Lys	Asp	Ala	Ile	Asn	Thr	Lys	Gly	Tyr	Ile	Ile	Leu	Ala
		115						120				125			
Tyr	Asp	Leu	Thr	Pro	Asn	Met	Ala	Ala	Asn	Ile	Arg	Asp	Leu	Asn	Lys
		130				135					140				
Lys	Phe	Leu	Ala	Phe	Gly	Val	Phe	Gln	Asn	Phe	Lys	Asp	Ala	His	Asp
145					150					155					160
Lys	Val	Trp	Gln	Lys	Gln	Gly	Leu	Asn	Ile	Glu	Val	Ser	Gly	Val	Ser
				165						170				175	
Arg	His	Tyr	Pro	Tyr	Gln	Asn	Ser	Leu	Glu	Pro	Ile	Ile	Gly	Tyr	Val
			180					185					190		
Gln	Lys	Gln	Glu	Glu	Asp	Lys	Leu	Thr	Leu	Thr	Thr	Gly	Lys	Lys	Gly
		195					200					205			
Val	Glu	Lys	Ser	Gln	Asp	His	Leu	Leu	Lys	Ala	Gln	Gln	Asn	Gly	Ile
		210				215					220				
Arg	Thr	Gly	Lys	Arg	Asp	Val	Ser	Phe	Asn	Phe	Ile	Gln	Asn	His	Ser
225					230				235						240
Tyr	Thr	Glu	Val	Glu	Arg	Leu	Asp	Gly	Tyr	Glu	Val	Tyr	Leu	Ser	Val
				245					250					255	
Pro	Leu	Lys	Leu	Gln	Arg	Glu	Ile	Glu	Thr	Leu	Leu	Asp	Lys	Thr	Lys
			260					265					270		
Asp	Lys	Leu	Lys	Ala	Lys	Glu	Ile	Leu	Val	Gly	Ile	Ile	Asn	Pro	Lys
		275					280					285			
Ser	Gly	Glu	Ile	Leu	Ser	Leu	Ala	Ser	Ser	Lys	Arg	Phe	Asn	Pro	Asn
		290				295					300				
Ala	Ile	Lys	Thr	Ser	Asp	Tyr	Glu	Ser	Leu	Asn	Leu	Ser	Val	Ala	Glu
305					310					315					320
Lys	Val	Phe	Glu	Pro	Gly	Ser	Thr	Ile	Lys	Pro	Ile	Val	Tyr	Ser	Leu
				325					330					335	
Leu	Leu	Asp	Lys	Asn	Leu	Ile	Asn	Pro	Lys	Glu	Arg	Ile	Asp	Leu	Asn
			340					345					350		
His	Gly	Tyr	Tyr	Gln	Leu	Gly	Lys	Tyr	Thr	Ile	Lys	Asp	Asp	Phe	Ile
		355					360					365			
Pro	Ser	Lys	Lys	Ala	Val	Val	Glu	Asp	Ile	Leu	Ile	Gln	Ser	Ser	Asn
		370				375					380				
Val	Gly	Met	Ile	Lys	Ile	Ser	Lys	Asn	Leu	Asn	Pro	Lys	Asp	Phe	Tyr
385					390					395					400
Asn	Gly	Leu													

Val	Ile	Tyr	Gly	Leu	Lys	Gly	Ala	Phe	Ser	Asn	Ala	His	Lys	Asp	Gly	
			95					100					105			
GCT	AGA	GTG	GAA	TTT	GCT	AAA	CGC	CCG	TGC	TGT	AAT	TCT	TGG	AGA	GGC	387
Ala	Arg	Val	Glu	Phe	Ala	Lys	Arg	Pro	Cys	Cys	Asn	Ser	Trp	Arg	Gly	
		110					115					120				
ATG	CCA	AGC	GGG	CAT	GCT	GGG	GGG	GTG	TTT	AGC	GCG	GCT	GGG	TTT	GTG	435
Met	Pro	Ser	Gly	His	Ala	Gly	Gly	Val	Phe	Ser	Ala	Ala	Gly	Phe	Val	
	125					130					135					
TAT	TAC	CGC	TAT	GGG	TGG	AAG	CCG	GCT	CTT	CCT	GTG	ATC	GCT	CTT	GCA	483
Tyr	Tyr	Arg	Tyr	Gly	Trp	Lys	Pro	Ala	Leu	Pro	Val	Ile	Ala	Leu	Ala	
140					145					150					155	
ATC	CTC	ACT	GAC	GCT	AGC	AGA	GTG	GTG	GCA	AGA	CAA	CAC	ACG	ATC	TTG	531
Ile	Leu	Thr	Asp	Ala	Ser	Arg	Val	Val	Ala	Arg	Gln	His	Thr	Ile	Leu	
				160					165					170		
CAA	GTT	ACG	ATC	GGC	AGC	CTT	ATC	GCA	TGG	GGG	TTT	GCT	TAT	TTA	TTC	579
Gln	Val	Thr	Ile	Gly	Ser	Leu	Ile	Ala	Trp	Gly	Phe	Ala	Tyr	Leu	Phe	
			175					180					185			
ACT	TCA	CGC	TAC	AAA	CCC	AAG	CAA	TGG	ATG	CTC	TAT	CCT	GAA	ATT	TCT	627
Thr	Ser	Arg	Tyr	Lys	Pro	Lys	Gln	Trp	Met	Leu	Tyr	Pro	Glu	Ile	Ser	
		190					195					200				
AGC	GAT	TTT	AAG	GGC	AGT	AGC	CGC	TAT	GGG	GTG	AGC	TTT	TCT	TAT	CAA	675
Ser	Asp	Phe	Lys	Gly	Ser	Ser	Arg	Tyr	Gly	Val	Ser	Phe	Ser	Tyr	Gln	
	205					210					215					
TGG	TAAAGGGATA	AAGTGCTAAA	AAAATTATTA	TTCATTGCAC	T											719
Trp																
220																

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

Met	Leu	Phe	Asn	Gly	Leu	Cys	Leu	Phe	Glu	Gln	Ala	Ser	Leu	Cys	Phe
1				5					10					15	
Arg	Lys	Ala	Ser	Val	Ser	Met	Lys	Lys	Leu	Lys	Gly	Leu	Phe	Leu	Ile
			20					25					30		
Leu	Leu	Leu	Trp	Val	Tyr	Pro	Leu	Arg	Ser	Glu	Pro	Ile	Asn	Glu	Gly
		35					40					45			
Ala	Tyr	Ile	Leu	Glu	Glu	Ile	Gly	Asp	Val	Leu	Arg	Phe	Leu	Pro	Ile
	50					55				60					
Phe	Val	Gly	Thr	Val	Ser	Leu	Ala	Met	Arg	Asp	Tyr	Arg	Gly	Leu	Gly
65					70				75					80	

Glu	Leu	Ala	Val	Gly	Thr	Leu	Val	Thr	Gln	Gly	Val	Ile	Tyr	Gly	Leu
				85					90					95	
Lys	Gly	Ala	Phe	Ser	Asn	Ala	His	Lys	Asp	Gly	Ala	Arg	Val	Glu	Phe
			100					105					110		
Ala	Lys	Arg	Pro	Cys	Cys	Asn	Ser	Trp	Arg	Gly	Met	Pro	Ser	Gly	His
		115					120					125			
Ala	Gly	Gly	Val	Phe	Ser	Ala	Ala	Gly	Phe	Val	Tyr	Tyr	Arg	Tyr	Gly
	130					135					140				
Trp	Lys	Pro	Ala	Leu	Pro	Val	Ile	Ala	Leu	Ala	Ile	Leu	Thr	Asp	Ala
145					150					155					160
Ser	Arg	Val	Val	Ala	Arg	Gln	His	Thr	Ile	Leu	Gln	Val	Thr	Ile	Gly
				165				170						175	
Ser	Leu	Ile	Ala	Trp	Gly	Phe	Ala	Tyr	Leu	Phe	Thr	Ser	Arg	Tyr	Lys
			180					185					190		
Pro	Lys	Gln	Trp	Met	Leu	Tyr	Pro	Glu	Ile	Ser	Ser	Asp	Phe	Lys	Gly
		195					200					205			
Ser	Ser	Arg	Tyr	Gly	Val	Ser	Phe	Ser	Tyr	Gln	Trp				
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1087 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1053
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

TTCAAGCAAA AACACCA	CCCC	AAATATAAAG	ATA	ATG	ATT	TTA	AGC	ATT	GAA	AGT	54
			Met	Ile	Leu	Ser	Ile	Glu	Ser		
			1				5				
TCT TGC GAT GAC AGC TCT TTA GCC CTT ACA AGA ATA GAG GAC GCT CAA	102										
Ser Cys Asp Asp Ser Ser Leu Ala Leu Thr Arg Ile Glu Asp Ala Gln											
	10 15 20										
CTC ATC GCT CAT TTT AAA ATC TCT CAA GAA AAG CAC CAT AGT TCT TAT	150										
Leu Ile Ala His Phe Lys Ile Ser Gln Glu Lys His His Ser Ser Tyr											
	25 30 35										
GGG GGC GTT GTG CCT GAG CTT GCA TCA CGT TTG CAT GCT GAG AAT TTG	198										
Gly Gly Val Val Pro Glu Leu Ala Ser Arg Leu His Ala Glu Asn Leu											
	40 45 50 55										
CCG CTT TTA TTA GAA CGC ATT AAA ATA AGC TTG AAT AAG GAT TTT TCC	246										
Pro Leu Leu Leu Glu Arg Ile Lys Ile Ser Leu Asn Lys Asp Phe Ser											
	60 65 70										
AAA ATT AAA GCC ATC GCT ATC ACT AAT CAG CCA GGT TTG AGC GTT ACT	294										

Lys	Ile	Lys	Ala	Ile	Ala	Ile	Thr	Asn	Gln	Pro	Gly	Leu	Ser	Val	Thr		
			75				80						85				
TTA	ATA	GAA	GGT	TTG	ATG	ATG	GCA	AAA	GCC	TTG	AGC	TTG	TCT	TTG	AAT	342	
Leu	Ile	Glu	Gly	Leu	Met	Met	Ala	Lys	Ala	Leu	Ser	Leu	Ser	Leu	Asn		
			90				95						100				
TTG	CCC	TTG	ATT	TTA	GAA	GAT	CAT	TTG	AGA	GGG	CAT	GTG	TAT	TCG	CTC	390	
Leu	Pro	Leu	Ile	Leu	Glu	Asp	His	Leu	Arg	Gly	His	Val	Tyr	Ser	Leu		
			105				110						115				
TTT	ATC	AAT	GAA	AAA	CAA	ACC	TGC	ATG	CCT	TTA	AGC	GTG	CTC	TTA	GTC	438	
Phe	Ile	Asn	Glu	Lys	Gln	Thr	Cys	Met	Pro	Leu	Ser	Val	Leu	Leu	Val		
			120				125						130	135			
TCT	GGG	GGG	CAT	TCT	TTG	ATT	TTA	GAG	GCT	AGA	GAT	TAT	GAG	AAT	ATT	486	
Ser	Gly	Gly	His	Ser	Leu	Ile	Leu	Glu	Ala	Arg	Asp	Tyr	Glu	Asn	Ile		
			140				145						150				
AAA	ATC	GTT	GCC	ACG	AGT	TTA	GAC	GAT	AGC	TTT	GGG	GAG	AGT	TTT	GAT	534	
Lys	Ile	Val	Ala	Thr	Ser	Leu	Asp	Asp	Ser	Phe	Gly	Glu	Ser	Phe	Asp		
			155				160						165				
AAG	GTT	TCC	AAA	ATG	CTT	GAT	TTA	GGC	TAT	CCA	GGA	GGC	CCT	ATA	GTG	582	
Lys	Val	Ser	Lys	Met	Leu	Asp	Leu	Gly	Tyr	Pro	Gly	Gly	Pro	Ile	Val		
			170				175						180				
GAA	AAA	TTA	GCC	CTT	GAT	TAT	AGG	CAC	CCA	AAC	GAG	CCT	TTA	ATG	TTC	630	
Glu	Lys	Leu	Ala	Leu	Asp	Tyr	Arg	His	Pro	Asn	Glu	Pro	Leu	Met	Phe		
			185				190						195				
CCT	ATC	CCT	TTA	AAA	AAC	AGC	CCG	AAT	CTG	GCT	TTT	AGT	TTT	TCA	GGT	678	
Pro	Ile	Pro	Leu	Lys	Asn	Ser	Pro	Asn	Leu	Ala	Phe	Ser	Phe	Ser	Gly		
			200				205						210	215			
TTA	AAA	AAT	GCG	GTG	CGT	TTG	GAG	GTT	GAA	AAA	AAC	GCC	CCC	AAC	TTG	726	
Leu	Lys	Asn	Ala	Val	Arg	Leu	Glu	Val	Glu	Lys	Asn	Ala	Pro	Asn	Leu		
			220				225						230				
AAT	GAA	GCG	ATC	AAA	CAA	AAG	ATT	GGC	TAT	CAT	TTT	CAA	AGT	GCA	GCG	774	
Asn	Glu	Ala	Ile	Lys	Gln	Lys	Ile	Gly	Tyr	His	Phe	Gln	Ser	Ala	Ala		
			235				240						245				
ATT	GAG	CAT	TTA	ATC	CAG	CAG	ACT	AAA	CGC	TAT	TTT	AAA	ATC	AAA	CGC	822	
Ile	Glu	His	Leu	Ile	Gln	Gln	Thr	Lys	Arg	Tyr	Phe	Lys	Ile	Lys	Arg		
			250				255						260				
CCT	AAA	ATT	TTT	GGC	ATT	GTG	GGG	GGA	GCG	AGC	CAA	AAT	TTG	GCT	TTA	870	
Pro	Lys	Ile	Phe	Gly	Ile	Val	Gly	Gly	Ala	Ser	Gln	Asn	Leu	Ala	Leu		
			265				270						275				
AGA	AAG	GCG	TTT	GAA	AAT	TTG	TGC	GAT	GCG	TTT	GAT	TGC	AAG	CTT	GTT	918	
Arg	Lys	Ala	Phe	Glu	Asn	Leu	Cys	Asp	Ala	Phe	Asp	Cys	Lys	Leu	Val		
			280				285						290	295			
TTA	GCC	CCT	TTA	GAA	TTT	TGC	AGC	GAC	AAT	GCC	GCC	ATG	ATA	GGG	CGA	966	
Leu	Ala	Pro	Leu	Glu	Phe	Cys	Ser	Asp	Asn	Ala							

TCC AGC CTA GAA GCT TAT CAA AAA AAG CGC TTT GTC CCT TTA GAA AAG 1014
 Ser Ser Leu Glu Ala Tyr Gln Lys Lys Arg Phe Val Pro Leu Glu Lys
 315 320 325

GCT AAC ATT TCG CCA AGA ACG CTG TTA AAA AGT TTT GAG TGAATGGATA CA 1065
 Ala Asn Ile Ser Pro Arg Thr Leu Leu Lys Ser Phe Glu
 330 335 340

AAAAGAAAGC GCATGATAAA AC 1087

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met	Ile	Leu	Ser	Ile	Glu	Ser	Ser	Cys	Asp	Asp	Ser	Ser	Leu	Ala	Leu	1	5	10	15
Thr	Arg	Ile	Glu	Asp	Ala	Gln	Leu	Ile	Ala	His	Phe	Lys	Ile	Ser	Gln	20	25	30	
Glu	Lys	His	His	Ser	Ser	Tyr	Gly	Gly	Val	Val	Pro	Glu	Leu	Ala	Ser	35	40	45	
Arg	Leu	His	Ala	Glu	Asn	Leu	Pro	Leu	Leu	Leu	Glu	Arg	Ile	Lys	Ile	50	55	60	
Ser	Leu	Asn	Lys	Asp	Phe	Ser	Lys	Ile	Lys	Ala	Ile	Ala	Ile	Thr	Asn	65	70	75	80
Gln	Pro	Gly	Leu	Ser	Val	Thr	Leu	Ile	Glu	Gly	Leu	Met	Met	Ala	Lys	85	90	95	
Ala	Leu	Ser	Leu	Ser	Leu	Asn	Leu	Pro	Leu	Ile	Leu	Glu	Asp	His	Leu	100	105	110	
Arg	Gly	His	Val	Tyr	Ser	Leu	Phe	Ile	Asn	Glu	Lys	Gln	Thr	Cys	Met	115	120	125	
Pro	Leu	Ser	Val	Leu	Leu	Val	Ser	Gly	Gly	His	Ser	Leu	Ile	Leu	Glu	130	135	140	
Ala	Arg	Asp	Tyr	Glu	Asn	Ile	Lys	Ile	Val	Ala	Thr	Ser	Leu	Asp	Asp	145	150	155	160
Ser	Phe	Gly	Glu	Ser	Phe	Asp	Lys	Val	Ser	Lys	Met	Leu	Asp	Leu	Gly	165	170	175	
Tyr	Pro	Gly	Gly	Pro	Ile	Val	Glu	Lys	Leu	Ala	Leu	Asp	Tyr	Arg	His	180	185	190	
Pro	Asn	Glu	Pro	Leu	Met	Phe	Pro	Ile	Pro	Leu	Lys	Asn	Ser	Pro	Asn	195	200	205	
Leu	Ala	Phe	Ser	Phe	Ser	Gly	Leu	Lys	Asn	Ala	Val	Arg	Leu	Glu	Val	210	215	220	
Glu	Lys	Asn	Ala	Pro	Asn	Leu	Asn	Glu	Ala	Ile	Lys	Gln	Lys	Ile	Gly	225	230	235	240
Tyr	His	Phe	Gln	Ser	Ala	Ala	Ile	Glu	His	Leu	Ile	Gln	Gln	Thr	Lys	245	250	255	
Arg	Tyr	Phe	Lys	Ile	Lys	Arg	Pro	Lys	Ile	Phe	Gly	Ile	Val	Gly	Gly	260	265	270	
Ala	Ser	Gln	Asn	Leu	Ala	Leu	Arg	Lys	Ala	Phe	Glu	Asn	Leu	Cys	Asp	275	280	285	

Ala	Phe	Asp	Cys	Lys	Leu	Val	Leu	Ala	Pro	Leu	Glu	Phe	Cys	Ser	Asp	
	290					295					300					
Asn	Ala	Ala	Met	Ile	Gly	Arg	Ser	Ser	Leu	Glu	Ala	Tyr	Gln	Lys	Lys	
305					310					315					320	
Arg	Phe	Val	Pro	Leu	Glu	Lys	Ala	Asn	Ile	Ser	Pro	Arg	Thr	Leu	Leu	
				325					330					335		
Lys	Ser	Phe	Glu													
			340													

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...498
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

TGCACTTGTT ATGATGAAGA TGGCGCACTA AGA ATG AAT GAA GAC TTG ACA AAT	54
Met Asn Glu Asp Leu Thr Asn	
1 5	
TCA ACA GAA TAT AAA AGA TAT GGC CAT GAT TAC GCC AAA TAC CCA AGA	102
Ser Thr Glu Tyr Lys Arg Tyr Gly His Asp Tyr Ala Lys Tyr Pro Arg	
10 15 20	
AGA ATC GCT GAA GAA TTG CAA CAT TAT GGG GGC AAT AGT TTT GCG AAT	150
Arg Ile Ala Glu Glu Leu Gln His Tyr Gly Gly Asn Ser Phe Ala Asn	
25 30 35	
TTT TTT AGA GAT GAA GGG GTC TTA TAC AAA GAG ATT TTG TGC GAT GCG	198
Phe Phe Arg Asp Glu Gly Val Leu Tyr Lys Glu Ile Leu Cys Asp Ala	
40 45 50 55	
TGC GAT CAT TTA AAG GTT AAT TAC AAT GAA GAA TCT GCA ACC TCT TTG	246
Cys Asp His Leu Lys Val Asn Tyr Asn Glu Glu Ser Ala Thr Ser Leu	
60 65 70	
ATT GAG CAA AAC ATG CTT TCT AAA CTC TTG AAA GAT AGT TTA GAA AAA	294
Ile Glu Gln Asn Met Leu Ser Lys Leu Leu Lys Asp Ser Leu Glu Lys	
75 80 85	
ATG AGT AGG AGA GAG ATT AAA GAA CTT TGC AAT GAA TTG GGC ATG ACA	342
Met Ser Arg Arg Glu Ile Lys Glu Leu Cys Asn Glu Leu Gly Met Thr	
90 95 100	
AAT ATT GAT AAA GTG ATT GGT GAA AAC AAA CAA GTC CTA ATC GCA TCT	390
Asn Ile Asp Lys Val Ile Gly Glu Asn Lys Gln Val Leu Ile Ala Ser	
105 110 115	

ACT TTA ACG CTG TTT AAA GCG GGT GGC TCT CAT TCT TAT GCG TTG GCT 438
 Thr Leu Thr Leu Phe Lys Ala Gly Gly Ser His Ser Tyr Ala Leu Ala
 120 125 130 135

GTA TCT GTT GCA GAT GCA ATG GTA AGA CAA ACT CTA GGG CAT GTT ATG 486
 Val Ser Val Ala Asp Ala Met Val Arg Gln Thr Leu Gly His Val Met
 140 145 150

TGG TGG GTA AAG TAGCACTTAA AAAAAGTTTG GCGGTTTTGG CTGGCCCTAT TGGTT 543
 Trp Trp Val Lys
 155

GGGT 547

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Met Asn Glu Asp Leu Thr Asn Ser Thr Glu Tyr Lys Arg Tyr Gly His
 1 5 10 15
 Asp Tyr Ala Lys Tyr Pro Arg Arg Ile Ala Glu Glu Leu Gln His Tyr
 20 25 30
 Gly Gly Asn Ser Phe Ala Asn Phe Arg Asp Glu Gly Val Leu Tyr
 35 40 45
 Lys Glu Ile Leu Cys Asp Ala Cys Asp His Leu Lys Val Asn Tyr Asn
 50 55 60
 Glu Glu Ser Ala Thr Ser Leu Ile Glu Gln Asn Met Leu Ser Lys Leu
 65 70 75 80
 Leu Lys Asp Ser Leu Glu Lys Met Ser Arg Arg Glu Ile Lys Glu Leu
 85 90 95
 Cys Asn Glu Leu Gly Met Thr Asn Ile Asp Lys Val Ile Gly Glu Asn
 100 105 110
 Lys Gln Val Leu Ile Ala Ser Thr Leu Thr Leu Phe Lys Ala Gly Gly
 115 120 125
 Ser His Ser Tyr Ala Leu Ala Val Ser Val Ala Asp Ala Met Val Arg
 130 135 140
 Gln Thr Leu Gly His Val Met Trp Trp Val Lys
 145 150 155

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 19...486
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

TTATTTTAAA	GGAATTTTC	ATG	CAA	ATC	ATA	GAA	GGG	AAA	TTG	CAA	TTA	CAA	51			
		Met	Gln	Ile	Ile	Glu	Gly	Lys	Leu	Gln	Leu	Gln				
		1				5					10					
GGG	AAT	GAA	AGA	GTC	GCT	ATT	TTA	ACA	TCG	CGC	TTC	AAT	CAT	ATC	ATC	99
Gly	Asn	Glu	Arg	Val	Ala	Ile	Leu	Thr	Ser	Arg	Phe	Asn	His	Ile	Ile	
		15					20					25				
ACA	GAC	AGA	TTG	CAA	GAA	GGG	GCG	ATG	GAC	TGC	TTT	AAA	AGG	CAT	GGG	147
Thr	Asp	Arg	Leu	Gln	Glu	Gly	Ala	Met	Asp	Cys	Phe	Lys	Arg	His	Gly	
		30					35					40				
GGC	GAT	GAG	GAT	CTT	TTA	GAC	ATC	GTG	CTG	GTG	CCT	GGG	GCT	TAT	GAA	195
Gly	Asp	Glu	Asp	Leu	Leu	Asp	Ile	Val	Leu	Val	Pro	Gly	Ala	Tyr	Glu	
		45				50					55					
TTG	CCT	TTT	ATT	TTA	GAC	AAA	TTA	TTA	GAG	AGC	GAA	AAA	TAC	GAT	GGC	243
Leu	Pro	Phe	Ile	Leu	Asp	Lys	Leu	Leu	Glu	Ser	Glu	Lys	Tyr	Asp	Gly	
		60			65				70						75	
GTG	TGC	GTT	TTG	GGA	GCG	ATC	ATT	AGA	GGG	GGG	ACT	CCG	CAT	TTT	GAT	291
Val	Cys	Val	Leu	Gly	Ala	Ile	Ile	Arg	Gly	Gly	Thr	Pro	His	Phe	Asp	
				80					85					90		
TAT	GTG	AGC	GCG	GAA	GCG	ACT	AAG	GGT	ATT	GCC	CAT	GCG	ATG	CTT	AAA	339
Tyr	Val	Ser	Ala	Glu	Ala	Thr	Lys	Gly	Ile	Ala	His	Ala	Met	Leu	Lys	
			95					100					105			
TAC	AGC	ATG	CCG	GTA	AGC	TTT	GGC	GTG	CTG	ACC	ACG	GAC	AAT	ATT	GAA	387
Tyr	Ser	Met	Pro	Val	Ser	Phe	Gly	Val	Leu	Thr	Thr	Asp	Asn	Ile	Glu	
		110					115					120				
CAA	GCG	ATT	GAA	AGA	GCG	GGC	AGT	AAA	GCC	GGC	AAT	AAG	GGC	TTT	GAA	435
Gln	Ala	Ile	Glu	Arg	Ala	Gly	Ser	Lys	Ala	Gly	Asn	Lys	Gly	Phe	Glu	
		125				130					135					
GCG	ATG	AGC	ACC	CTC	ATT	GAA	TTG	TTG	AGC	TTG	TGC	CAA	ACT	CTC	AAG	483
Ala	Met	Ser	Thr	Leu	Ile	Glu	Leu	Leu	Ser	Leu	Cys	Gln	Thr	Leu	Lys	
		140			145				150						155	
GGT	TAAAATGGCG	ACACGAACTC	AAGCCAGGGG	GGCTGTG												523
Gly																

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Met Gln Ile Ile Glu Gly Lys Leu Gln Leu Gln Gly Asn Glu Arg Val
1 5 10 15
Ala Ile Leu Thr Ser Arg Phe Asn His Ile Ile Thr Asp Arg Leu Gln
20 25 30
Glu Gly Ala Met Asp Cys Phe Lys Arg His Gly Gly Asp Glu Asp Leu
35 40 45
Leu Asp Ile Val Leu Val Pro Gly Ala Tyr Glu Leu Pro Phe Ile Leu
50 55 60
Asp Lys Leu Leu Glu Ser Glu Lys Tyr Asp Gly Val Cys Val Leu Gly
65 70 75 80
Ala Ile Ile Arg Gly Gly Thr Pro His Phe Asp Tyr Val Ser Ala Glu
85 90 95
Ala Thr Lys Gly Ile Ala His Ala Met Leu Lys Tyr Ser Met Pro Val
100 105 110
Ser Phe Gly Val Leu Thr Thr Asp Asn Ile Glu Gln Ala Ile Glu Arg
115 120 125
Ala Gly Ser Lys Ala Gly Asn Lys Gly Phe Glu Ala Met Ser Thr Leu
130 135 140
Ile Glu Leu Leu Ser Leu Cys Gln Thr Leu Lys Gly
145 150 155

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1656
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

TATTATTAAG GATACAAA ATG GCA AAA GAA ATC AAA TTT TCA GAT AGC GCG 51
Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala
1 5 10
AGA AAC CTT TTA TTT GAA GGC GTG AGA CAA CTC CAT GAC GCT GTT AAA 99
Arg Asn Leu Leu Phe Glu Gly Val Arg Gln Leu His Asp Ala Val Lys
15 20 25
GTA ACC ATG GGG CCA AGA GGC AGG AAC GTG TTG ATC CAA AAA AGC TAT 147
Val Thr Met Gly Pro Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr
30 35 40
GGC GCT CCA AGC ATC ACT AAA GAT GGC GTG AGC GTG GCT AAA GAG ATT 195

Gly	Ala	Pro	Ser	Ile	Thr	Lys	Asp	Gly	Val	Ser	Val	Ala	Lys	Glu	Ile	
45						50					55					
GAA	TTA	AGT	TGC	CCG	GTA	GCT	AAC	ATG	GGC	GCT	CAA	CTC	GTT	AAA	GAA	243
Glu	Leu	Ser	Cys	Pro	Val	Ala	Asn	Met	Gly	Ala	Gln	Leu	Val	Lys	Glu	
60					65				70						75	
GTA	GCG	AGC	AAA	ACC	GCT	GAT	GCT	GCC	GGC	GAT	GGC	ACG	ACC	ACA	GCG	291
Val	Ala	Ser	Lys	Thr	Ala	Asp	Ala	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	
				80					85						90	
ACC	GTG	CTG	GCT	TAT	AGC	ATT	TTT	AAA	GAA	GGT	TTG	AGG	AAC	ATC	ACG	339
Thr	Val	Leu	Ala	Tyr	Ser	Ile	Phe	Lys	Glu	Gly	Leu	Arg	Asn	Ile	Thr	
			95					100					105			
GCT	GGG	GCT	AAC	CCT	ATT	GAA	GTG	AAA	CGA	GGC	ATG	GAT	AAA	GCC	GCT	387
Ala	Gly	Ala	Asn	Pro	Ile	Glu	Val	Lys	Arg	Gly	Met	Asp	Lys	Ala	Ala	
		110					115					120				
GAA	GCC	ATT	ATT	AAT	GAG	CTT	AAA	AAA	GCG	AGC	AAA	AAA	GTG	GGC	GGT	435
Glu	Ala	Ile	Ile	Asn	Glu	Leu	Lys	Lys	Ala	Ser	Lys	Lys	Val	Gly	Gly	
	125					130					135					
AAA	GAA	GAA	ATC	ACC	CAA	GTG	GCG	ACC	ATT	TCT	GCA	AAC	TCC	GAT	CAC	483
Lys	Glu	Glu	Ile	Thr	Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Ser	Asp	His	
140					145					150					155	
AAT	ATC	GGG	AAA	CTC	ATC	GCT	GAC	GCT	ATG	GAA	AAA	GTG	GGT	AAA	GAC	531
Asn	Ile	Gly	Lys	Leu	Ile	Ala	Asp	Ala	Met	Glu	Lys	Val	Gly	Lys	Asp	
				160					165					170		
GGC	GTG	ATC	ACC	GTT	GAA	GAA	GCT	AAG	GGC	ATT	GAA	GAT	GAA	CTA	GAT	579
Gly	Val	Ile	Thr	Val	Glu	Glu	Ala	Lys	Gly	Ile	Glu	Asp	Glu	Leu	Asp	
			175					180					185			
GTT	GTA	GAA	GGC	ATG	CAA	TTT	GAT	AGA	GGC	TAC	CTC	TCC	CCT	TAT	TTT	627
Val	Val	Glu	Gly	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	
		190					195					200				
GTA	ACA	AAC	GCT	GAG	AAA	ATG	ACC	GCT	CAA	TTG	GAT	AAC	GCT	TAC	ATC	675
Val	Thr	Asn	Ala	Glu	Lys	Met	Thr	Ala	Gln	Leu	Asp	Asn	Ala	Tyr	Ile	
	205					210					215					
CTT	TTA	ACG	GAT	AAA	AAA	ATC	TCT	AGC	ATG	AAA	GAC	ATT	CTC	CCG	CTA	723
Leu	Leu	Thr	Asp	Lys	Lys	Ile	Ser	Ser	Met	Lys	Asp	Ile	Leu	Pro	Leu	
220					225					230					235	
CTA	GAA	AAA	ACC	ATG	AAA	GAG	GGC	AAA	CCG	CTT	TTA	ATC	ATC	GCT	GAA	771
Leu	Glu	Lys	Thr	Met	Lys	Glu	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	
				240					245					250		
GAC	ATT	GAG	GGC	GAA	GCT	TTA	ACG	ACT	CTA							

AGA Arg	AAA Lys	GAA Glu	ATG Met	CTC Leu	AAA Lys	GAC Asp	ATC Ile	GCT Ala	ATT Ile	TTA Leu	ACC Thr	GGC Gly	GGT Gly	CAA Gln	GTT Val	915
285290295																
ATT Ile	AGC Ser	GAA Glu	GAA Glu	TTG Leu	GGC Gly	TTG Leu	AGT Ser	CTA Leu	GAA Glu	AAC Asn	GCT Ala	GAA Glu	GTG Val	GAG Glu	TTT Phe	963
300305310315																
TTA Leu	GGC Gly	AAA Lys	GCC Ala	GGA Gly	AGG Arg	ATT Ile	GTG Val	ATT Ile	GAC Asp	AAA Lys	GAC Asp	AAC Asn	ACC Thr	ACG Thr	ATC Ile	1011
320325330																
GTA Val	GAT Asp	GGC Gly	AAA Lys	GGC Gly	CAT His	AGC Ser	CAT His	GAT Asp	GTC Val	AAA Lys	GAC Asp	AGA Arg	GTC Val	GCG Ala	CAA Gln	1059
335340345																
ATC Ile	AAA Lys	ACC Thr	CAA Gln	ATT Ile	GCA Ala	AGC Ser	ACG Thr	ACA Thr	AGC Ser	GAT Asp	TAT Tyr	GAC Asp	AAA Lys	GAA Glu	AAA Lys	1107
350355360																
TTG Leu	CAA Gln	GAA Glu	AGG Arg	TTG Leu	GCT Ala	AAA Lys	CTC Leu	TCT Ser	GGC Gly	GGT Gly	GTG Val	GCT Ala	GTG Val	ATT Ile	AAA Lys	1155
365370375																
GTG Val	GGC Gly	GCT Ala	GCG Ala	AGT Ser	GAA Glu	GTG Val	GAA Glu	ATG Met	AAA Lys	GAG Glu	AAA Lys	AAA Lys	GAC Asp	CGG Arg	GTT Val	1203
380385390395																
GAT Asp	GAT Asp	GCG Ala	TTG Leu	AGC Ser	GCG Ala	ACT Thr	AAA Lys	GCG Ala	GCT Ala	GTT Val	GAA Glu	GAA Glu	GGT Gly	ATT Ile	GTG Val	1251
400405410																
ATT Ile	GGC Gly	GGC Gly	GGT Gly	GCG Ala	GCT Ala	CTC Leu	ATT Ile	CGC Arg	GCG Ala	GCT Ala	CAA Gln	AAA Lys	GTG Val	CAT His	TTG Leu	1299
415420425																
AAT Asn	TTG Leu	CAC His	GAT Asp	GAT Asp	GAA Glu	AAA Lys	GTG Val	GGC Gly	TAT Tyr	GAA Glu	ATC Ile	ATC Ile	ATG Met	CGC Arg	GCC Ala	1347
430435440																
ATT Ile	AAA Lys	GCC Ala	CCA Pro	TTA Leu	GCT Ala	CAA Gln	ATC Ile	GCT Ala	ATC Ile	AAT Asn	GCC Ala	GGT Gly	TAT Tyr	GAT Asp	GGC Gly	1395
445450455																
GGT Gly	GTG Val	GTC Val	GTG Val	AAT Asn	GAA Glu	GTA Val	GAA Glu	AAA Lys	CAC His	GAA Glu	GGG Gly	CAT His	TTT Phe	GGT Gly	TTT Phe	1443
460465470475																
AAC Asn	GCT Ala	AGC Ser	AAT Asn	GGC Gly	AAG Lys	TAT Tyr	GTG Val	GAT Asp	ATG Met	TTT Phe	AAA Lys	GAA Glu	GGC Gly	ATT Ile	ATT Ile	1491
480485490																
GAC Asp	CCC Pro	TTA Leu	AAA Lys	GTA Val	GAA Glu	AGG Arg	ATC Ile	GCT Ala	TTA Leu	CAA Gln	AAT Asn	GCG Ala	GTT Val	TCG Ser	GTT Val	1539
495500505																
TCA Ser	AGC Ser	CTG Leu	CTT Leu	TTA Leu	ACC Thr	ACA Thr	GAA Glu	GCC Ala	ACC Thr	GTG Val	CAT His	GAA Glu	ATC Ile	AAA Lys	GAA Glu	1587

TTT Phe	GCA Ala	GGG Gly 15	CAT His	TTG Leu	GAG Glu	CAA Gln 20	GCA Ala 20	GGA Gly	GAG Glu	AGT Ser	CAT His 25	AGT Ser 25	TTT Phe	ATT Ile	AAC Asn	97
ATG Met	AAA Lys 30	AGC Ser	GAA Glu	GAA Glu	AAG Lys 35	GAC Asp 35	GCC Ala	CCT Pro	AAG Lys	GGG Gly 40	CTA Leu 40	TTC Phe	CCT Pro	TTT Phe	TAT Tyr	145
ATC Ile 45	CCC Pro	TAT Tyr	GAA Glu	AAT Asn 50	TGT Cys 50	TAT Tyr	TTG Leu	GGG Gly	CGT Arg 55	TGT Cys 55	TGC Cys	ATT Ile	GAT Asp	AAC Asn 60	CAT His 60	193
AAG Lys	ATT Ile	ATT Ile	TTG Leu 65	CCT Pro 65	AGT Ser	GAT Asp	CTA Leu	GAT Asp 70	TTA Leu 70	AGG Arg	GTG Val	CAA Gln	GCA Ala 75	GAG Glu 75	CCA Pro	241
GAA Glu	ATC Ile	GCT Ala 80	TTA Leu 80	GAA Glu	TGC Cys	GAT Asp	GTT Val 85	AAA Lys 85	TAC Tyr	GAT Asp	GAA Glu	AAA Lys 90	CAT His 90	TTG Leu	GTT Val	289
GCA Ala	AAG Lys 95	CTC Leu 95	GTG Val	CCT Pro	AAT Asn	TTT Phe 100	TTC Phe 100	ATG Met	GCG Ala	TTT Phe 105	AAT Asn 105	GAC Asp 105	GCT Ala	TCT Ser	GTG Val	337
CGC Arg 110	AAT Asn 110	TTA Leu	GAC Asp	GCC Ala	GCA Ala	AAA Lys 115	CTC Leu 115	TCC Ser	CAA Gln	AAA Lys 120	AAG Lys 120	AAT Asn	TTT Phe	TCA Ser	CCG Pro	385
GCT Ala 125	TCT Ser	AAA Lys	GGT Gly	ATA Ile 130	GGG Gly 130	CAG Gln	AAA Lys	TTG Leu	CCC Pro 135	ATT Ile 135	GAC Asp	AGG Arg	TTT Phe	GTT Val	TAT Tyr 140	433
GGG Gly	GGG Gly	GTG Val	TGT Cys	AAC Asn 145	AAT Asn 145	TTC Phe	TCT Ser	ATC Ile 150	GCG Ala 150	TCT Ser	TTT Phe 155	TTG Leu	AAA Lys 155	TAC Tyr 155	AAT Asn	481
AAT Asn 160	GTT Val	TGG Trp 160	CAC His 160	ATT Ile	TAT Tyr	GGG Gly 165	GAA Glu 165	AAC Asn 165	AGC Ser	AAA Lys 170	TTG Leu 170	CTC Leu 170	AAA Lys 170	TAC Tyr	GAG Glu	529
TTT Phe 175	TTT Phe 175	TAT Tyr 175	CAA Gln	AAG Lys	CTT Leu	TTA Leu 180	GAT Asp 180	TGG Trp 180	ATT Ile	AAA Lys 185	GAC Asp 185	CAA Gln 185	TTA Leu	AAC Asn	CAC His	577
CAA Gln 190	CAA Gln 190	GAT Asp	GGC Gly	GAC Asp	TCT Ser	TTA Leu 195	GAG Glu 195	GCT Ala	CTA Leu	AGA Arg 200	CCT Pro 200	TTT Phe	TTA Leu	GAG Glu	CGC Arg	625
CAT His 205	AAT Asn	TTC Phe	CCC Pro	ACT Thr	AAA Lys 210	ATG Met	ATT Ile	TTT Phe	GCA Ala 215	ATA Ile 215	GGG Gly 215	GCT Ala	ACC Thr	CCT Pro	TAT Tyr 220	673
ATG Met	CCT Pro	TTT Phe	GCG Ala 225	CAA Gln 225	GAG Glu	CAT His	TTT Phe	TTG Leu 230	CAA Gln 230	AAA Lys 235	GGC Gly 235	GAT Asp	GAG Glu	GTG Val 235	GTG Val	721
ATC Ile	GTT Val	GCT Ala	TAC Tyr	AAC Asn	CAT His	TTA Leu	CAA Gln	TAC Tyr	AGT Ser	TTT Phe	GAA Glu	AAG Lys	ATT Ile	CAA Gln	AAC Asn	769

Ile Val Glu
275

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...300
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

AGCTCCGAGT TTAGCGAATT GGTTTATGGG AATTTTTTA ATG ATT ATC CTG TCA	54
Met Ile Ile Leu Ser	
1 5	
GCG AGC GTG AAG AAT TTG CGT GAA ATT TCG GTT AAA GAA AAA TTT TTA	102
Ala Ser Val Lys Asn Leu Arg Glu Ile Ser Val Lys Glu Lys Phe Leu	
10 15 20	
TGG CTG AAC GCT AAG TCT TAT TTG ATT TCT GTT TTT GCG CCT TTT ATC	150
Trp Leu Asn Ala Lys Ser Tyr Leu Ile Ser Val Phe Ala Pro Phe Ile	
25 30 35	
TTG CTC CCT TGG ATT GAT TTG TTG AGC GCT TTT TTA TTG TAT TTA GGG	198
Leu Leu Pro Trp Ile Asp Leu Leu Ser Ala Phe Leu Leu Tyr Leu Gly	
40 45 50	
TTT TTA GCG CTC TTT AGC GTG CTG GAA TTT TTT GAT GAA GAC ATT GCA	246
Phe Leu Ala Leu Phe Ser Val Leu Glu Phe Phe Asp Glu Asp Ile Ala	
55 60 65	
GAT ATT ATC GTG GCT AAA AGC AAA ATA AAG ACT AAA ACC AAA TGT TAT	294
Asp Ile Ile Val Ala Lys Ser Lys Ile Lys Thr Lys Thr Lys Cys Tyr	
70 75 80 85	
AGA GCG TAGAATGTTA GAAAAGCTTT TAAGCGCTAT CAAACAA	337
Arg Ala	

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

```
Met Ile Ile Leu Ser Ala Ser Val Lys Asn Leu Arg Glu Ile Ser Val
 1           5           10           15
Lys Glu Lys Phe Leu Trp Leu Asn Ala Lys Ser Tyr Leu Ile Ser Val
      20           25           30
Phe Ala Pro Phe Ile Leu Leu Pro Trp Ile Asp Leu Leu Ser Ala Phe
      35           40           45
Leu Leu Tyr Leu Gly Phe Leu Ala Leu Phe Ser Val Leu Glu Phe Phe
      50           55           60
Asp Glu Asp Ile Ala Asp Ile Ile Val Ala Lys Ser Lys Ile Lys Thr
65           70           75           80
Lys Thr Lys Cys Tyr Arg Ala
      85
```

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1044 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 15...977
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```
ATTAAGGGGA AGTC ATG GCT GAT AGT TTA GCG GGC ATT GAT CAA GTT ACG      50
      Met Ala Asp Ser Leu Ala Gly Ile Asp Gln Val Thr
      1           5           10

AGT TTG CAT AAA AAT AAC GAG TTA CAA TTG TTG TGT TTC AGG CTG GGT      98
Ser Leu His Lys Asn Asn Glu Leu Gln Leu Leu Cys Phe Arg Leu Gly
      15           20           25

AAA AAC AAG GAT TTG TAT GCG GTC AAT GTT TTT AAG ATC CGT GAA GTG      146
Lys Asn Lys Asp Leu Tyr Ala Val Asn Val Phe Lys Ile Arg Glu Val
      30           35           40

GTG AAA TAC CAT GGC AAT CTC ACC ATC ATT AGC CAC GAA AAC AAT TCG      194
Val Lys Tyr His Gly Asn Leu Thr Ile Ile Ser His Glu Asn Asn Ser
45           50           55           60

CTC GTT GAG GGG CTA ATC ATT ATA AGA GAA CTC ACC ATT CCC TTG ATT      242
Leu Val Glu Gly Leu Ile Ile Ile Arg Glu Leu Thr Ile Pro Leu Ile
      65           70           75

GAT ATG AAA AAA TGG TTT TAT TAT GAC AGC CAA AAC AAA AAC AAG GAT      290
Asp Met Lys Lys Trp Phe Tyr Tyr Asp Ser Gln Asn Lys Asn Lys Asp
      80           85           90
```

TTA Leu	CGC Arg	CCT Pro 95	TAT Tyr	AGG Arg	ATA Ile	GAA Glu	AAA Lys 100	GAA Glu	AAA Lys	GGC Gly	GAA Glu	GAT Asp 105	GAT Asp	ATT Ile	GTT Val	338
ATG Met	ATT Ile 110	TGT Cys	GAG Glu	TTT Phe	TCT Ser	CGC Arg	TGG Trp 115	ACT Thr	ATA Ile	GGG Gly	GTT Val 120	AGG Arg	ATC Ile	TAT Tyr	GAA Glu	386
GCG Ala 125	GAT Asp	AGG Arg	ATT Ile	TTG Leu	AGC Ser 130	AAG Lys	AAA Lys	TGG Trp	ACT Thr	GAA Glu 135	ATG Met	GAG Glu	CAA Gln	AGC Ser	GCT Ala 140	434
GGG Gly	CTA Leu	GGG Gly	GGA Gly	TCT Ser 145	GCA Ala	GGC Gly	AAT Asn	AAC Asn	AAA Lys 150	CTC Leu	GTG Val	AGC Ser	CGC Arg	ACG Thr 155	CGC Arg	482
TAT Tyr	TTT Phe	GAT Asp	GGG Gly 160	CGC Arg	TTG Leu	GTG Val	CAA Gln 165	GTG Val	GTG Val	GAT Asp	ATT Ile	GAA Glu 170	AAA Lys	ATG Met	CTT Leu	530
ATA Ile	GAC Asp 175	GTG Val	TTC Phe	CCT Pro	TGG Trp	ATT Ile	GAA Glu 180	GAT Asp	GAA Glu	AAA Lys	CAC His	AAC Asn 185	GAT Asp	TTA Leu	GAG Glu	578
ACG Thr 190	CTT Leu	TCT Ser	AAA Lys	ATC Ile	CAT His	TCT Ser 195	AAC Asn	CAA Gln	TGC Cys	GTT Val 200	TTG Leu	CTT Leu	GCT Ala	GAT Asp	GAC Asp	626
TCC Ser 205	CCA Pro	AGC Ser	GTT Val	TTG Leu	AAA Lys 210	ACC Thr	ATG Met	CAA Gln	ATG Met	ATT Ile 215	TTA Leu	GAC Asp	AAG Lys	CTG Leu	GGC Gly 220	674
GTC Val	AAG Lys	CAT His	ATA Ile	GAT Asp 225	TTT Phe	ATC Ile	AAT Asn	GGT Gly	AAA Lys 230	ACC Thr	TTA Leu	CTA Leu	GAG Glu	CAT His 235	TTA Leu	722
TTC Phe	AAC Asn	CCC Pro	ACA Thr 240	ACC Thr	GAT Asp	GTG Val	AGT Ser	AAT Asn 245	ATT Ile	GGC Gly	CTG Leu	ATT Ile 250	ATT Ile	ACC Thr	GAT Asp	770
TTG Leu	GAA Glu	ATG Met 255	CCA Pro	GAG Glu	GCG Ala	AGC Ser	GGT Gly 260	TTT Phe	GAA Glu	GTG Val	ATC Ile	AAG Lys 265	CAG Gln	GTT Val	AAA Lys	818
AAC Asn 270	AAT Asn	CCT Pro	TTG Leu	ACT Thr	TCA Ser	AAA Lys 275	ATC Ile	CCT Pro	ATC Ile	GTG Val 280	GTC Val	AAT Asn	TCT Ser	TCT Ser	ATG Met	866
AGC Ser 285	GGG Gly	AGT Ser	TCT Ser	AAT Asn	GAA Glu 290	GAC Asp	ATG Met	GCC Ala	AGG Arg	AGT Ser 295	TTG Leu	AAG Lys	GCC Ala	GAT Asp	GAT Asp 300	914
TTC Phe	ATT Ile	TCC Ser	AAG Lys	TCT Ser 305	AAC Asn	CCC Pro	AAA Lys	GAC Asp 310	ATC Ile	CAG Gln	CGA Arg	GTG Val	GTT Val	AAG Lys 315	CAA Gln	962
TTT Phe	TTG Leu	GAA Glu	TTA Leu	GCA Ala	TGAAAAAATA	CAGCACTATC	CCCACCCCTT	GCTACGTGTT	A	1018						

GAGAGCGAAC GCTTAGAAAA AAACGC

1044

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

```

Met Ala Asp Ser Leu Ala Gly Ile Asp Gln Val Thr Ser Leu His Lys
 1      5      10      15
Asn Asn Glu Leu Gln Leu Leu Cys Phe Arg Leu Gly Lys Asn Lys Asp
      20      25      30
Leu Tyr Ala Val Asn Val Phe Lys Ile Arg Glu Val Val Lys Tyr His
      35      40      45
Gly Asn Leu Thr Ile Ile Ser His Glu Asn Asn Ser Leu Val Glu Gly
 50      55      60
Leu Ile Ile Ile Arg Glu Leu Thr Ile Pro Leu Ile Asp Met Lys Lys
 65      70      75      80
Trp Phe Tyr Tyr Asp Ser Gln Asn Lys Asn Lys Asp Leu Arg Pro Tyr
      85      90      95
Arg Ile Glu Lys Glu Lys Gly Glu Asp Asp Ile Val Met Ile Cys Glu
      100      105      110
Phe Ser Arg Trp Thr Ile Gly Val Arg Ile Tyr Glu Ala Asp Arg Ile
      115      120      125
Leu Ser Lys Lys Trp Thr Glu Met Glu Gln Ser Ala Gly Leu Gly Gly
      130      135      140
Ser Ala Gly Asn Asn Lys Leu Val Ser Arg Thr Arg Tyr Phe Asp Gly
 145      150      155      160
Arg Leu Val Gln Val Val Asp Ile Glu Lys Met Leu Ile Asp Val Phe
      165      170      175
Pro Trp Ile Glu Asp Glu Lys His Asn Asp Leu Glu Thr Leu Ser Lys
      180      185      190
Ile His Ser Asn Gln Cys Val Leu Ala Asp Asp Ser Pro Ser Val
      195      200      205
Leu Lys Thr Met Gln Met Ile Leu Asp Lys Leu Gly Val Lys His Ile
      210      215      220
Asp Phe Ile Asn Gly Lys Thr Leu Leu Glu His Leu Phe Asn Pro Thr
 225      230      235      240
Thr Asp Val Ser Asn Ile Gly Leu Ile Ile Thr Asp Leu Glu Met Pro
      245      250      255
Glu Ala Ser Gly Phe Glu Val Ile Lys Gln Val Lys Asn Asn Pro Leu
      260      265      270
Thr Ser Lys Ile Pro Ile Val Val Asn Ser Ser Met Ser Gly Ser Ser
      275      280      285
Asn Glu Asp Met Ala Arg Ser Leu Lys Ala Asp Asp Phe Ile Ser Lys
      290      295      300
Ser Asn Pro Lys Asp Ile Gln Arg Val Val Lys Gln Phe Leu Glu Leu
 305      310      315      320
Ala

```

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...618
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

ATCTGCTTAA	ACACAAAAAA	GAGTAAAATA	ACACGC	ATG	AAA	AAA	TTC	TTA	TTT		54
				Met	Lys	Lys	Phe	Leu	Phe		
				1				5			
AAA CAA AAA	TTT TGT GAA	AGC CTG CCC	AAA AGC	TTT TCT	AAA ACT	TTG					102
Lys Gln Lys	Phe Cys Glu	Ser Leu Pro	Lys Ser	Phe Ser	Lys Thr	Leu					
	10		15		20						
TTA GCG CTC	AGT TTG GGC	TTG ATT TTA	TTA GGC	ATT TTT	GCG CCT	TTC					150
Leu Ala Leu	Ser Leu Gly	Leu Ile Leu	Leu Gly	Ile Phe	Ala Pro	Phe					
	25		30		35						
CCT AAA GTC	CCT AAA CAG	CCT AGC GTG	CCT TTA	ATG TTT	CAT TTC	ACC					198
Pro Lys Val	Pro Lys Gln	Pro Ser Val	Pro Leu	Met Phe	His Phe	Thr					
	40		45		50						
GAG CAT TAT	GCG CGC TTT	ATC CCT ACG	ATT TTA	TCT GTG	GCG ATT	CCC					246
Glu His Tyr	Ala Arg Phe	Ile Pro Thr	Ile Leu	Ser Val	Ala Ile	Pro					
	55		60		65						
TTA ATC CAA	AGA GAT GCG	GTA GGG CTT	TTT CAA	GTC GCT	AAC GCT	TCT					294
Leu Ile Gln	Arg Asp Ala	Val Gly Leu	Phe Gln	Val Ala	Asn Ala	Ser					
	75		80		85						
ATC GCT ACA	ACC CTT CTC	ACG CAC ACC	ACC AAA	AGA GCC	TTA AAC	CAT					342
Ile Ala Thr	Thr Leu Leu	Thr His Thr	Thr Lys	Arg Ala	Leu Asn	His					
	90		95		100						
GTA ACA ATC	AAC GAT CAG	CGT TTG GGC	GAG CGC	CCT TAT	GGA GGT	AAT					390
Val Thr Ile	Asn Asp Gln	Arg Leu Gly	Glu Arg	Pro Tyr	Gly Gly	Asn					
	105		110		115						
TTC AAC ATG	CCA AGC GGG	CAT TCG TCT	ATG GTG	GGT TTG	GCG GTG	GCG					438
Phe Asn Met	Pro Ser Gly	His Ser Ser	Met Val	Gly Leu	Ala Val	Ala					
	120		125		130						
TTT TTA ATG	CGC CGC TAT	TCT TTT AAA	AAA TAC	TTT TGG	CTC TTG	CCC					486
Phe Leu Met	Arg Arg Tyr	Ser Phe Lys	Lys Tyr	Phe Trp	Leu Leu	Pro					
	135		140		145						
											150

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 57...1040

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

ATTTCCCTTT GTTCGTTTAT GTTTATAAAG AAAGCAACCA GGTCAGTTTT ATCGCC ATG	59
Met	
1	
ATG GTT GTG GTG CTT TTT TGC GTT AAT GGC GCT CTT TTT TTG GCG TTA	107
Met Val Val Val Leu Phe Cys Val Asn Gly Ala Leu Phe Leu Ala Leu	
5 10 15	
GGC TTG ATC TCT GCT TCT TTG ATG CGT TGG AGT GCG ATA GTT TTT AGC	155
Gly Leu Ile Ser Ala Ser Leu Met Arg Trp Ser Ala Ile Val Phe Ser	
20 25 30	
CTG CTC AAT TCC GTT GCT TTC TAT TTC ATT AGC GCT TAT AAG GTG TTT	203
Leu Leu Asn Ser Val Ala Phe Tyr Phe Ile Ser Ala Tyr Lys Val Phe	
35 40 45	
TTA AAT AAG AGC ATG ATG GGT AAT GTC TTA AAC ACC AAC ACG CAT GAA	251
Leu Asn Lys Ser Met Met Gly Asn Val Leu Asn Thr Asn Thr His Glu	
50 55 60 65	
GTT TTA GGC TTT TTG AGC GTC AAA TTA TTC GTT TTT ATC GTT GTT TTT	299
Val Leu Gly Phe Leu Ser Val Lys Leu Phe Val Phe Ile Val Val Phe	
70 75 80	
GGG GTG TTG CCT GGC TAT GTC ATC TAT AAA ATC CCC CTT AAA AAT TCT	347
Gly Val Leu Pro Gly Tyr Val Ile Tyr Lys Ile Pro Leu Lys Asn Ser	
85 90 95	
TCT AAA AAA GCG CCC TTT TTA GCG ATC TTG GCG TTA GTG TTT ATC TTT	395
Ser Lys Lys Ala Pro Phe Leu Ala Ile Leu Ala Leu Val Phe Ile Phe	
100 105 110	
ATC GCT AGC GCT TTA GCT AAC ACT AAA AAT TGG CTG TGG TTT GAC AAG	443
Ile Ala Ser Ala Leu Ala Asn Thr Lys Asn Trp Leu Trp Phe Asp Lys	
115 120 125	
CAT GCG AAA TTC ATA GGG GGC TTA ATT TTG CCC TTC GCT TAT AGC GTG	491
His Ala Lys Phe Ile Gly Gly Leu Ile Leu Pro Phe Ala Tyr Ser Val	
130 135 140 145	
AAC GCT TTT AGA GTG AGC GCT CTC AAA TTT TTC GCC CCC ACC ATC AAG	539
Asn Ala Phe Arg Val Ser Ala Leu Lys Phe Phe Ala Pro Thr Ile Lys	
150 155 160	
CCG CTC CCT CTT TTT TCA CCC AAT CAT TCC CAT TCG TTT GTG GTG CTA	587
Pro Leu Pro Leu Phe Ser Pro Asn His Ser His Ser Phe Val Val Leu	

165							170					175					
GTC Val	ATT Ile	GGC Gly 180	GAA Glu	AGC Ser	GCT Ala	AGG Arg	AAA Lys 185	CAT His	AAT Asn	TAC Tyr	GCC Ala	CTT Leu 190	TAT Tyr	GGC Gly	TAT Tyr	635	
CAA Gln	AAA Lys 195	CCC Pro	ACC Thr	ACC Thr	CCA Pro	AGA Arg 200	CTA Leu	AGC Ser	AAG Lys	CGT Arg	TTA Leu 205	GCC Ala	GAT Asp	AAT Asn	GAA Glu	683	
CTC Leu 210	ACT Thr	CTT Leu	TTC Phe	AAC Asn	GCC Ala 215	ACT Thr	TCT Ser	TGC Cys	GCC Ala	ACT Thr 220	TAC Tyr	ACG Thr	ACA Thr	GCG Ala	AGT Ser 225	731	
TTG Leu	GAA Glu	TGC Cys	ATT Ile	TTA Leu 230	GAT Asp	TCT Ser	TCT Ser	TTT Phe	AAA Lys 235	AAC Asn	AAC Asn	GCT Ala	TAT Tyr	GAA Glu 240	AAT Asn	779	
TTG Leu	CCA Pro	ACT Thr	TAC Tyr 245	TTG Leu	ACT Thr	AAA Lys	GCC Ala	GGT Gly 250	ATC Ile	AAA Lys	GTC Val	TTT Phe 255	TGG Trp	TAT Tyr	AGC Ser	827	
GCG Ala	AAC Asn	GAC Asp 260	GGC Gly	GAA Glu	AAG Lys	AAT Asn	GTT Val 265	AAG Lys	GTT Val	ACA Thr	AGC Ser	TAT Tyr 270	CTT Leu	AAA Lys	AAC Asn	875	
TAT Tyr	GAA Glu 275	TTG Leu	ATT Ile	CAA Gln	AAA Lys	TGC Cys 280	CCC Pro	AAT Asn	TGT Cys	GAA Glu	GCG Ala 285	ATC Ile	GCT Ala	CCT Pro	TAT Tyr	923	
GAT Asp 290	GAA Glu	TCT Ser	TTA Leu	CTT Leu	TAT Tyr 295	AAT Asn	TTG Leu	CCT Pro	GAC Asp	CTT Leu 300	TTA Leu	AAA Lys	GAA Glu	CAC His	TCT Ser 305	971	
AAT Asn	GAA Glu	AAT Asn	GTC Val 310	TTG Leu	CTC Leu	ATC Ile	TTA Leu	CAC His	TTG Leu 315	CAG Gln	GCT Ala	CGC Arg	ATG Met	GCC Ala 320	CAA Gln	1019	
ACT Thr	ACG Thr	ACA Thr	ACA Thr 325	AAG Lys	TGC Cys	CTT Leu	TAAATTTTAG	GGTGTTTAAG				CCTTATTGCT			CAAG	1074	
CGCTGATCTG TCTTCTT																1091	

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

Met Met Val Val Val Leu Phe Cys Val Asn Gly Ala Leu Phe Leu Ala
1 5 10 15

AAGCTCAAAG	ATAAAGCGCT	ACAATCTCGC	TTAGAAAAAG	GACACAAA	ATG	CTA	TTG								57	
					Met	Leu	Leu									
					1											
AAT	TAC	GAT	TTT	TTA	GAA	TTT	GTT	GAT	GAG	CCG	AAA	AGA	AAC	ACT	TCT	105
Asn	Tyr	Asp	Phe	Leu	Glu	Phe	Val	Asp	Glu	Pro	Lys	Arg	Asn	Thr	Ser	
5						10				15						
TTG	ACA	GCA	TCT	ATT	GAT	AAA	GCG	TTA	GCG	GAC	AGG	AAG	TTA	GCT	AGA	153
Leu	Thr	Ala	Ser	Ile	Asp	Lys	Ala	Leu	Ala	Asp	Arg	Lys	Leu	Ala	Arg	
20					25				30				35			
CAA	AAT	AAA	CCT	AGC	GTT	AGG	GTG	CTT	GGT	AAG	GCG	ATG	CCC	TTA	AGC	201
Gln	Asn	Lys	Pro	Ser	Val	Arg	Val	Leu	Gly	Lys	Ala	Met	Pro	Leu	Ser	
				40				45				50				
AAG	TTT	TTA	GAT	GCT	GTT	GGC	GAT	GAA	ATC	TCA	CGA	CTT	AAA	TAT	GAT	249
Lys	Phe	Leu	Asp	Ala	Val	Gly	Asp	Glu	Ile	Ser	Arg	Leu	Lys	Tyr	Asp	
		55				60						65				
ATG	AGC	CAC	AAG	ACT	ATT	AAA	GGC	TCT	ACA	ATT	GAG	AGT	TCT	AAT	CTT	297
Met	Ser	His	Lys	Thr	Ile	Lys	Gly	Ser	Thr	Ile	Glu	Ser	Ser	Asn	Leu	
70						75						80				
ATC	AGC	ATT	TAT	AAA	AAG	ATT	GCG	AGC	GGA	CTA	CCT	TTT	GGG	ACT	ATC	345
Ile	Ser	Ile	Tyr	Lys	Lys	Ile	Ala	Ser	Gly	Leu	Pro	Phe	Gly	Thr	Ile	
85						90				95						
TCG	GCG	TTT	AGA	CCT	TTT	AAA	GAC	GCT	TTT	TAT	AAA	GAC	TTT	ACC	GAA	393
Ser	Ala	Phe	Arg	Pro	Phe	Lys	Asp	Ala	Phe	Tyr	Lys	Asp	Phe	Thr	Glu	
100					105				110				115			
AAA	GAA	CAA	AAC	GCT	CTA	ATC	TAT	GCT	TAT	AAG	AGC	GGA	GCA	GAC	CCT	441
Lys	Glu	Gln	Asn	Ala	Leu	Ile	Tyr	Ala	Tyr	Lys	Ser	Gly	Ala	Asp	Pro	
				120				125				130				
AAA	AAT	GCG	GAC	ATA	ATA	GCC	AAA	TAT	TGG	TTA	AGT	CAA	TCT	GTG	GAT	489
Lys	Asn	Ala	Asp	Ile	Ile	Ala	Lys	Tyr	Trp	Leu	Ser	Gln	Ser	Val	Asp	
		135				140						145				
TTA	GAC	CCA	TAC	GAC	CCT	ATT	AAA	GTT	GTA	GAT	TTC	TTT	CAC	CCA	CAA	537
Leu	Asp	Pro	Tyr	Asp	Pro	Ile	Lys	Val	Val	Asp	Phe	Phe	His	Pro	Gln	
		150				155						160				
CCT	GAA	AAT	GGT	AAA	GAG	ACT	ACA	AAA	TTT	AAG	AAC	TAC	AAA	GAT	AGG	585
Pro	Glu	Asn	Gly	Lys	Glu	Thr	Lys	Phe	Lys	Asn	Tyr	Lys	Asp	Arg		
165						170				175						
ATT	GAG	AAC	ATT	TAT	GCG	ACA	CTC	TAT	AAC	ACA	TTG	GGT	AGG	GGT	TAT	633
Ile	Glu	Asn	Ile	Tyr	Ala	Thr	Leu	Tyr	Asn	Thr	Leu	Gly	Arg	Gly	Tyr	
180				185				190						195		
GTG	GAT	AAA	TTT	TTT	AAA	AAA	GAA	GCC	ACA	ATG	AGG	GAC	TTT	ATG	TCT	681
Val	Asp	Lys	Phe	Phe	Lys	Lys	Glu	Ala	Thr	Met	Arg	Asp	Phe	Met	Ser	

				215				220				225							
GCA Ala	AGG Arg	ACA Thr 230	CAA Gln	GCA Ala	TTA Leu	AAA Lys	GAC Asp 235	ATA Ile	ATG Met	AAT Asn	ATT Ile	GAC Asp 240	AGA Arg	GAT Asp	TTC Phe	777			
ATT Ile	GGT Gly 245	TAT Tyr	ATT Ile	GAA Glu	GTG Val 250	TTA Leu	GGG Gly	TAT Tyr	TGG Trp	AAA Lys 255	GAC Asp	AAC Asn	CCT Pro	AAA Lys	GAC Asp	825			
AAT Asn 260	ATC Ile	TTA Leu	CCA Pro	GAC Asp 265	AAA Lys	GAG Glu	GTT Val	AGC Ser	TTT Phe 270	TTT Phe	GTA Val	TTC Phe	CAA Gln	AAC Asn	GAA Glu 275	873			
CCT Pro	AGT Ser	AGC Ser	ACA Thr 280	TTT Phe	GAT Asp	TTG Leu	AAA Lys	AAC Asn 285	CAC His	TTA Leu	TTG Leu	ATA Ile	TGG Trp 290	GGT Gly	AAA Lys	921			
CAA Gln	TTC Phe	AGA Arg 295	CAA Gln	GTA Val	GCG Ala	ATT Ile	TGC Cys 300	TAT Tyr	GGC Gly	GGA Gly	CAA Gln	TTG Leu 305	ATT Ile	GCT Ala	AAT Asn	969			
AAG Lys	AAT Asn 310	AAG Lys	ACT Thr	TAT Tyr	AGG Arg	ATA Ile 315	GAT Asp	TTG Leu	ATA Ile	AGT Ser	TGC Cys 320	AGA Arg	CCT Pro	GAT Asp	AAT Asn	1017			
TTT Phe	GGT Gly 325	GAG Glu	GTT Val	TGG Trp	GCT Ala 330	AAA Lys	TTC Phe 335	ACA Thr	GGG Gly	ATT Ile 335	AAA Lys	TTT Phe	TCA Ser	GTT Val	CCT Pro	1065			
AGC Ser 340	GAC Asp	TTA Leu	CCA Pro	CAA Gln 345	GCT Ala	CTC Leu	ACA Thr	CGC Arg	ATA Ile 350	AAT Asn	GAC Asp	AGC Ser	GTT Val	TAT Tyr 355	ACT Thr	1113			
TTT Phe	CTC Leu	TCT Ser	AGG Arg 360	AAT Asn	AAA Lys	GAG Glu	GGT Gly	ATC Ile 365	GGT Gly	CTT Leu	AAT Asn	AAA Lys	CTC Leu 370	GCT Ala	CTC Leu	1161			
AAT Asn	AAA Lys	GTC Val 375	GTT Val	AAG Lys	ACA Thr	GAA Glu	TTA Leu 380	AAA Lys	GCG Ala	ACT Thr	TGT Cys	ATG Met 385	CCC Pro	TAT Tyr	GAT Asp	1209			
TAC Tyr	TCT Ser 390	AAA Lys	TTG Leu	GGT Gly	ATA Ile	GAG Glu	ACT Thr 395	ATT Ile	GGC Gly	GAG Glu	GAC Asp 400	ATT Ile	AGA Arg	AGC Ser	AAT Asn	1257			
ATT Ile	AAA Lys 405	GCA Ala	TTA Leu	CAG Gln	AAA Lys 410	ATG Met	TCT Ser 415	CGT Arg	GGG Gly	TAT Tyr 415	GGA Gly	CAC His	CCT Pro	AAA Lys	GAG Glu	1305			
TTC Phe 420	TTT Phe	TTG Leu	GAC Asp	GCA Ala 425	ATG Met	ATA Ile	AAA Lys	AAA Lys	CAG Gln 430	GAA Glu	AAT Asn 435	GCG Ala	ATT Ile	AAA Lys	CGC Arg 435	1353			
ATA Ile	GAA Glu	GCA Ala	CGA Arg 440	AAA Lys	TGT Cys	GCG Ala	GTA Val 445	AGC Ser	GAT Asp 445	GAC Asp	TTC Phe	AAA Lys	CAA Gln 450	GGT Gly 450	ATG Met	1401			

Lys 65	Tyr	Asp	Met	Ser	His 70	Lys	Thr	Ile	Lys	Gly 75	Ser	Thr	Ile	Glu	Ser 80
Ser	Asn	Leu	Ile	Ser 85	Ile	Tyr	Lys	Lys	Ile 90	Ala	Ser	Gly	Leu	Pro 95	Phe
Gly	Thr	Ile	Ser 100	Ala	Phe	Arg	Pro	Phe 105	Lys	Asp	Ala	Phe	Tyr 110	Lys	Asp
Phe	Thr	Glu	Lys 115	Glu	Gln	Asn	Ala 120	Leu	Ile	Tyr	Ala	Tyr 125	Lys	Ser	Gly
Ala	Asp 130	Pro	Lys	Asn	Ala	Asp 135	Ile	Ile	Ala	Lys	Tyr 140	Trp	Leu	Ser	Gln
Ser 145	Val	Asp	Leu	Asp	Pro 150	Tyr	Asp	Pro	Ile	Lys 155	Val	Val	Asp	Phe 160	Phe
His	Pro	Gln	Pro	Glu 165	Asn	Gly	Lys	Glu	Thr 170	Thr	Lys	Phe	Lys 175	Asn	Tyr
Lys	Asp	Arg	Ile 180	Glu	Asn	Ile	Tyr	Ala 185	Thr	Leu	Tyr	Asn	Thr 190	Leu	Gly
Arg	Gly	Tyr 195	Val	Asp	Lys	Phe	Phe 200	Lys	Lys	Glu	Ala	Thr 205	Met	Arg	Asp
Phe 210	Met	Ser	Ser	Asp	Lys	Phe 215	Val	Glu	Arg	Tyr 220	Arg	Tyr	Thr	Arg	Lys
Glu 225	Asn	Met	Ala	Arg	Thr 230	Gln	Ala	Leu	Lys	Asp 235	Ile	Met	Asn	Ile	Asp
Arg	Asp	Phe	Ile 245	Gly	Tyr	Ile	Glu	Val	Leu 250	Gly	Tyr	Trp	Lys	Asp 255	Asn
Pro	Lys	Asp	Asn 260	Ile	Leu	Pro	Asp 265	Lys	Glu	Val	Ser	Phe	Phe 270	Val	Phe
Gln	Asn 275	Glu	Pro	Ser	Ser	Thr	Phe 280	Asp	Leu	Lys	Asn	His 285	Leu	Leu	Ile
Trp	Gly 290	Lys	Gln	Phe	Arg	Gln	Val 295	Ala	Ile	Cys	Tyr 300	Gly	Gly	Gln	Leu
Ile 305	Ala	Asn	Lys	Asn	Lys 310	Thr	Tyr	Arg	Ile	Asp 315	Leu	Ile	Ser	Cys	Arg
Pro	Asp	Asn	Phe 325	Gly	Glu	Val	Trp	Ala	Lys 330	Phe	Thr	Gly	Ile	Lys 335	Phe
Ser	Val	Pro	Ser 340	Asp	Leu	Pro	Gln	Ala 345	Leu	Thr	Arg	Ile	Asn 350	Asp	Ser
Val	Tyr 355	Thr	Phe	Leu	Ser	Arg	Asn 360	Lys	Glu	Gly	Ile	Gly 365	Leu	Asn	Lys
Leu	Ala 370	Leu	Asn	Lys	Val	Val	Lys 375	Thr	Glu	Leu	Lys 380	Ala	Thr	Cys	Met
Pro 385	Tyr	Asp	Tyr	Ser	Lys 390	Leu	Gly	Ile	Glu	Thr 395	Ile	Gly	Glu	Asp	Ile
Arg	Ser	Asn	Ile 405	Lys	Ala	Leu	Gln	Lys	Met 410	Ser	Arg	Gly	Tyr	Gly 415	His
Pro	Lys	Glu	Phe 420	Phe	Leu	Asp	Ala	Met 425	Ile	Lys	Lys	Gln	Glu 430	Asn	Ala
Ile	Lys 435	Arg	Ile	Glu	Ala	Arg	Lys 440	Cys	Ala	Val	Ser	Asp 445	Asp	Phe	Lys
Gln	Gly 450	Met	Lys	Arg	Asn	Ile 455	Lys	Val	Asn	Asn	Leu 460	Val	Lys	Ala	Met
Arg 465	Gln	Gly	Lys	Lys	Val 470	Ser	Arg	Thr	Leu	Ile 475	Ala	Lys	Val	Leu	Ala
Asn	Thr	Ile	Asp 485	Thr	Asp	Ala	Gly	Tyr	Cys 490	Phe	Ile	Ser	Pro	Thr 495	Asp
Leu	Ala	Thr	Gln 500	Leu	Gly	Asn	Ile	Ser 505	Pro	Arg	Leu	Ser	Lys 510	Ser	Ile
Val	Thr	Ala 515	Ile	Glu	Gln	Ala	Glu 520	Gly	Val	Arg	Leu	Asn 525	Tyr	Ala	Leu

Ile	Asp	Lys	Ile	Thr	Tyr	Asn	Ser	Leu	His	Asn	Ile	Leu	Ser	Phe	Ile
530						535					540				
Phe	Asp	Ile	Asp	Asn	Pro	Leu	Ser	Asp	Gln	Val	Phe	Glu	Arg	Leu	Val
545					550				555						560
Ile	Glu	Val	Pro	Arg	Glu	Ala	Leu	Lys	Asn	Val	Lys	Leu	Pro	Gln	Ile
			565					570						575	
Lys	Asn	Val	Leu	Thr	Ser	Gln	Ile	Phe	Asp	Gly	Ala	Tyr	His	Phe	Lys
		580						585					590		

Ser

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1063 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...1014
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

TGCTAAATTG TG ATG TTT CAC AAA GCC CTT ATT ACC TTT ATC GTT CTA TGG	51
Met Phe His Lys Ala Leu Ile Thr Phe Ile Val Leu Trp	
1 5 10	
TTT TTT TTG AAT GGC TTA GGG GCT TAT GAT TTC AAG CAT TGT CAA GCG	99
Phe Phe Leu Asn Gly Leu Gly Ala Tyr Asp Phe Lys His Cys Gln Ala	
15 20 25	
TTT TTT AAA AAA GCG AGC CTT CAA AAA GGA GGC GTG GCT TTA AAA GAA	147
Phe Phe Lys Lys Ala Ser Leu Gln Lys Gly Gly Val Ala Leu Lys Glu	
30 35 40 45	
TTG CCT AAA GGC GTG TAT TTG TAT TAT TCC AAA ACC TAT CCC AAA CAC	195
Leu Pro Lys Gly Val Tyr Leu Tyr Tyr Ser Lys Thr Tyr Pro Lys His	
50 55 60	
GCC AAA GTC ATC AAA TCC GAT CCC TTT GTA GGG TTG TAT TTG TTG CAA	243
Ala Lys Val Ile Lys Ser Asp Pro Phe Val Gly Leu Tyr Leu Leu Gln	
65 70 75	
AGC GCA CCA AGC GAG TAT GTT TAT ACC TTA AGG GAT TTA GAC AAA GAC	291
Ser Ala Pro Ser Glu Tyr Val Tyr Thr Leu Arg Asp Leu Asp Lys Asp	
80 85 90	
GCC CTT ATA AGG CCA ATG GCT AGC ATA GGG GAT AAA GAA GCC CTA GAA	339
Ala Leu Ile Arg Pro Met Ala Ser Ile Gly Asp Lys Glu Ala Leu Glu	
95 100 105	
ACG CGA TTA TTG GTG GGG CAA AGA GGC TAT GAG CGC TAC GCT CAA ATT	387

[illegible]

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

Met	Phe	His	Lys	Ala	Leu	Ile	Thr	Phe	Ile	Val	Leu	Trp	Phe	Phe	Leu	1	5	10	15
Asn	Gly	Leu	Gly	Ala	Tyr	Asp	Phe	Lys	His	Cys	Gln	Ala	Phe	Phe	Lys	20	25	30	
Lys	Ala	Ser	Leu	Gln	Lys	Gly	Gly	Val	Ala	Leu	Lys	Glu	Leu	Pro	Lys	35	40	45	
Gly	Val	Tyr	Leu	Tyr	Tyr	Ser	Lys	Thr	Tyr	Pro	Lys	His	Ala	Lys	Val	50	55	60	
Ile	Lys	Ser	Asp	Pro	Phe	Val	Gly	Leu	Tyr	Leu	Gln	Ser	Ala	Pro		65	70	75	80
Ser	Glu	Tyr	Val	Tyr	Thr	Leu	Arg	Asp	Leu	Asp	Lys	Asp	Ala	Leu	Ile	85	90	95	
Arg	Pro	Met	Ala	Ser	Ile	Gly	Asp	Lys	Glu	Ala	Leu	Glu	Thr	Arg	Leu	100	105	110	
Leu	Val	Gly	Gln	Arg	Gly	Tyr	Glu	Arg	Tyr	Ala	Gln	Ile	Ser	Gln	Lys	115	120	125	
Thr	Gln	Lys	Asn	Gly	Val	Ile	Ser	Asn	Ile	Cys	Tyr	Gln	Met	Leu	Gly	130	135	140	
Leu	Gly	Val	Gly	Gly	Asn	Gly	Phe	Ile	Glu	Thr	Lys	Phe	Ile	Lys	Arg	145	150	155	160
Phe	Leu	Asn	Gln	Gln	Glu	Pro	Tyr	Tyr	Gly	Asp	Ile	Gly	Val	Arg	Leu	165	170	175	
Glu	Glu	His	His	Lys	Arg	Leu	Val	Val	Val	Gln	Phe	Asp	Pro	Phe	Phe	180	185	190	
Pro	Lys	Asn	Pro	Phe	Leu	Lys	Asn	Asp	Glu	Ile	Leu	Ala	Ile	Asn	His	195	200	205	
Gln	Lys	Ile	His	Ser	Leu	Ala	Glu	Phe	Glu	Trp	Val	Val	Ser	Asn	Leu	210	215	220	
Lys	Tyr	Gln	Ser	Leu	Ala	Lys	Val	Glu	Ile	Lys	Arg	Asn	His	Lys	Val	225	230	235	240
Lys	Glu	Val	Thr	Leu	Lys	Val	Asn	Lys	Arg	Tyr	Gly	Gly	Phe	Leu	Leu	245	250	255	
Lys	Asp	Thr	Phe	Leu	Glu	Arg	Tyr	Gly	Ile	Ala	Leu	Asp	Glu	Arg	Phe	260	265	270	
Ile	Ile	Thr	Lys	Ile	Gly	Ala	His	Leu	Pro	Lys	Gly	Leu	Asp	Phe	Leu	275	280	285	
Lys	Leu	Gly	Asp	Arg	Ile	Leu	Trp	Val	Asn	Tyr	Lys	Ser	Val	Ala	Ser	290	295	300	
Asn	Pro	Lys	Ala	Leu	Arg	Glu	Ala	Leu	Ser	Ala	Pro	Lys	Ile	Glu	Leu	305	310	315	320
Leu	Val	Leu	Arg	Lys	Gly	Phe	Glu	Phe	Tyr	Ile	Lys	Val	Arg			325	330		

(2) INFORMATION FOR SEQ ID NO:433:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 52...1104
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

TAGTCTTGCG TAAAGGCTTT GAATTTTACA TTAAAGTCCG TTGAAGTATT G ATG AAA	57
Met Lys	
1	
AAT GAC GCT TAT GAA ATT ATT CTT TCT TGG TTT ATC ACG CCT CTC ACG	105
Asn Asp Ala Tyr Glu Ile Ile Leu Ser Trp Phe Ile Thr Pro Leu Thr	
5 10 15	
GCG ATT TTA GGG CGT TTC GCT GAA TTT TTT CTC TAC ACT TTG CAT GCG	153
Ala Ile Leu Gly Arg Phe Ala Glu Phe Phe Leu Tyr Thr Leu His Ala	
20 25 30	
CAA TTG GTG TTT AAT AGC GTG GTC GCT TTG GCG TTC ATG CTC TTT GCT	201
Gln Leu Val Phe Asn Ser Val Val Ala Leu Ala Phe Met Leu Phe Ala	
35 40 45 50	
TAT AGG AGT TTG AAA GAA CAG AAT TTC TTC AGC GCT AGC GCG CTA ACA	249
Tyr Arg Ser Leu Lys Glu Gln Asn Phe Phe Ser Ala Ser Ala Leu Thr	
55 60 65	
GAA GCG TTA TTG TTT GTG GGG TTT TTT GCA CTT TTC AAC TAC GCT TTA	297
Glu Ala Leu Leu Phe Val Gly Phe Phe Ala Leu Phe Asn Tyr Ala Leu	
70 75 80	
AAA AAT CCC ATG CAT TTT TAT GAA TTT TTC CAA AAC GCT ATT TTT ATT	345
Lys Asn Pro Met His Phe Tyr Glu Phe Phe Gln Asn Ala Ile Phe Ile	
85 90 95	
GCG CCT AAC ATG ATC GCG CAA AGC CTC TCT CAA AGC TTG AGT AAC TTT	393
Ala Pro Asn Met Ile Ala Gln Ser Leu Ser Gln Ser Leu Ser Asn Phe	
100 105 110	
TCT GAC CAT GCG CTT TCT TTA GAT TTT ATC TTT AAT CAT GGT TTT TAT	441
Ser Asp His Ala Leu Ser Leu Asp Phe Ile Phe Asn His Gly Phe Tyr	
115 120 125 130	
GCC CTT AGT TTC ATC AGC GAT TTG AGC CAT AAT GAA ATG TCT GTG TGG	489
Ala Leu Ser Phe Ile Ser Asp Leu Ser His Asn Glu Met Ser Val Trp	
135 140 145	
CTT TTT TTA AGC GTT TTG CAA GGG CTT TTT TTG AGC GTG CTG TTT GCA	537
Leu Phe Leu Ser Val Leu Gln Gly Leu Phe Leu Ser Val Leu Phe Ala	

150						155						160						
ATC	ATC	ATT	TTA	GTG	TAT	TTA	GAA	GTG	CAT	GTG	TGG	TGC	TCT	TTA	GGG	585		
Ile	Ile	Ile	Leu	Val	Tyr	Leu	Glu	Val	His	Val	Trp	Cys	Ser	Leu	Gly			
165						170						175						
GTG	CTG	TTT	TTA	GCG	TTT	GGG	TTT	TTT	AAA	ACC	TGG	AGG	AGC	GTT	GTG	633		
Val	Leu	Phe	Leu	Ala	Phe	Gly	Phe	Phe	Lys	Thr	Trp	Arg	Ser	Val	Val			
180						185						190						
GTT	ATA	TGC	CTA	AAA	AAG	TGC	TTC	GCT	CTT	GGG	TTT	TAC	AAG	CCT	TTT	681		
Val	Ile	Cys	Leu	Lys	Lys	Cys	Phe	Ala	Leu	Gly	Phe	Tyr	Lys	Pro	Phe			
195						200						205				210		
TTG	TTG	TTG	GTA	GGG	TTT	TTG	AAT	GTG	TCG	GTT	ACT	AAG	GCT	TTA	ATA	729		
Leu	Leu	Leu	Val	Gly	Phe	Leu	Asn	Val	Ser	Val	Thr	Lys	Ala	Leu	Ile			
215						220						225						
GAC	GCT	CAT	ATG	CAA	GAA	AAA	CAA	GAC	TTA	AGC	CTT	TTA	TTG	GTG	GTA	777		
Asp	Ala	His	Met	Gln	Glu	Lys	Gln	Asp	Leu	Ser	Leu	Leu	Leu	Val	Val			
230						235						240						
GCG	TTA	TTT	TTG	TGT	TGC	GTT	TTT	ATC	ATC	GGC	GTG	CCT	TTT	TTC	ATC	825		
Ala	Leu	Phe	Leu	Cys	Cys	Val	Phe	Ile	Ile	Gly	Val	Pro	Phe	Phe	Ile			
245						250						255						
AAC	GCT	TTG	TTT	AGG	GTG	CAA	AAC	AGC	CTT	AAA	GAA	ACT	TAC	AAA	CTC	873		
Asn	Ala	Leu	Phe	Arg	Val	Gln	Asn	Ser	Leu	Lys	Glu	Thr	Tyr	Lys	Leu			
260						265						270						
GCC	ACC	AAT	TTG	AGT	GCC	AAC	CTC	AGC	CAA	AAC	GCC	CTT	AAT	TCC	TTA	921		
Ala	Thr	Asn	Leu	Ser	Ala	Asn	Leu	Ser	Gln	Asn	Ala	Leu	Asn	Ser	Leu			
275						280						285				290		
CAA	TAC	ATC	ACG	ACC	CCA	CCC	GCT	TCT	TCT	AGC	GTT	TCT	TCT	TCT	ATG	969		
Gln	Tyr	Ile	Thr	Thr	Pro	Pro	Ala	Ser	Ser	Ser	Val	Ser	Ser	Ser	Met			
295						300						305						
AGT	GAA	AGC	GTC	TCT	AAA	GAA	AAA	GAA	ACG	CAT	TCC	CCC	ACA	TTT	AAG	1017		
Ser	Glu	Ser	Val	Ser	Lys	Glu	Lys	Glu	Thr	His	Ser	Pro	Thr	Phe	Lys			
310						315						320						
GTA	GAA	ACC	ACT	CAA	TTA	GAT	GTA	AAA	ATC	CCA	AAT	TTC	AAG	CAA	AAA	1065		
Val	Glu	Thr	Thr	Gln	Leu	Asp	Val	Lys	Ile	Pro	Asn	Phe	Lys	Gln	Lys			
325						330						335						
AAG	GTT	AAA	AAG	GAT	ACA	ATA	AAT	ACA	AAA	AAT	GAA	ATT	TAA	TAA	TAA	GG	1116	
Lys	Val	Lys	Lys	Asp	Thr	Ile	Asn	Thr	Lys	Asn	Glu	Ile						
340						345						350						
AATTTAATGA GAATTTT																1133		

(2) INFORMATION FOR SEQ ID NO:434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met Lys Asn Asp Ala Tyr Glu Ile Ile Leu Ser Trp Phe Ile Thr Pro
1 5 10 15
Leu Thr Ala Ile Leu Gly Arg Phe Ala Glu Phe Phe Leu Tyr Thr Leu
20 25 30
His Ala Gln Leu Val Phe Asn Ser Val Val Ala Leu Ala Phe Met Leu
35 40 45
Phe Ala Tyr Arg Ser Leu Lys Glu Gln Asn Phe Phe Ser Ala Ser Ala
50 55 60
Leu Thr Glu Ala Leu Leu Phe Val Gly Phe Phe Ala Leu Phe Asn Tyr
65 70 75 80
Ala Leu Lys Asn Pro Met His Phe Tyr Glu Phe Phe Gln Asn Ala Ile
85 90 95
Phe Ile Ala Pro Asn Met Ile Ala Gln Ser Leu Ser Gln Ser Leu Ser
100 105 110
Asn Phe Ser Asp His Ala Leu Ser Leu Asp Phe Ile Phe Asn His Gly
115 120 125
Phe Tyr Ala Leu Ser Phe Ile Ser Asp Leu Ser His Asn Glu Met Ser
130 135 140
Val Trp Leu Phe Leu Ser Val Leu Gln Gly Leu Phe Leu Ser Val Leu
145 150 155 160
Phe Ala Ile Ile Ile Leu Val Tyr Leu Glu Val His Val Trp Cys Ser
165 170 175
Leu Gly Val Leu Phe Leu Ala Phe Gly Phe Phe Lys Thr Trp Arg Ser
180 185 190
Val Val Val Ile Cys Leu Lys Lys Cys Phe Ala Leu Gly Phe Tyr Lys
195 200 205
Pro Phe Leu Leu Leu Val Gly Phe Leu Asn Val Ser Val Thr Lys Ala
210 215 220
Leu Ile Asp Ala His Met Gln Glu Lys Gln Asp Leu Ser Leu Leu Leu
225 230 235 240
Val Val Ala Leu Phe Leu Cys Cys Val Phe Ile Ile Gly Val Pro Phe
245 250 255
Phe Ile Asn Ala Leu Phe Arg Val Gln Asn Ser Leu Lys Glu Thr Tyr
260 265 270
Lys Leu Ala Thr Asn Leu Ser Ala Asn Leu Ser Gln Asn Ala Leu Asn
275 280 285
Ser Leu Gln Tyr Ile Thr Thr Pro Pro Ala Ser Ser Ser Val Ser Ser
290 295 300
Ser Met Ser Glu Ser Val Ser Lys Glu Lys Glu Thr His Ser Pro Thr
305 310 315 320
Phe Lys Val Glu Thr Thr Gln Leu Asp Val Lys Ile Pro Asn Phe Lys
325 330 335
Gln Lys Lys Val Lys Lys Asp Thr Ile Asn Thr Lys Asn Glu Ile
340 345 350

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 50...748
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

CCCTTTCAAA CAAGGCCCTA AAAATTACGA AGAAAACCTG ATTTTCCCC ATG GAT AAC	58
Met Asp Asn	
1	
CCT AAA GGC ATT GAT GGT TTT ACT AAC CTT AAA GAA AAA GAC ATC GCC	106
Pro Lys Gly Ile Asp Gly Phe Thr Asn Leu Lys Glu Lys Asp Ile Ala	
5 10 15	
ACT AAT GAA AAT AAG CTT TTA CGC ACC ATT ACA GCG GAT AAA ATG ATA	154
Thr Asn Glu Asn Lys Leu Leu Arg Thr Ile Thr Ala Asp Lys Met Ile	
20 25 30 35	
CCC GCC TTT CTC ATC ACG CCT ATT TCT AGC CAG ATC GCT GGT AAA GTC	202
Pro Ala Phe Leu Ile Thr Pro Ile Ser Ser Gln Ile Ala Gly Lys Val	
40 45 50	
ATC GCG CAG GTG GAG AGC GAT ATT TTT GCT CAC ATG GGC AAG GCC GTC	250
Ile Ala Gln Val Glu Ser Asp Ile Phe Ala His Met Gly Lys Ala Val	
55 60 65	
TTA ATC CCC AAA GGC TCT AAA GTC ATA GGT TAT TAC AGC AAC AAT AAC	298
Leu Ile Pro Lys Gly Ser Lys Val Ile Gly Tyr Tyr Ser Asn Asn Asn	
70 75 80	
AAA ATG GGC GAA TAC CGC TTG GAT ATT GTA TGG AGC CGC ATC ATC ACT	346
Lys Met Gly Glu Tyr Arg Leu Asp Ile Val Trp Ser Arg Ile Ile Thr	
85 90 95	
CCC CAT GGC ATC AAT ATC ATG CTC ACT AAC GCT AAA GGG GCG GAC ATT	394
Pro His Gly Ile Asn Ile Met Leu Thr Asn Ala Lys Gly Ala Asp Ile	
100 105 110 115	
AAA GGC TAT AAC GGC TTG GTG GGG GAA TTG ATT GAA AGG AAT TTC CAG	442
Lys Gly Tyr Asn Gly Leu Val Gly Glu Leu Ile Glu Arg Asn Phe Gln	
120 125 130	
CGC TAT GGC GTG CCG TTA CTG CTT TCT ACT CTC ACT AAC GGC CTA TTG	490
Arg Tyr Gly Val Pro Leu Leu Leu Ser Thr Leu Thr Asn Gly Leu Leu	
135 140 145	
ATT GGG ATC ACT TCG GCT TTA AAC AAC AGA GGC AAT AAA GAA GGA GCC	538
Ile Gly Ile Thr Ser Ala Leu Asn Asn Arg Gly Asn Lys Glu Gly Ala	
150 155 160	
ACC AAT TTC TTT GGG GAT TAT CTT TTA ATG CAA TTG ATG AGG CAA AGC	586
Thr Asn Phe Phe Gly Asp Tyr Leu Leu Met Gln Leu Met Arg Gln Ser	
165 170 175	

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 27...1169
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

AAATAAAATT CAATAAAGGA AAAATA ATG AAA GAA AAA ATC GCT TTA ATC ACC	53
Met Lys Glu Lys Ile Ala Leu Ile Thr	
1 5	
GGG GTT ACC GGG CAA GAC GGG AGC TAT CTG GCT GAA TAC TTG CTG AAT	101
Gly Val Thr Gly Gln Asp Gly Ser Tyr Leu Ala Glu Tyr Leu Leu Asn	
10 15 20 25	
TTG GGT TAT GAA GTG CAT GGG TTA AAA AGG CGC TCT TCT AGC ATC AAC	149
Leu Gly Tyr Glu Val His Gly Leu Lys Arg Arg Ser Ser Ser Ile Asn	
30 35 40	
ACT TCT AGG ATC GAT CAT CTG TAT GAA GAT TTG CAT AGC GAT CAT AAA	197
Thr Ser Arg Ile Asp His Leu Tyr Glu Asp Leu His Ser Asp His Lys	
45 50 55	
AGG CGT TTT TTC TTA CAC TAT GGG GAT ATG ACC GAT AGC TCT AAT CTT	245
Arg Arg Phe Phe Leu His Tyr Gly Asp Met Thr Asp Ser Ser Asn Leu	
60 65 70	
ATC CAT TTA ATC GCT ACC ACT AAG CCT ACA GAG ATT TAT AAT TTA GCC	293
Ile His Leu Ile Ala Thr Thr Lys Pro Thr Glu Ile Tyr Asn Leu Ala	
75 80 85	
GCT CAA AGC CAT GTA AAA GTC TCT TTT GAA ACC CCC GAA TAC ACC GCT	341
Ala Gln Ser His Val Lys Val Ser Phe Glu Thr Pro Glu Tyr Thr Ala	
90 95 100 105	
AAC GCT GAT GGT ATT GGC ACG CTA AGG ATT TTA GAA GCC ATG CGG ATT	389
Asn Ala Asp Gly Ile Gly Thr Leu Arg Ile Leu Glu Ala Met Arg Ile	
110 115 120	
TTA GGA TTA GAA AAG AAA ACG CGC TTT TAT CAA GCC AGC ACG AGC GAA	437
Leu Gly Leu Glu Lys Lys Thr Arg Phe Tyr Gln Ala Ser Thr Ser Glu	
125 130 135	
TTG TAT GGC GAA GTC TTA GAA ACC CCG CAA AAT GAA AAC ACC CCC TTT	485
Leu Tyr Gly Glu Val Leu Glu Thr Pro Gln Asn Glu Asn Thr Pro Phe	

	140					145					150					
AAC Asn	CCA Pro	CGA Arg	AGC Ser	CCC Pro	TAT Tyr	GCG Ala	GTC Val	GCT Ala	AAA Lys	ATG Met	TAT Tyr	GCC Ala	TTT Phe	TAC Tyr	ATC Ile	533
	155					160				165						
ACC Thr	AAA Lys	AAT Asn	TAC Tyr	AGA Arg	GAG Glu	GCC Ala	TAT Tyr	AAC Asn	TTG Leu	TTT Phe	GCG Ala	GTT Val	AAT Asn	GGC Gly	ATT Ile	581
170					175					180					185	
CTT Leu	TTT Phe	AAC Asn	CAT His	GAG Glu	AGC Ser	AGG Arg	GTA Val	AGG Arg	GGC Gly	GAA Glu	ACT Thr	TTT Phe	GTA Val	ACC Thr	CGT Arg	629
				190					195					200		
AAA Lys	ATC Ile	ACA Thr	CGA Arg	GCC Ala	GCT Ala	AGC Ser	GCG Ala	ATA Ile	GCG Ala	TAT Tyr	AAC Asn	TTA Leu	ACG Thr	GAT Asp	TGC Cys	677
			205					210					215			
TTG Leu	TAT Tyr	TTA Leu	GGG Gly	AAT Asn	TTA Leu	GAC Asp	GCT Ala	AAA Lys	AGA Arg	GAC Asp	TGG Trp	GGG Gly	CAT His	GCC Ala	AAA Lys	725
		220				225						230				
GAT Asp	TAC Tyr	GTG Val	AAA Lys	ATG Met	ATG Met	CAT His	TTA Leu	ATG Met	CTC Leu	CAA Gln	GCG Ala	CCC Pro	ATC Ile	CCA Pro	CAA Gln	773
	235					240					245					
GAT Asp	TAT Tyr	GTG Val	ATC Ile	GCC Ala	ACA Thr	GGA Gly	AAG Lys	ACC Thr	ACA Thr	AGC Ser	GTG Val	CGC Arg	GAT Asp	TTT Phe	GTG Val	821
250					255					260					265	
AAA Lys	ATG Met	AGC Ser	TTT Phe	GAA Glu	TTT Phe	ATC Ile	GGT Gly	ATC Ile	AAT Asn	TTA Leu	GAA Glu	TTT Phe	CAA Gln	AAT Asn	ACA Thr	869
				270					275					280		
GGG Gly	ATT Ile	AAA Lys	GAA Glu	ATC Ile	GGT Gly	TTG Leu	ATT Ile	AAA Lys	AGC Ser	GTT Val	GAT Asp	GAA Glu	AAA Lys	AGA Arg	GCG Ala	917
			285					290					295			
AAC Asn	GCT Ala	TTA Leu	AAA Lys	TTG Leu	AAC Asn	TTA Leu	AGC Ser	CAT His	TTA Leu	AAA Lys	AAA Lys	GGC Gly	CAA Gln	ATC Ile	GTG Val	965
		300					305					310				
GTG Val	CGC Arg	ATA Ile	GAC Asp	GAG Glu	CGT Arg	TAT Tyr	TTC Phe	AGG Arg	CCT Pro	ACC Thr	GAA Glu	GTG Val	GAT Asp	TTG Leu	CTT Leu	1013
	315					320					325					
TTA Leu	GGC Gly	GAT Asp	CCC Pro	ACT Thr	AAG Lys	GCA Ala	GAG Glu	AAA Lys	GAG Glu	CTA Leu	GAC Asp	TGG Trp	GTT Val	AGG Arg	GAA Glu	1061
330					335					340					345	
TAC Tyr	GAT Asp	TTA Leu	AAA Lys	GAG Glu	TTG Leu	GTT Val	AAG Lys	GAC Asp	ATG Met	TTA Leu	GAA Glu	TAC Tyr	GAT Asp	TTA Leu	AAA Lys	1109
				350					355					360		
GAA Glu	TGC Cys	CAA Gln	AAA Lys	AAC Asn	CTT Leu	TAC Tyr	TTG Leu	CAA Gln	GAT Asp	GGG Gly	GGT Gly	TAT Tyr	ATT Ile	TTA Leu	AGG Arg	1157
			365					370					375			

AAT TTT TAT GAA TGAGATTATT TTAATCACTG GTGCCTATGG CATGGTGGGG CAGAA 1214
Asn Phe Tyr Glu
380

CACGGCGTTG TATTT 1229

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

```

Met Lys Glu Lys Ile Ala Leu Ile Thr Gly Val Thr Gly Gln Asp Gly
 1      5      10      15
Ser Tyr Leu Ala Glu Tyr Leu Leu Asn Leu Gly Tyr Glu Val His Gly
      20      25      30
Leu Lys Arg Arg Ser Ser Ser Ile Asn Thr Ser Arg Ile Asp His Leu
      35      40      45
Tyr Glu Asp Leu His Ser Asp His Lys Arg Arg Phe Phe Leu His Tyr
      50      55      60
Gly Asp Met Thr Asp Ser Ser Asn Leu Ile His Leu Ile Ala Thr Thr
65      70      75      80
Lys Pro Thr Glu Ile Tyr Asn Leu Ala Ala Gln Ser His Val Lys Val
      85      90      95
Ser Phe Glu Thr Pro Glu Tyr Thr Ala Asn Ala Asp Gly Ile Gly Thr
      100      105      110
Leu Arg Ile Leu Glu Ala Met Arg Ile Leu Gly Leu Glu Lys Lys Thr
      115      120      125
Arg Phe Tyr Gln Ala Ser Thr Ser Glu Leu Tyr Gly Glu Val Leu Glu
      130      135      140
Thr Pro Gln Asn Glu Asn Thr Pro Phe Asn Pro Arg Ser Pro Tyr Ala
145      150      155      160
Val Ala Lys Met Tyr Ala Phe Tyr Ile Thr Lys Asn Tyr Arg Glu Ala
      165      170      175
Tyr Asn Leu Phe Ala Val Asn Gly Ile Leu Phe Asn His Glu Ser Arg
      180      185      190
Val Arg Gly Glu Thr Phe Val Thr Arg Lys Ile Thr Arg Ala Ala Ser
      195      200      205
Ala Ile Ala Tyr Asn Leu Thr Asp Cys Leu Tyr Leu Gly Asn Leu Asp
      210      215      220
Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val Lys Met Met His
225      230      235      240
Leu Met Leu Gln Ala Pro Ile Pro Gln Asp Tyr Val Ile Ala Thr Gly
      245      250      255
Lys Thr Thr Ser Val Arg Asp Phe Val Lys Met Ser Phe Glu Phe Ile
      260      265      270
Gly Ile Asn Leu Glu Phe Gln Asn Thr Gly Ile Lys Glu Ile Gly Leu
      275      280      285
Ile Lys Ser Val Asp Glu Lys Arg Ala Asn Ala Leu Lys Leu Asn Leu
      290      295      300
Ser His Leu Lys Lys Gly Gln Ile Val Val Arg Ile Asp Glu Arg Tyr
305      310      315      320
Phe Arg Pro Thr Glu Val Asp Leu Leu Leu Gly Asp Pro Thr Lys Ala
      325      330      335
Glu Lys Glu Leu Asp Trp Val Arg Glu Tyr Asp Leu Lys Glu Leu Val
      340      345      350
Lys Asp Met Leu Glu Tyr Asp Leu Lys Glu Cys Gln Lys Asn Leu Tyr
      355      360      365

```

Leu Gln Asp Gly Gly Tyr Ile Leu Arg Asn Phe Tyr Glu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...1065
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

CAGCAGTATC CCTATCGGTC AAGCCTTAAT GCGTATTTTC AACCTACAA TCATCAAAAA	60
AGGATAAAA ATG GAT AGC GTA ACT CTA GCA TGC GGG AAC GGA GGG AAA GAA	111
Met Asp Ser Val Thr Leu Ala Cys Gly Asn Gly Gly Lys Glu	
1 5 10	
ACA AAC GCT TTG ATT GAG CGA GTC TTT ATG CCC TAT TTA AAA GAA TGG	159
Thr Asn Ala Leu Ile Glu Arg Val Phe Met Pro Tyr Leu Lys Glu Trp	
15 20 25 30	
ATT GTT GCA TTT GAT GAA GAC GCC CCT AAA TTT GAA GCT AGT GGG GAA	207
Ile Val Ala Phe Asp Glu Asp Ala Pro Lys Phe Glu Ala Ser Gly Glu	
35 40 45	
TAT TGC GTG AGC ACG GAT AGT TTT GTC ATC ACG CCC TTA ATT TTT AAT	255
Tyr Cys Val Ser Thr Asp Ser Phe Val Ile Thr Pro Leu Ile Phe Asn	
50 55 60	
GGG GGC GAT ATA GGC AAG CTT TGC GTT TGC GGG AGT GCG AAT GAT GTG	303
Gly Gly Asp Ile Gly Lys Leu Cys Val Cys Gly Ser Ala Asn Asp Val	
65 70 75	
AGC GTG CAA GGG GGC GAA CCT TTG TAT TTG AAT ATG GGT TTT ATT TTA	351
Ser Val Gln Gly Gly Glu Pro Leu Tyr Leu Asn Met Gly Phe Ile Leu	
80 85 90	
GAA GAA GGC TTA GAA ATT TCT CTT TTA AAA CAA ATT TTA CAA TCC ATA	399
Glu Glu Gly Leu Glu Ile Ser Leu Leu Lys Gln Ile Leu Gln Ser Ile	
95 100 105 110	
CAA AAA GAA TTG TTT AAA GCC AAC CTG AAA CTC CTC TCC CTA GAC ACT	447
Gln Lys Glu Leu Phe Lys Ala Asn Leu Lys Leu Leu Ser Leu Asp Thr	
115 120 125	
AAA GTC GTG CCA AAG GGG AGC GTG GAT AAG CTT TTT ATC AAC ACA ACC	495
Lys Val Val Pro Lys Gly Ser Val Asp Lys Leu Phe Ile Asn Thr Thr	
130 135 140	

TGC ATT GGT AAA ATC ATC AAG CCA GGG ATT TCT TCG TAC CAT TTA CAA	543
Cys Ile Gly Lys Ile Ile Lys Pro Gly Ile Ser Ser Tyr His Leu Gln	
145 150 155	
CAA GGG CAA GCC ATT ATC CTA AGC GAC ACT ATC GCC AAT CAT GGG GCA	591
Gln Gly Gln Ala Ile Ile Leu Ser Asp Thr Ile Ala Asn His Gly Ala	
160 165 170	
AGC TTA TTT GCG ATG CGT AAT GAA ATC AAG CTT AAA ACG AAT CTA GAA	639
Ser Leu Phe Ala Met Arg Asn Glu Ile Lys Leu Lys Thr Asn Leu Glu	
175 180 185 190	
AGC GAT TGC CAA CTG CTC TAT CCC TTA TTA AAA CCC CTA TTT TTA AGC	687
Ser Asp Cys Gln Leu Leu Tyr Pro Leu Leu Lys Pro Leu Phe Leu Ser	
195 200 205	
GAT CTC AAA ATT GAT GCT TTA AGA GAT GCG ACT AGG GGC GGG TTA GCG	735
Asp Leu Lys Ile Asp Ala Leu Arg Asp Ala Thr Arg Gly Gly Leu Ala	
210 215 220	
AGC GTG CTG AAC GAA TGG GCG AAC AGC TCT AGA GTG AAA ATC GTT ATA	783
Ser Val Leu Asn Glu Trp Ala Asn Ser Ser Arg Val Lys Ile Val Ile	
225 230 235	
GAA GAA GAA AAA ATC CCC TTA AAA GAA GAA ACG AAA GGG ATT TGT GAG	831
Glu Glu Glu Lys Ile Pro Leu Lys Glu Glu Thr Lys Gly Ile Cys Glu	
240 245 250	
ATT TTA GGG TTA GAA CCC TAC GCG CTA GCC AAT GAG GGG GTG TTT GTT	879
Ile Leu Gly Leu Glu Pro Tyr Ala Leu Ala Asn Glu Gly Val Phe Val	
255 260 265 270	
TTA GCG CTC AAT CAA AAA GAC GCC CCT AAA GCC TTA GAA ATT TTA AAA	927
Leu Ala Leu Asn Gln Lys Asp Ala Pro Lys Ala Leu Glu Ile Leu Lys	
275 280 285	
AGT AAC GAA AAA GCT AAA AAC GCT TGC GTG ATT GGC AAA GTG TTT GAA	975
Ser Asn Glu Lys Ala Lys Asn Ala Cys Val Ile Gly Lys Val Phe Glu	
290 295 300	
AAC CCT TAT CCT AGC GTG GTT TTA AAG AAC GCA TGG GGT TTT GAA AGG	1023
Asn Pro Tyr Pro Ser Val Val Leu Lys Asn Ala Trp Gly Phe Glu Arg	
305 310 315	
ATT TTA GAG GTG CCA GAG GGC GAA TTA TTG CCT AGG ATT TGT TAACACGCC	1074
Ile Leu Glu Val Pro Glu Gly Glu Leu Leu Pro Arg Ile Cys	
320 325 330	
GTCATTTTTT AATCGTTTTA AGCCTGCCCT AAAAATGGTT TA	1116

(2) INFORMATION FOR SEQ ID NO:440:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Met Asp Ser Val Thr Leu Ala Cys Gly Asn Gly Gly Lys Glu Thr Asn
1 5 10 15
Ala Leu Ile Glu Arg Val Phe Met Pro Tyr Leu Lys Glu Trp Ile Val
20 25 30
Ala Phe Asp Glu Asp Ala Pro Lys Phe Glu Ala Ser Gly Glu Tyr Cys
35 40 45
Val Ser Thr Asp Ser Phe Val Ile Thr Pro Leu Ile Phe Asn Gly Gly
50 55 60
Asp Ile Gly Lys Leu Cys Val Cys Gly Ser Ala Asn Asp Val Ser Val
65 70 75 80
Gln Gly Gly Glu Pro Leu Tyr Leu Asn Met Gly Phe Ile Leu Glu Glu
85 90 95
Gly Leu Glu Ile Ser Leu Leu Lys Gln Ile Leu Gln Ser Ile Gln Lys
100 105 110
Glu Leu Phe Lys Ala Asn Leu Lys Leu Leu Ser Leu Asp Thr Lys Val
115 120 125
Val Pro Lys Gly Ser Val Asp Lys Leu Phe Ile Asn Thr Thr Cys Ile
130 135 140
Gly Lys Ile Ile Lys Pro Gly Ile Ser Ser Tyr His Leu Gln Gln Gly
145 150 155 160
Gln Ala Ile Ile Leu Ser Asp Thr Ile Ala Asn His Gly Ala Ser Leu
165 170 175
Phe Ala Met Arg Asn Glu Ile Lys Leu Lys Thr Asn Leu Glu Ser Asp
180 185 190
Cys Gln Leu Leu Tyr Pro Leu Leu Lys Pro Leu Phe Leu Ser Asp Leu
195 200 205
Lys Ile Asp Ala Leu Arg Asp Ala Thr Arg Gly Gly Leu Ala Ser Val
210 215 220
Leu Asn Glu Trp Ala Asn Ser Ser Arg Val Lys Ile Val Ile Glu Glu
225 230 235 240
Glu Lys Ile Pro Leu Lys Glu Glu Thr Lys Gly Ile Cys Glu Ile Leu
245 250 255
Gly Leu Glu Pro Tyr Ala Leu Ala Asn Glu Gly Val Phe Val Leu Ala
260 265 270
Leu Asn Gln Lys Asp Ala Pro Lys Ala Leu Glu Ile Leu Lys Ser Asn
275 280 285
Glu Lys Ala Lys Asn Ala Cys Val Ile Gly Lys Val Phe Glu Asn Pro
290 295 300
Tyr Pro Ser Val Val Leu Lys Asn Ala Trp Gly Phe Glu Arg Ile Leu
305 310 315 320
Glu Val Pro Glu Gly Glu Leu Leu Pro Arg Ile Cys
325 330

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 16...1005
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

AAAAGGATAT TTTGA ATG AAA AGA ATG TTA GCG GAG TTT GAA AAA ATC CAA	51
Met Lys Arg Met Leu Ala Glu Phe Glu Lys Ile Gln	
1 5 10	
GCG ATT CTA ATG GCT TTC CCC CAT GAG TTT AGC GAC TGG GCG TAT TGT	99
Ala Ile Leu Met Ala Phe Pro His Glu Phe Ser Asp Trp Ala Tyr Cys	
15 20 25	
ATC AAA GAG GCT AGG GAA AGT TTT TTA AAC ATC ATT CAA ACC ATA GCC	147
Ile Lys Glu Ala Arg Glu Ser Phe Leu Asn Ile Ile Gln Thr Ile Ala	
30 35 40	
AAA CAC GCT AAA GTG CTA GTG TGC GTC CAC ACT AAC GAT ATT ATC GGT	195
Lys His Ala Lys Val Leu Val Cys Val His Thr Asn Asp Ile Ile Gly	
45 50 55 60	
TAT GAA ACG CTT AAA AAC TTA CCC GGT GTA GAG ATC GCA AGG ATT GAC	243
Tyr Glu Thr Leu Lys Asn Leu Pro Gly Val Glu Ile Ala Arg Ile Asp	
65 70 75	
ACT AAC GAC ACA TGG GCT AGG GAT TTT GGA GCG ATC AGC GTT GAA AAT	291
Thr Asn Asp Thr Trp Ala Arg Asp Phe Gly Ala Ile Ser Val Glu Asn	
80 85 90	
CAT GGC GTT TTA GAG TGC TTG GAT TTT GGC TTT AAT GGC TGG GGG TTA	339
His Gly Val Leu Glu Cys Leu Asp Phe Gly Phe Asn Gly Trp Gly Leu	
95 100 105	
AAA TAC CCG TCC AAT TTA GAC AAT CAA GTG AAT TTC AAA CTC AAA AGT	387
Lys Tyr Pro Ser Asn Leu Asp Asn Gln Val Asn Phe Lys Leu Lys Ser	
110 115 120	
TTA GGG TTT TTA AAA CAC CCT TTA AAA ACG ATG CCC TAT ATT TTA GAG	435
Leu Gly Phe Leu Lys His Pro Leu Lys Thr Met Pro Tyr Ile Leu Glu	
125 130 135 140	
GGC GGG AGT ATA GAA AGC GAT GGG GCT GGG AGC GTT TTA ACC AAC ACC	483
Gly Gly Ser Ile Glu Ser Asp Gly Ala Gly Ser Val Leu Thr Asn Thr	
145 150 155	
CAA TGC CTG TTA GAA AAA AAT CGT AAC CCC CAT TTG AAT CAA AAT GGA	531
Gln Cys Leu Leu Glu Lys Asn Arg Asn Pro His Leu Asn Gln Asn Gly	
160 165 170	
ATA GAA AAC ATG CTT AAA AAG GAA TTA GGG GCT AAA CAA GTG CTG TGG	579
Ile Glu Asn Met Leu Lys Lys Glu Leu Gly Ala Lys Gln Val Leu Trp	
175 180 185	
TAT TCT TAT GGC TAT CTC AAA GGC GAT GAT ACC GAT AGC CAT ACC GAC	627
Tyr Ser Tyr Gly Tyr Leu Lys Gly Asp Asp Thr Asp Ser His Thr Asp	
190 195 200	

ACG CTC GCT CGT TTT TTA GAT AAA GAC ACC ATT GTT TAT AGC ACA TGC	675
Thr Leu Ala Arg Phe Leu Asp Lys Asp Thr Ile Val Tyr Ser Thr Cys	
205 210 215 220	
GAA GAT GAA AAC GAT GAG CAC TAC ACA GCC TTA AAA AAA ATG CAA GAA	723
Glu Asp Glu Asn Asp Glu His Tyr Thr Ala Leu Lys Lys Met Gln Glu	
225 230 235	
GAA TTA AAA ACC TTT AAA AAA CTA GAC GGC ACG CCC TAT AAA CTC ATC	771
Glu Leu Lys Thr Phe Lys Lys Leu Asp Gly Thr Pro Tyr Lys Leu Ile	
240 245 250	
CCC CTA GAA ATC CCT AAA GCC ATT TTT GAT GAA AAC CAA CAA CGC TTG	819
Pro Leu Glu Ile Pro Lys Ala Ile Phe Asp Glu Asn Gln Gln Arg Leu	
255 260 265	
CCG GCA ACT TAT GTG AAT TTT TTA TTG TGC AAT AAC GCT TTA ATC GTG	867
Pro Ala Thr Tyr Val Asn Phe Leu Leu Cys Asn Asn Ala Leu Ile Val	
270 275 280	
CCC ACT TAC AAC GAC CCT AAA GAC GCG CTC ATT TTA GAA ACC TTG AAA	915
Pro Thr Tyr Asn Asp Pro Lys Asp Ala Leu Ile Leu Glu Thr Leu Lys	
285 290 295 300	
CAA CAC ACG CCC TTA GAA GTG ATA GGG GTT GAT TGC AAC ACC TTA ATC	963
Gln His Thr Pro Leu Glu Val Ile Gly Val Asp Cys Asn Thr Leu Ile	
305 310 315	
AAA CAG CAT GGA AGT TTG CAT TGT GTA ACG ATG CAA CTT TAT TGAACAAAA	1014
Lys Gln His Gly Ser Leu His Cys Val Thr Met Gln Leu Tyr	
320 325 330	
TCACGCTTTT TGGCGTGGT	1033

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

Met Lys Arg Met Leu Ala Glu Phe Glu Lys Ile Gln Ala Ile Leu Met	
1 5 10 15	
Ala Phe Pro His Glu Phe Ser Asp Trp Ala Tyr Cys Ile Lys Glu Ala	
20 25 30	
Arg Glu Ser Phe Leu Asn Ile Ile Gln Thr Ile Ala Lys His Ala Lys	
35 40 45	
Val Leu Val Cys Val His Thr Asn Asp Ile Ile Gly Tyr Glu Thr Leu	
50 55 60	
Lys Asn Leu Pro Gly Val Glu Ile Ala Arg Ile Asp Thr Asn Asp Thr	
65 70 75 80	
Trp Ala Arg Asp Phe Gly Ala Ile Ser Val Glu Asn His Gly Val Leu	
85 90 95	

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 25...375

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

AAAAACTGGA ATCAAGGGGT TAAA ATG TTT TCT CAT GAA GTT TAT TTG GAG	51
Met Phe Ser His Glu Val Tyr Leu Glu	
1 5	
GGT TGC ACC CTT GAA TTA AGA AAG ATT TGC GAT GAT TTT GAA AAA AAT	99
Gly Cys Thr Leu Glu Leu Arg Lys Ile Cys Asp Asp Phe Glu Lys Asn	
10 15 20 25	
GCC ATG CAA GAT GAT TTA GGG CAG AAA CTC AGG AGT GAT GTG CTA GAG	147
Ala Met Gln Asp Asp Leu Gly Gln Lys Leu Arg Ser Asp Val Leu Glu	
30 35 40	
GAC ATG CTA AAA ATC GCG CAT GAT TTA GAA AAT TTA GAA GAT GAC ACC	195
Asp Met Leu Lys Ile Ala His Asp Leu Glu Asn Leu Glu Asp Asp Thr	
45 50 55	
CAA TAC CAA AGA AGA ATA ATT GAC GAG CAA ATT GAA GAA GCC AAA TCT	243
Gln Tyr Gln Arg Arg Ile Ile Asp Glu Gln Ile Glu Glu Ala Lys Ser	
60 65 70	
TTG ATG AGG CAA ATT GAT ATG AAT TTC CAT CCA TCA AGC GAG ATC GAT	291
Leu Met Arg Gln Ile Asp Met Asn Phe His Pro Ser Ser Glu Ile Asp	
75 80 85	
AGG CTT ATG CGT GAA GCC AAA GAG CAT GAA AGA GAA GCT AGT AAA AGA	339
Arg Leu Met Arg Glu Ala Lys Glu His Glu Arg Glu Ala Ser Lys Arg	
90 95 100 105	
TAT GAT GAG TAT CTT AAA TCT AAG GAT AAA AAT GAT TGATGTGAAT GGTTTA	391
Tyr Asp Glu Tyr Leu Lys Ser Lys Asp Lys Asn Asp	
110 115	
TTAAAAGAAC TGGATGATGC CTTAGATAA	420

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

[illegible]

(2) INFORMATION FOR SEQ ID NO:448:

Asp	Asp	His	Lys	Val	Leu	Gly	Ile	Thr	Glu	Gly	Asp	Trp	Trp	Ala	Ile
130						135					140				
Ile	Trp	Leu	Ala	Trp	Gly	Val	Leu	Trp	Leu	Thr	Ala	Phe	Ile	Glu	Asn
145					150					155					160
Ile	Leu	Lys	Ile	Pro	Leu	Gly	Lys	Phe	Thr	Pro	Trp	Leu	Ala	Ile	Ile
				165					170					175	
Glu	Gly	Ile	Leu	Thr	Ala	Trp	Ile	Pro	Ala	Trp	Leu	Leu	Phe	Ile	Gln
			180					185					190		
His	Trp	Val													
		195													

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 48...482
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

GAAGGGCATT TGTGCTAAAA ACCACTAAAA AAAGCCTGTT GGTTTTT	ATG GGG GTT	56
	Met Gly Val	
	1	
TTT TTC CTT ATT TTT GGC GTG GAT CAA GCG ATT AAA TAC GCT ATT TTA		104
Phe Phe Leu Ile Phe Gly Val Asp Gln Ala Ile Lys Tyr Ala Ile Leu		
5 10 15		
GAA GGG TTT CGC TAT GAA AGT TTG ATG ATA GAT ATT GTT TTA GTG TTC		152
Glu Gly Phe Arg Tyr Glu Ser Leu Met Ile Asp Ile Val Leu Val Phe		
20 25 30 35		
AAT AAA GGC GTG GCG TTT TCC TTG CTC AGT TTT TTA GAG GGG GGT TTG		200
Asn Lys Gly Val Ala Phe Ser Leu Leu Ser Phe Leu Glu Gly Gly Leu		
40 45 50		
AAA TAC TTG CAA ATC CTT TTG ATT TTA GGG CTT TTT ATC TTT TTA ATG		248
Lys Tyr Leu Gln Ile Leu Leu Ile Leu Gly Leu Phe Ile Phe Leu Met		
55 60 65		
CGC CAA AGG GAG CTT TTT AAA AAC CAT GCG ATA GAG TTT GGC ATG GTG		296
Arg Gln Arg Glu Leu Phe Lys Asn His Ala Ile Glu Phe Gly Met Val		
70 75 80		
TTT GGC GCC GGG GTT TCT AAT GTT TTA GAC CGG TTT GTG CAT GGG GGC		344
Phe Gly Ala Gly Val Ser Asn Val Leu Asp Arg Phe Val His Gly Gly		
85 90 95		
GTG GTG GAT TAT GTG TAT TAT CAT TAT GGC TTT GAT TTT GCC ATT TTT		392

(B) LOCATION: 22...1356
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

TTTAAAAGGT ATTTTATAAC G ATG AAA ATT TTT GGG ACT GAT GGC GTG AGG	51
Met Lys Ile Phe Gly Thr Asp Gly Val Arg	
1 5 10	
GGT AAA GCA GGG GTG AAA CTC ACC CCC ATG TTT GTG ATG CGT TTA GGC	99
Gly Lys Ala Gly Val Lys Leu Thr Pro Met Phe Val Met Arg Leu Gly	
15 20 25	
ATT GCT GCC GGA TTG TAT TTT AAA AAA CAT TCT CAA ACG AAT AAA ATT	147
Ile Ala Ala Gly Leu Tyr Phe Lys Lys His Ser Gln Thr Asn Lys Ile	
30 35 40	
CTA ATC GGT AAA GAC ACC AGA AAA AGC GGC TAT ATG GTA GAA AAC GCT	195
Leu Ile Gly Lys Asp Thr Arg Lys Ser Gly Tyr Met Val Glu Asn Ala	
45 50 55	
TTA GTG AGC GCT CTA ACT TCC ATA GGC TAT AAT GTG ATT CAA ATA GGC	243
Leu Val Ser Ala Leu Thr Ser Ile Gly Tyr Asn Val Ile Gln Ile Gly	
60 65 70	
CCT ATG CCC ACC CCT GCG ATT GCG TTT TTA ACT GAA GAC ATG CGC TGT	291
Pro Met Pro Thr Pro Ala Ile Ala Phe Leu Thr Glu Asp Met Arg Cys	
75 80 85 90	
GAT GCG GGT ATT ATG ATA AGC GCG AGC CAC AAC CCT TTT GAA GAT AAT	339
Asp Ala Gly Ile Met Ile Ser Ala Ser His Asn Pro Phe Glu Asp Asn	
95 100 105	
GGC ATT AAG TTT TTC AAT TCT TAT GGC TAT AAG CTT AAA GAA GAA GAA	387
Gly Ile Lys Phe Phe Asn Ser Tyr Gly Tyr Lys Leu Lys Glu Glu Glu	
110 115 120	
GAA AAA GCG ATT GAA GAA ATC TTT CAT GAT GAA GAA TTA CTG CAT TCT	435
Glu Lys Ala Ile Glu Glu Ile Phe His Asp Glu Glu Leu Leu His Ser	
125 130 135	
AGC TAT AAA GTG GGT GAG AGC GTC GGT AGC GCT AAA AGG ATA GAC GAT	483
Ser Tyr Lys Val Gly Glu Ser Val Gly Ser Ala Lys Arg Ile Asp Asp	
140 145 150	
GTC ATA GGG CGC TAT ATT GCA CAT TTA AAA CAC TCT TTC CCC AAA CAT	531
Val Ile Gly Arg Tyr Ile Ala His Leu Lys His Ser Phe Pro Lys His	
155 160 165 170	
TTG AAT TTA CAG AGT TTA AGG ATC GTG CTA GAT ACG GCT AAT GGC GCG	579
Leu Asn Leu Gln Ser Leu Arg Ile Val Leu Asp Thr Ala Asn Gly Ala	
175 180 185	
GCT TAT AAG GTG GCT CCG GTC GTT TTT AGC GAG CTT GGG GCT GAT GTG	627
Ala Tyr Lys Val Ala Pro Val Val Phe Ser Glu Leu Gly Ala Asp Val	
190 195 200	

TTA GTG ATT AAT GAT GAG CCT AAC GGG TGT AAC ATT AAT GAT CAA TGC Leu Val Ile Asn Asp Glu Pro Asn Gly Cys Asn Ile Asn Asp Gln Cys 205 210 215	675
GGG GCT TTA CAC CCC AAC CAA TTA AGC CAG GAA GTG AAA AAA TAC CGC Gly Ala Leu His Pro Asn Gln Leu Ser Gln Glu Val Lys Lys Tyr Arg 220 225 230	723
GCA GAT TTA GGC TTT GCT TTT GAT GGC GAT GCT GAC AGG CTA GTG GTG Ala Asp Leu Gly Phe Ala Phe Asp Gly Asp Ala Asp Arg Leu Val Val 235 240 245 250	771
GTG GAT AAT TTA GGG AAT ATC GTG CAT GGG GAT AAG CTT TTA GGG GTG Val Asp Asn Leu Gly Asn Ile Val His Gly Asp Lys Leu Leu Gly Val 255 260 265	819
TTA GGG GTT TAT CAA AAA TCT AAA AAC GCC CTT TCT TCT CAA GCG GTT Leu Gly Val Tyr Gln Lys Ser Lys Asn Ala Leu Ser Ser Gln Ala Val 270 275 280	867
GTC GCC ACA AAC ATG AGC AAT TTA GCC CTT AAA GAA TAT TTA AAA TCC Val Ala Thr Asn Met Ser Asn Leu Ala Leu Lys Glu Tyr Leu Lys Ser 285 290 295	915
CAA GAT TTG GAA TTG AAG CAT TGC GCG ATT GGG GAT AAG TTT GTG AGC Gln Asp Leu Glu Leu Lys His Cys Ala Ile Gly Asp Lys Phe Val Ser 300 305 310	963
GAA TGC ATG CAA TTG AAT AAA GCC AAT TTT GGA GGC GAG CAA AGC GGG Glu Cys Met Gln Leu Asn Lys Ala Asn Phe Gly Gly Glu Gln Ser Gly 315 320 325 330	1011
CAT ATC ATT TTT AGC GAT TAC GCT AAA ACA GGC GAT GGT TTG GTG TGC His Ile Ile Phe Ser Asp Tyr Ala Lys Thr Gly Asp Gly Leu Val Cys 335 340 345	1059
GCT TTG CAA GTG AGC GCG TTA GTG TTA GAA AGC AAG CAG GTA AGC TCT Ala Leu Gln Val Ser Ala Leu Val Leu Glu Ser Lys Gln Val Ser Ser 350 355 360	1107
GTT GCG TTA AAC CCC TTT GAA TTA TAC CCC CAA AGC CTA GTG AAT TTG Val Ala Leu Asn Pro Phe Glu Leu Tyr Pro Gln Ser Leu Val Asn Leu 365 370 375	1155
AAT GTC CAA AAA AAG CCC CCT TTA GAA AGC CTG AAA GGT TAT AGC GCT Asn Val Gln Lys Lys Pro Pro Leu Glu Ser Leu Lys Gly Tyr Ser Ala 380 385 390	1203
CTT TTA AAA GAA TTA GAC AAG CTA GAA ATC CGC CAT TTG ATC CGT TAT Leu Leu Lys Glu Leu Asp Lys Leu Glu Ile Arg His Leu Ile Arg Tyr 395 400 405 410	1251
AGC GGC ACT GAA AAC AAA TTG CGA ATC CTT TTA GAA GCT AAA GAT GAA Ser Gly Thr Glu Asn Lys Leu Arg Ile Leu Leu Glu Ala Lys Asp Glu 415 420 425	1299
AAG CTT TTA GAA TCC AAA ATG CAA GAA TTA AAA GAG TTT TTT GAA GGG Lys Leu Leu Glu Ser Lys Met Gln Glu Leu Lys Glu Phe Phe Glu Gly 430 435 440 445	1347

430

435

440

CAT TTG TGC TAAAAACCAC TAAAAAAGC CTGTTGGTTT TTATGG
 His Leu Cys
 445

1392

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Met Lys Ile Phe Gly Thr Asp Gly Val Arg Gly Lys Ala Gly Val Lys
 1 5 10 15
 Leu Thr Pro Met Phe Val Met Arg Leu Gly Ile Ala Ala Gly Leu Tyr
 20 25 30
 Phe Lys Lys His Ser Gln Thr Asn Lys Ile Leu Ile Gly Lys Asp Thr
 35 40 45
 Arg Lys Ser Gly Tyr Met Val Glu Asn Ala Leu Val Ser Ala Leu Thr
 50 55 60
 Ser Ile Gly Tyr Asn Val Ile Gln Ile Gly Pro Met Pro Thr Pro Ala
 65 70 75 80
 Ile Ala Phe Leu Thr Glu Asp Met Arg Cys Asp Ala Gly Ile Met Ile
 85 90 95
 Ser Ala Ser His Asn Pro Phe Glu Asp Asn Gly Ile Lys Phe Phe Asn
 100 105 110
 Ser Tyr Gly Tyr Lys Leu Lys Glu Glu Glu Glu Lys Ala Ile Glu Glu
 115 120 125
 Ile Phe His Asp Glu Glu Leu Leu His Ser Ser Tyr Lys Val Gly Glu
 130 135 140
 Ser Val Gly Ser Ala Lys Arg Ile Asp Asp Val Ile Gly Arg Tyr Ile
 145 150 155 160
 Ala His Leu Lys His Ser Phe Pro Lys His Leu Asn Leu Gln Ser Leu
 165 170 175
 Arg Ile Val Leu Asp Thr Ala Asn Gly Ala Ala Tyr Lys Val Ala Pro
 180 185 190
 Val Val Phe Ser Glu Leu Gly Ala Asp Val Leu Val Ile Asn Asp Glu
 195 200 205
 Pro Asn Gly Cys Asn Ile Asn Asp Gln Cys Gly Ala Leu His Pro Asn
 210 215 220
 Gln Leu Ser Gln Glu Val Lys Lys Tyr Arg Ala Asp Leu Gly Phe Ala
 225 230 235 240
 Phe Asp Gly Asp Ala Asp Arg Leu Val Val Val Asp Asn Leu Gly Asn
 245 250 255
 Ile Val His Gly Asp Lys Leu Leu Gly Val Leu Gly Val Tyr Gln Lys
 260 265 270
 Ser Lys Asn Ala Leu Ser Ser Gln Ala Val Val Ala Thr Asn Met Ser
 275 280 285
 Asn Leu Ala Leu Lys Glu Tyr Leu Lys Ser Gln Asp Leu Glu Leu Lys
 290 295 300
 His Cys Ala Ile Gly Asp Lys Phe Val Ser Glu Cys Met Gln Leu Asn

305					310					315				320	
Lys	Ala	Asn	Phe	Gly	Gly	Glu	Gln	Ser	Gly	His	Ile	Ile	Phe	Ser	Asp
				325					330					335	
Tyr	Ala	Lys	Thr	Gly	Asp	Gly	Leu	Val	Cys	Ala	Leu	Gln	Val	Ser	Ala
			340					345					350		
Leu	Val	Leu	Glu	Ser	Lys	Gln	Val	Ser	Ser	Val	Ala	Leu	Asn	Pro	Phe
		355					360					365			
Glu	Leu	Tyr	Pro	Gln	Ser	Leu	Val	Asn	Leu	Asn	Val	Gln	Lys	Lys	Pro
	370					375					380				
Pro	Leu	Glu	Ser	Leu	Lys	Gly	Tyr	Ser	Ala	Leu	Leu	Lys	Glu	Leu	Asp
	385				390					395					400
Lys	Leu	Glu	Ile	Arg	His	Leu	Ile	Arg	Tyr	Ser	Gly	Thr	Glu	Asn	Lys
			405					410					415		
Leu	Arg	Ile	Leu	Glu	Ala	Lys	Asp	Glu	Lys	Leu	Leu	Glu	Ser	Lys	
		420					425					430			
Met	Gln	Glu	Leu	Lys	Glu	Phe	Phe	Glu	Gly	His	Leu	Cys			
	435					440						445			

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...441
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

TTTTATCAAA	GGATTCTT	ATG	ACA	AAG	ACC	GCT	AAA	GTC	AAT	GAC	ATC	GTT	51
		Met	Thr	Lys	Thr	Ala	Lys	Val	Asn	Asp	Ile	Val	
		1				5					10		
CGT	GAT	TGG	GTC	GTT	TTA	GAC	GCC	AAA	GAC	AAG	GTT	TTT	99
Arg	Asp	Trp	Val	Val	Leu	Asp	Ala	Lys	Asp	Lys	Val	Phe	
		15				20					25		
ATC	ACT	GAA	ATC	GCT	GTG	CTT	TTA	AGA	GGG	AAA	CAC	CGC	147
Ile	Thr	Glu	Ile	Ala	Val	Leu	Leu	Arg	Gly	Lys	His	Arg	
		30				35					40		
ACC	CCT	AAT	GTG	GAT	TGT	GGG	GAT	TTT	GTG	GTG	GTT	ATC	195
Thr	Pro	Asn	Val	Asp	Cys	Gly	Asp	Phe	Val	Val	Val	Ile	
	45				50						55		
AAG	GTT	AAA	TTT	TCA	GGC	ATG	AAA	TTA	GAG	GAT	AAA	GAG	243
Lys	Val	Lys	Phe	Ser	Gly	Met	Lys	Leu	Glu	Asp	Lys	Glu	
	60				65				70			75	
CAT	TCA	GGC	TAT	TTT	GGC	AGC	ACT	AAG	AGC	AAG	ACT	CTC	291
His	Ser	Gly	Tyr	Phe	Gly	Ser	Thr	Lys	Ser	Lys	Thr	Leu	
												Gln	
												Glu	
												Met	

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 19...2058
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

TAGCTTTTGA	TTGAAAGC	ATG	GGT	TCT	TAC	TTT	ATG	GAG	TGT	CCA	ATG	AAA	51
		Met	Gly	Ser	Tyr	Phe	Met	Glu	Cys	Pro	Met	Lys	
		1				5					10		
AAG	AAA	GCT	AAC	GAA	GAA	AAA	GCC	CAA	AAA	AGA	GCT	AAA	99
Lys	Lys	Ala	Asn	Glu	Glu	Lys	Ala	Gln	Lys	Arg	Ala	Lys	
		15					20				25		
AAA	GCA	GAA	GCC	ACA	CAA	GAA	AAT	AAA	ACT	AAA	GAA	AAC	147
Lys	Ala	Glu	Ala	Thr	Gln	Glu	Asn	Lys	Thr	Lys	Glu	Asn	
		30				35					40		
AAA	GAA	AGC	AAA	ATT	AAA	GAA	AGC	AAA	ATC	AAA	GAA	GCT	195
Lys	Glu	Ser	Lys	Ile	Lys	Glu	Ser	Lys	Ile	Lys	Glu	Ala	
	45					50					55		
GAA	CCT	ATT	CCT	GTT	AAA	AAG	CTT	AGT	TTT	AAT	GAA	GCG	243
Glu	Pro	Ile	Pro	Val	Lys	Lys	Leu	Ser	Phe	Asn	Glu	Ala	
	60				65					70		75	
TTG	TTC	GCT	AAT	TCC	TTA	AGC	GAT	TGC	GTT	TCT	TAT	GAG	291
Leu	Phe	Ala	Asn	Ser	Leu	Ser	Asp	Cys	Val	Ser	Tyr	Glu	
			80					85				90	
CAA	ATC	AGC	GCG	AAA	GTC	CCC	ACT	CTA	GCC	CAA	ATC	AAA	339
Gln	Ile	Ser	Ala	Lys	Val	Pro	Thr	Leu	Ala	Gln	Ile	Lys	
		95						100				105	
GAA	TTG	TGC	CAA	AAA	TAC	CAA	AAG	AAA	TTA	GTC	AGC	TCT	387
Glu	Leu	Cys	Gln	Lys	Tyr	Gln	Lys	Lys	Leu	Val	Ser	Ser	
		110				115					120		
GCT	AAA	AAA	CTC	AAT	GCG	ATT	GAC	AAG	ATT	AAA	AAA	ACC	435
Ala	Lys	Lys	Leu	Asn	Ala	Ile	Asp	Lys	Ile	Lys	Lys	Thr	
	125					130					135		
CAA	AAA	GTT	TTA	GAT	GAA	GAA	TTA	GAA	GAT	GGC	TAT	GAC	483
Gln	Lys	Val	Leu	Asp	Glu	Glu	Leu	Glu	Asp	Gly	Tyr	Asp	
	140				145					150			155
GAA	AAG	GAT	TTT	TTA	GAG	TGG	AGC	AGA	AGC	GAT	AGC	CCA	531
Glu	Lys	Asp	Phe	Leu	Glu	Trp	Ser	Arg	Ser	Asp	Ser	Pro	
			160					165				170	
TAT	TTG	CGC	GAA	ATG	GGG	GAT	ATA	AAA	CTT	TTA	AGC	AAA	579
Tyr	Leu	Arg	Glu	Met	Gly	Asp	Ile	Lys	Leu	Leu	Ser	Lys	
			175					180				185	

ATT Ile	GAA Glu	TTG Leu 190	AGC Ser	AAG Lys	CAA Gln	ATC Ile	CGC Arg 195	TTG Leu	GGT Gly	GAA Glu	GAC Asp	ATT Ile 200	ATT Ile	TTA Leu	GAC Asp	627
GCG Ala	ATC Ile 205	TGC Cys	TCG Ser	GTG Val	CCG Pro	TAT Tyr 210	TTG Leu	ATT Ile	GAT Asp	TTT Phe 215	ATC Ile 215	TAT Tyr	GCG Ala	TAT Tyr	AAA Lys	675
GAC Asp 220	GCT Ala	TTA Leu	ATC Ile	AAT Asn 225	CGT Arg	GAA Glu	AGA Arg	AGG Arg	GTT Val	AAA Lys 230	GAG Glu	CTT Leu	TTC Phe	AGG Arg	AGC Ser 235	723
TTT Phe	GAT Asp	GAT Asp	GAC Asp 240	GAT Asp	GAA Glu	AAT Asn	AGC Ser	GTG Val	AGC Ser 245	GAT Asp	TCT Ser	AAA Lys	AAA Lys	GAT Asp 250	GAA Glu	771
GAC Asp	AAC Asn	GAA Glu 255	GAA Glu	GAT Asp	GAA Glu	GAA Glu	AAC Asn 260	GAA Glu	GAA Glu	AGG Arg	AAA Lys	AAA Lys	GTC Val 265	GTT Val	TCT Ser	819
GAA Glu	AAA Lys 270	GAC Asp	AAG Lys	AAG Lys	CGT Arg	GTA Val	GAA Glu 275	AAG Lys	GTT Val	CAA Gln	GAA Glu 280	AGC Ser 280	TTT Phe	AAA Lys	GCC Ala	867
CTA Leu 285	GAC Asp	AAG Lys	GCT Ala	AAA Lys	AAA Lys	GAA Glu 290	TGG Trp	CTT Leu	AAA Lys	GCC Ala 295	CTT Leu 295	GAA Glu	GCC Ala	CCC Pro	ATA Ile	915
GAT Asp 300	GAA Glu	AGA Arg	GAA Glu	GAC Asp 305	GAA Glu	TTG Leu	GTG Val	CGT Arg	TCA Ser	TTG Leu 310	ACC Thr	CTA Leu	GCT Ala	TAC Tyr	AAA Lys 315	963
CGC Arg	CAA Gln	ACA Thr	CTC Leu 320	AAA Lys	GAC Asp	AGA Arg	CTC Leu	TAT Tyr	GAT Asp 325	TTA Leu	GAA Glu	CCT Pro	ACC Thr	AGC Ser 330	AAA Lys	1011
CTG Leu	ATT Ile	AAT Asn	GAA Glu 335	TTA Leu	GTC Val	AAA Lys	ACG Thr	ATG Met 340	GAA Glu	ACC Thr	ACT Thr	TTA Leu 345	AAA Lys	AGC Ser	GGC Gly	1059
GAT Asp	GGG Gly 350	TTT Phe	GAA Glu	AAA Lys	GAG Glu	TTG Leu	AAA Lys 355	CGC Arg	TTG Leu	GAA Glu	TAC Tyr 360	AAA Lys 360	CTG Leu	CCC Pro	TTA Leu	1107
TTC Phe 365	AAT Asn	GAC Asp	ACT Thr	CTC Leu	ATC Ile	GCA Ala 370	AAC Asn	CAT His	AAA Lys	AAA Lys 375	ATC Ile 375	CTT Leu	GCC Ala	AAT Asn	ATC Ile	1155
ACT Thr 380	AAC Asn	ATG Met	ACT Thr	AAA Lys	GAA Glu 385	GAT Asp	ATT Ile	ATC Ile	GCT Ala	CAA Gln 390	GTG Val	CCA Pro	GAA Glu	GCG Ala	ACT Thr 395	1203
ATG Met	GTG Val	AGC Ser	GTG Val 400	TAT Tyr	ATG Met	GAT Asp	CTT Leu	AAA Lys	AAG Lys 405	CTT Leu	TTT Phe	TTG Leu	ACT Thr 410	AAA Lys	GAA Glu	1251
GCG Ala	AGC Ser	GAA Glu	GAA Glu	GGC Gly	TTT Phe	GAT Asp	CTA Leu	GCC Ala	CCC Pro	AAC Asn	AAG Lys	CTA Leu	AAA Lys	GAA Glu	ATT Ile	1299

	415						420						425						
TTA Leu	GAG Glu	CAA Gln	ATC Ile	AAA Lys	AGA Arg	GGG Gly	AAG Lys	TTG Leu	ATT Ile	TCC Ser	GAT Asp	CGC Arg	GCT Ala	AAA Lys	AAC Asn	1347			
	430					435					440								
AAA Lys	ATG Met	GCT Ala	AAA Lys	TCC Ser	AAT Asn	TTA Leu	AGG Arg	TTG Leu	GTG Val	GTG Val	AGC Ser	ATC Ile	GCT Ala	AAA Lys	CGA Arg	1395			
	445					450					455								
TTC Phe	ACG Thr	AGC Ser	AGA Arg	GGC Gly	TTA Leu	CCA Pro	TTC Phe	TTG Leu	GAT Asp	TTG Leu	ATT Ile	CAA Gln	GAG Glu	GGC Gly	AAT Asn	1443			
	460				465					470					475				
ATT Ile	GGC Gly	TTG Leu	ATG Met	AAA Lys	GCG Ala	GTG Val	GAT Asp	AAG Lys	TTT Phe	GAG Glu	CAT His	GAA Glu	AAG Lys	GGC Gly	TTC Phe	1491			
				480					485					490					
AAG Lys	TTT Phe	TCT Ser	ACC Thr	TAT Tyr	GCG Ala	ACC Thr	TGG Trp	TGG Trp	ATC Ile	AAA Lys	CAA Gln	GCT Ala	ATC Ile	AGC Ser	AGA Arg	1539			
				495				500					505						
GCC Ala	ATA Ile	GCC Ala	GAT Asp	CAG Gln	GCC Ala	CGC Arg	ACT Thr	ATC Ile	CGC Arg	ATC Ile	CCC Pro	ATT Ile	CAC His	ATG Met	ATT Ile	1587			
	510					515					520								
GAT Asp	ACG Thr	ATT Ile	AAT Asn	CGC Arg	ATC Ile	AAT Asn	AAA Lys	GTC Val	ATG Met	CGC Arg	AAA Lys	CAC His	ATT Ile	CAA Gln	GAA Glu	1635			
	525					530					535								
AAC Asn	GGC Gly	AAA Lys	GAG Glu	CCT Pro	GAT Asp	TTA Leu	GAA Glu	GTG Val	GTG Val	GCT Ala	GAA Glu	GAA Glu	GTG Val	GGG Gly	CTT Leu	1683			
	540				545					550					555				
TCG Ser	TTA Leu	GAT Asp	AAA Lys	GTG Val	AAG Lys	AAT Asn	GTG Val	ATT Ile	AAG Lys	GTG Val	ACT Thr	AAA Lys	GAG Glu	CCT Pro	ATC Ile	1731			
				560					565					570					
AGT Ser	TTG Leu	GAA Glu	ACC Thr	CCA Pro	GTC Val	GGC Gly	AAT Asn	GAT Asp	GAT Asp	GAT Asp	GGC Gly	AAG Lys	TTT Phe	GGG Gly	GAT Asp	1779			
	575					580					585								
TTC Phe	GTG Val	GAA Glu	GAT Asp	AAG Lys	AAT Asn	ATC Ile	GTC Val	AGC Ser	TCC Ser	ATT Ile	GAT Asp	CAC His	ATC Ile	ATG Met	CGA Arg	1827			
	590					595					600								
GAA Glu	GAT Asp	TTG Leu	AAA Lys	GCA Ala	CAA Gln	ATT Ile	GAA Glu	AGC Ser	GTT Val	TTG Leu	GAT Asp	CAG Gln	TTG Leu	AAT Asn	GAG Glu	1875			
	605					610					615								
CGA Arg	GAA Glu	AAA Lys	GCG Ala	GTG Val	ATC Ile	CGC Arg	ATG Met	CGT Arg	TTT Phe	GGG Gly	CTT Leu	TTA Leu	GAC Asp	GAT Asp	GAA Glu	1923			
	620				625					630					635				
AGC Ser	GAT Asp	CGA Arg	ACT Thr	TTA Leu	GAA Glu	GAA Glu	ATT Ile	GGC Gly	AAG Lys	GAA Glu	TTG Leu	AAT Asn	GTT Val	ACT Thr	AGA Arg	1971			
				640					645					650					

Lys	Glu	Trp	Leu	Lys	Ala	Leu	Glu	Ala	Pro	Ile	Asp	Glu	Arg	Glu	Asp
290						295					300				
Glu	Leu	Val	Arg	Ser	Leu	Thr	Leu	Ala	Tyr	Lys	Arg	Gln	Thr	Leu	Lys
305					310					315					320
Asp	Arg	Leu	Tyr	Asp	Leu	Glu	Pro	Thr	Ser	Lys	Leu	Ile	Asn	Glu	Leu
				325					330					335	
Val	Lys	Thr	Met	Glu	Thr	Thr	Leu	Lys	Ser	Gly	Asp	Gly	Phe	Glu	Lys
			340					345					350		
Glu	Leu	Lys	Arg	Leu	Glu	Tyr	Lys	Leu	Pro	Leu	Phe	Asn	Asp	Thr	Leu
		355					360					365			
Ile	Ala	Asn	His	Lys	Lys	Ile	Leu	Ala	Asn	Ile	Thr	Asn	Met	Thr	Lys
	370					375					380				
Glu	Asp	Ile	Ile	Ala	Gln	Val	Pro	Glu	Ala	Thr	Met	Val	Ser	Val	Tyr
385					390					395					400
Met	Asp	Leu	Lys	Lys	Leu	Phe	Leu	Thr	Lys	Glu	Ala	Ser	Glu	Glu	Gly
				405					410					415	
Phe	Asp	Leu	Ala	Pro	Asn	Lys	Leu	Lys	Glu	Ile	Leu	Glu	Gln	Ile	Lys
			420					425					430		
Arg	Gly	Lys	Leu	Ile	Ser	Asp	Arg	Ala	Lys	Asn	Lys	Met	Ala	Lys	Ser
		435					440					445			
Asn	Leu	Arg	Leu	Val	Val	Ser	Ile	Ala	Lys	Arg	Phe	Thr	Ser	Arg	Gly
	450					455					460				
Leu	Pro	Phe	Leu	Asp	Leu	Ile	Gln	Glu	Gly	Asn	Ile	Gly	Leu	Met	Lys
465					470					475					480
Ala	Val	Asp	Lys	Phe	Glu	His	Glu	Lys	Gly	Phe	Lys	Phe	Ser	Thr	Tyr
				485					490					495	
Ala	Thr	Trp	Trp	Ile	Lys	Gln	Ala	Ile	Ser	Arg	Ala	Ile	Ala	Asp	Gln
			500					505					510		
Ala	Arg	Thr	Ile	Arg	Ile	Pro	Ile	His	Met	Ile	Asp	Thr	Ile	Asn	Arg
		515					520					525			
Ile	Asn	Lys	Val	Met	Arg	Lys	His	Ile	Gln	Glu	Asn	Gly	Lys	Glu	Pro
	530					535					540				
Asp	Leu	Glu	Val	Val	Ala	Glu	Glu	Val	Gly	Leu	Ser	Leu	Asp	Lys	Val
545					550					555					560
Lys	Asn	Val	Ile	Lys	Val	Thr	Lys	Glu	Pro	Ile	Ser	Leu	Glu	Thr	Pro
				565					570					575	
Val	Gly	Asn	Asp	Asp	Asp	Gly	Lys	Phe	Gly	Asp	Phe	Val	Glu	Asp	Lys
			580					585					590		
Asn	Ile	Val	Ser	Ser	Ile	Asp	His	Ile	Met	Arg	Glu	Asp	Leu	Lys	Ala
		595				600						605			
Gln	Ile	Glu	Ser	Val	Leu	Asp	Gln	Leu	Asn	Glu	Arg	Glu	Lys	Ala	Val
	610					615					620				
Ile	Arg	Met	Arg	Phe	Gly	Leu	Leu	Asp	Asp	Glu	Ser	Asp	Arg	Thr	Leu
625					630					635					640
Glu															

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 745 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 25...717
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

AAGAATACGT GTGATTGGGA GAAA ATG GTG CAA AAA ATT GGC ATT TTA GGG	51
Met Val Gln Lys Ile Gly Ile Leu Gly	
1 5	
GCG ATG AGA GAA GAA ATA ACC CCT ATA CTA GAA TTG TTT GGC GTG GAT	99
Ala Met Arg Glu Glu Ile Thr Pro Ile Leu Glu Leu Phe Gly Val Asp	
10 15 20 25	
TTT GAA GAG ATC CCT TTA GGG GGG AAT GTC TTC CAT AAA GGC GTT TAT	147
Phe Glu Glu Ile Pro Leu Gly Gly Asn Val Phe His Lys Gly Val Tyr	
30 35 40	
CAC AAC AAG GAA ATC ATT GTC GCT TAT AGC AAG ATT GGC AAG GTG CAT	195
His Asn Lys Glu Ile Ile Val Ala Tyr Ser Lys Ile Gly Lys Val His	
45 50 55	
TCC ACT TTA ACC ACA ACG AGC ATG ATT TTA GCG TTT GGC GTT CAA AAG	243
Ser Thr Leu Thr Thr Thr Ser Met Ile Leu Ala Phe Gly Val Gln Lys	
60 65 70	
GTG CTT TTT AGC GGG GTG GCT GGA AGC TTA GTT AAA GAT TTA AAA ATC	291
Val Leu Phe Ser Gly Val Ala Gly Ser Leu Val Lys Asp Leu Lys Ile	
75 80 85	
AAT GAT TTA CTA GTG GCT ATT CAA TTA GTC CAG CAT GAT GTG GAT TTG	339
Asn Asp Leu Leu Val Ala Ile Gln Leu Val Gln His Asp Val Asp Leu	
90 95 100 105	
AGC GCG TTT GAT CAC CCT TTA GGG TTC ATC CCA GAA AGC GCG ATT TTT	387
Ser Ala Phe Asp His Pro Leu Gly Phe Ile Pro Glu Ser Ala Ile Phe	
110 115 120	
ATT GAA ACG AGC GAA AGT TTG AAC GCT TTG GCT AAA GAA GTC GCT AAT	435
Ile Glu Thr Ser Glu Ser Leu Asn Ala Leu Ala Lys Glu Val Ala Asn	
125 130 135	
GAA CAG CAT ATC GTG CTC AAA GAA GGC GTC ATC GCA TCA GGC GAT CAG	483
Glu Gln His Ile Val Leu Lys Glu Gly Val Ile Ala Ser Gly Asp Gln	
140 145 150	
TTT GTG CAT AGC AAA GAA AGG AAA GAG TTT TTA GTT AGC GAG TTT AAA	531
Phe Val His Ser Lys Glu Arg Lys Glu Phe Leu Val Ser Glu Phe Lys	
155 160 165	
GCG AGC GCG GTG GAA ATG GAG GGG GCG AGC GTG GCG TTT GTG TGC CAA	579
Ala Ser Ala Val Glu Met Glu Gly Ala Ser Val Ala Phe Val Cys Gln	
170 175 180 185	

AAA TTT GGC GTG CCA TGC TGT GTG TTA AGG AGC ATT AGC GAT AAC GCT 627
 Lys Phe Gly Val Pro Cys Cys Val Leu Arg Ser Ile Ser Asp Asn Ala
 190 195 200

GAT GAG GAA GCT AAC ATG AGC TTT GAT GCG TTT TTA GAA AAA AGC GCT 675
 Asp Glu Glu Ala Asn Met Ser Phe Asp Ala Phe Leu Glu Lys Ser Ala
 205 210 215

CAA ACT TCA GCG AAA TTC TTA AAA AGC ATG GTG GAT GAG CTT TAGGGTTTG 726
 Gln Thr Ser Ala Lys Phe Leu Lys Ser Met Val Asp Glu Leu
 220 225 230

TTTTTATAGA GGGGTGGAA 745

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met Val Gln Lys Ile Gly Ile Leu Gly Ala Met Arg Glu Glu Ile Thr
 1 5 10 15
 Pro Ile Leu Glu Leu Phe Gly Val Asp Phe Glu Glu Ile Pro Leu Gly
 20 25 30
 Gly Asn Val Phe His Lys Gly Val Tyr His Asn Lys Glu Ile Ile Val
 35 40 45
 Ala Tyr Ser Lys Ile Gly Lys Val His Ser Thr Leu Thr Thr Thr Ser
 50 55 60
 Met Ile Leu Ala Phe Gly Val Gln Lys Val Leu Phe Ser Gly Val Ala
 65 70 75 80
 Gly Ser Leu Val Lys Asp Leu Lys Ile Asn Asp Leu Leu Val Ala Ile
 85 90 95
 Gln Leu Val Gln His Asp Val Asp Leu Ser Ala Phe Asp His Pro Leu
 100 105 110
 Gly Phe Ile Pro Glu Ser Ala Ile Phe Ile Glu Thr Ser Glu Ser Leu
 115 120 125
 Asn Ala Leu Ala Lys Glu Val Ala Asn Glu Gln His Ile Val Leu Lys
 130 135 140
 Glu Gly Val Ile Ala Ser Gly Asp Gln Phe Val His Ser Lys Glu Arg
 145 150 155 160
 Lys Glu Phe Leu Val Ser Glu Phe Lys Ala Ser Ala Val Glu Met Glu
 165 170 175
 Gly Ala Ser Val Ala Phe Val Cys Gln Lys Phe Gly Val Pro Cys Cys
 180 185 190
 Val Leu Arg Ser Ile Ser Asp Asn Ala Asp Glu Glu Ala Asn Met Ser
 195 200 205
 Phe Asp Ala Phe Leu Glu Lys Ser Ala Gln Thr Ser Ala Lys Phe Leu
 210 215 220
 Lys Ser Met Val Asp Glu Leu
 225 230

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 56...1945

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GGTGTCTTA AACAGCAGGG TGAAAGAGAT TTAAAAGAA AGCGCTCTGC ATTCT ATG	58
Met	
1	
CAA GAT AGT TTG CAT TTT AAG GTT AAT GAA GTG CAA GGG GTT TTA GAA	106
Gln Asp Ser Leu His Phe Lys Val Asn Glu Val Gln Gly Val Leu Glu	
5 10 15	
AAC ACT TAT ACG AGC ATG GGC ATT GTT AAA GAA ATG CTC CCT AAA GAC	154
Asn Thr Tyr Thr Ser Met Gly Ile Val Lys Glu Met Leu Pro Lys Asp	
20 25 30	
ACC AAA AGA GAA ATC AAA ATC GGC TTG TTA AAA AAC TTC ATT TTA GCC	202
Thr Lys Arg Glu Ile Lys Ile Gly Leu Leu Lys Asn Phe Ile Leu Ala	
35 40 45	
AAT TCG CAT GTC GCT GGG GTG AGC ATG TTT TTT AAA GGC AGA GAA GAT	250
Asn Ser His Val Ala Gly Val Ser Met Phe Phe Lys Gly Arg Glu Asp	
50 55 60 65	
TTA AGA TTA ACG CTT TTA AGG GAT AAC AAT ACG ATT AAG CTA GTG GAA	298
Leu Arg Leu Thr Leu Leu Arg Asp Asn Asn Thr Ile Lys Leu Val Glu	
70 75 80	
AAT CCG TCA TTA GAG AAT AGC CCT TTA GCG CAA AAA GCG ATG AAA AAT	346
Asn Pro Ser Leu Glu Asn Ser Pro Leu Ala Gln Lys Ala Met Lys Asn	
85 90 95	
AAA GAA ATT TCT AAA AGT TTG GGT TAT TAT AGG AAA ATG CCT AAT GGG	394
Lys Glu Ile Ser Lys Ser Leu Gly Tyr Tyr Arg Lys Met Pro Asn Gly	
100 105 110	
GCG GAA GTT TAT GGG GTG GAT ATT CTT TTA CCT TTA TTG AAT GAG AAC	442
Ala Glu Val Tyr Gly Val Asp Ile Leu Leu Pro Leu Leu Asn Glu Asn	
115 120 125	
GCT CAA GAG GTT GTA GGG GCT TTG ATG ATT TTT ATT TCC ATT GAC AGC	490
Ala Gln Glu Val Val Gly Ala Leu Met Ile Phe Ile Ser Ile Asp Ser	
130 135 140 145	
TTC AGC AAT GAA ATC ACT AAA AAC AGG AGC GAT TTA TTT TTA ATT GGC	538
Phe Ser Asn Glu Ile Thr Lys Asn Arg Ser Asp Leu Phe Leu Ile Gly	

150								155					160					
ACT Thr	AAA Lys	GGT Gly	AAA Lys	GTG Val	CTT Leu	TTG Leu	AGC Ser	GCG Ala	AAT Asn	AAG Lys	AGT Ser	TTG Leu	CAA Gln	GAC Asp	AAA Lys	586		
165								170					175					
CCT Pro	ATC Ile	GCA Ala	GAA Glu	ATT Ile	TAT Tyr	AAG Lys	AGC Ser	GTG Val	CCT Pro	AAA Lys	GCC Ala	ACC Thr	AAC Asn	GAA Glu	GTG Val	634		
180								185					190					
ATG Met	GCT Ala	ATT Ile	TTA Leu	GAA Glu	AAC Asn	GGC Gly	TCT Ser	AAA Lys	GCG Ala	ACT Thr	TTA Leu	GAA Glu	TAC Tyr	TTA Leu	GAT Asp	682		
195								200					205					
CCC Pro	TTT Phe	AGC Ser	CAT His	AAG Lys	GAA Glu	AAT Asn	TTT Phe	TTA Leu	GCC Ala	GTT Val	GAA Glu	ACC Thr	TTT Phe	AAA Lys	ATG Met	730		
210								220					225					
CTA Leu	GGC Gly	AAA Lys	ACA Thr	GAA Glu	AGT Ser	AAA Lys	GAC Asp	AAT Asn	CTT Leu	AAT Asn	TGG Trp	ATG Met	ATC Ile	GCT Ala	TTA Leu	778		
230								235					240					
ATC Ile	ATT Ile	GAA Glu	AAA Lys	GAC Asp	AAG Lys	GTC Val	TAT Tyr	GAG Glu	CAA Gln	GTA Val	GGC Gly	TCG Ser	GTG Val	CGT Arg	TTT Phe	826		
245								250					255					
GTG Val	GTG Val	ATC Ile	ATA Ile	GCG Ala	AGC Ser	GCA Ala	ATC Ile	ATG Met	GTG Val	TTA Leu	GCC Ala	TTG Leu	ATT Ile	ATA Ile	GCG Ala	874		
260								265					270					
ATC Ile	ACT Thr	CTC Leu	TTA Leu	ATG Met	CGA Arg	GCG Ala	ATC Ile	GTG Val	AGC Ser	AGT Ser	CGT Arg	TTG Leu	GAA Glu	GCC Ala	GTT Val	922		
275								280					285					
TCT Ser	AGC Ser	ACC Thr	TTG Leu	TCT Ser	CAT His	TTC Phe	TTT Phe	AAA Lys	TTA Leu	TTG Leu	AAC Asn	AAT Asn	CAA Gln	GCC Ala	AAT Asn	970		
290								295					300					
TCT Ser	AGC Ser	GGT Gly	ATT Ile	AAA Lys	TTG Leu	ATT Ile	GAA Glu	GCG Ala	AAA Lys	TCC Ser	AAT Asn	GAC Asp	GAG Glu	TTA Leu	GGC Gly	1018		
310								315					320					
CGC Arg	ATG Met	CAA Gln	ACA Thr	GCG Ala	ATC Ile	AAT Asn	AAA Lys	AAT Asn	ATC Ile	TTG Leu	CAA Gln	ACC Thr	CAA Gln	AAA Lys	ATC Ile	1066		
325								330					335					
ATG Met	CAA Gln	GAA Glu	GAC Asp	AGG Arg	CAA Gln	GCC Ala	GTC Val	CAA Gln	GAC Asp	ACC Thr	ATT Ile	AAA Lys	GTG Val	GTT Val	TCA Ser	1114		
340								345					350					
GAT Asp	GTG Val	AAA Lys	GCA Ala	GGG Gly	AAT Asn	TTT Phe	GCG Ala	GTG Val	CGC Arg	ATC Ile	ACG Thr	GCT Ala	GAG Glu	CCC Pro	GCA Ala	1162		
355								360					365					
AGC Ser	CCT Pro	GAT Asp	TTG Leu	AAA Lys	GAA Glu	TTG Leu	AGG Arg	GAC Asp	GCG Ala	CTA Leu	AAT Asn	GGG Gly	ATC Ile	ATG Met	GAT Asp	1210		
370								375					380					
385																		

TAT Tyr	TTG Leu	CAA Gln	GAA Glu	AGC Ser 390	GTA Val	GGG Gly	ACT Thr	CAC His	ATG Met 395	CCA Pro	AGC Ser	ATT Ile	TTC Phe	AAA Lys 400	ATC Ile	1258
TTT Phe	GAA Glu	AGC Ser	TAT Tyr 405	TCT Ser	GGT Gly	TTG Leu	GAT Asp	TTT Phe 410	AGA Arg	GGC Gly	CGG Arg	ATC Ile	CAA Gln 415	AAC Asn	GCT Ala	1306
TCG Ser	GGT Gly	AGG Arg 420	GTG Val	GAA Glu	CTG Leu	GTT Val	ACT Thr 425	AAC Asn	GCT Ala	TTA Leu	GGG Gly	CAA Gln 430	GAA Glu	ATC Ile	CAA Gln	1354
AAA Lys	ATG Met 435	CTA Leu	GAA Glu	ACT Thr	TCG Ser	TCT Ser 440	AAT Asn	TTT Phe	GCC Ala	AAA Lys	GAT Asp 445	TTA Leu	GCG Ala	AAC Asn	GAT Asp	1402
AGC Ser 450	GCG Ala	AAT Asn	TTA Leu	AAA Lys	GAG Glu 455	TGC Cys	GTG Val	CAA Gln	AAT Asn	TTA Leu 460	GAA Glu	AAA Lys	GCT Ala	TCA Ser	AAC Asn 465	1450
TCC Ser	CAA Gln	CAC His	AAA Lys	AGC Ser 470	TTG Leu	ATG Met	GAA Glu	ACT Thr	TCC Ser 475	AAA Lys	ACG Thr	ATA Ile	GAA Glu	AAT Asn 480	ATC Ile	1498
ACC Thr	ACT Thr	TCC Ser	ATT Ile 485	CAA Gln	GGC Gly	GTG Val	AGC Ser	TCT Ser 490	CAA Gln	AGT Ser	GAA Glu	GCC Ala	ATG Met 495	ATT Ile	GAA Glu	1546
CAA Gln	GGG Gly 500	CAA Gln	GAC Asp	ATT Ile	AAA Lys	AGC Ser	ATT Ile 505	GTA Val	GAA Glu	ATC Ile	ATT Ile	AGA Arg 510	GAT Asp	ATT Ile	GCT Ala	1594
GAT Asp	CAA Gln 515	ACC Thr	AAT Asn	CTT Leu	TTA Leu	GCC Ala 520	TTA Leu	AAC Asn	GCC Ala	GCT Ala	ATT Ile 525	GAA Glu	GCC Ala	GCA Ala	AGG Arg	1642
GCC Ala 530	GGC Gly	GAG Glu	CAT His	GGC Gly	AGA Arg 535	GGC Gly	TTT Phe	GCG Ala	GTG Val	GTG Val 540	GCT Ala	GAT Asp	GAG Glu	GTA Val	AGA Arg 545	1690
AAG Lys	CTC Leu	GCT Ala	GAA Glu	AGG Arg 550	ACG Thr	CAA Gln	AAA Lys	TCG Ser	CTC Leu 555	AGC Ser	GAG Glu	ATT Ile	GAA Glu	GCC Ala 560	AAT Asn	1738
ATC Ile	AAT Asn	ATT Ile	TTA Leu 565	GTG Val	CAA Gln	AGC Ser	ATT Ile	TCA Ser 570	GAC Asp	ACG Thr	AGC Ser	GAA Glu	AGC Ser 575	ATT Ile	AAA Lys	1786
AAC Asn	CAG Gln	GTT Val 580	AAA Lys	GAA Glu	GTG Val	GAA Glu	GAA Glu 585	ATC Ile	AAC Asn	GCT Ala	TCT Ser	ATT Ile 590	GAA Glu	GCC Ala	TTA Leu	1834
AGA Arg	TCG Ser 595	GTT Val	ACT Thr	GAG Glu	GGC Gly	AAT Asn 600	CTA Leu	AAA Lys	ATC Ile	GCT Ala	AGC Ser 605	GAT Asp	TCT Ser	TTA Leu	GAA Glu	1882
ATC Ile	AGT Ser	CAA Gln	GAA Glu	ATT Ile	GAC Asp	AAA Lys	GTT Val	TCT Ser	AAC Asn	GAT Asp	ATT Ile	TTA Leu	GAA Glu	GAT Asp	GTG Val	1930

610

615

620

625

AAT AAA AAG CAG TTT TAATGCTCAT TCATATTTGC TGCTCAGTGG ATAACCTCTA T 1986
 Asn Lys Lys Gln Phe
 630

1986

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

Met	Gln	Asp	Ser	Leu	His	Phe	Lys	Val	Asn	Glu	Val	Gln	Gly	Val	Leu
1				5				10						15	
Glu	Asn	Thr	Tyr	Thr	Ser	Met	Gly	Ile	Val	Lys	Glu	Met	Leu	Pro	Lys
			20					25					30		
Asp	Thr	Lys	Arg	Glu	Ile	Lys	Ile	Gly	Leu	Leu	Lys	Asn	Phe	Ile	Leu
		35					40					45			
Ala	Asn	Ser	His	Val	Ala	Gly	Val	Ser	Met	Phe	Phe	Lys	Gly	Arg	Glu
		50				55					60				
Asp	Leu	Arg	Leu	Thr	Leu	Leu	Arg	Asp	Asn	Asn	Thr	Ile	Lys	Leu	Val
65					70					75				80	
Glu	Asn	Pro	Ser	Leu	Glu	Asn	Ser	Pro	Leu	Ala	Gln	Lys	Ala	Met	Lys
				85					90					95	
Asn	Lys	Glu	Ile	Ser	Lys	Ser	Leu	Gly	Tyr	Tyr	Arg	Lys	Met	Pro	Asn
			100					105					110		
Gly	Ala	Glu	Val	Tyr	Gly	Val	Asp	Ile	Leu	Leu	Pro	Leu	Leu	Asn	Glu
		115					120					125			
Asn	Ala	Gln	Glu	Val	Val	Gly	Ala	Leu	Met	Ile	Phe	Ile	Ser	Ile	Asp
		130				135					140				
Ser	Phe	Ser	Asn	Glu	Ile	Thr	Lys	Asn	Arg	Ser	Asp	Leu	Phe	Leu	Ile
145					150					155				160	
Gly	Thr	Lys	Gly	Lys	Val	Leu	Leu	Ser	Ala	Asn	Lys	Ser	Leu	Gln	Asp
			165						170					175	
Lys	Pro	Ile	Ala	Glu	Ile	Tyr	Lys	Ser	Val	Pro	Lys	Ala	Thr	Asn	Glu
			180					185					190		
Val	Met	Ala	Ile	Leu	Glu	Asn	Gly	Ser	Lys	Ala	Thr	Leu	Glu	Tyr	Leu
		195					200					205			
Asp	Pro	Phe	Ser	His	Lys	Glu	Asn	Phe	Leu	Ala	Val	Glu	Thr	Phe	Lys
		210				215					220				
Met	Leu	Gly	Lys	Thr	Glu	Ser	Lys	Asp	Asn	Leu	Asn	Trp	Met	Ile	Ala
225					230					235				240	
Leu	Ile	Ile	Glu	Lys	Asp	Lys	Val	Tyr	Glu	Gln	Val	Gly	Ser	Val	Arg
			245						250					255	
Phe	Val	Val	Ile	Ile	Ala	Ser	Ala	Ile	Met	Val	Leu	Ala	Leu	Ile	Ile
			260					265					270		
Ala	Ile	Thr	Leu	Leu	Met	Arg	Ala	Ile	Val	Ser	Ser	Arg	Leu	Glu	Ala
		275					280					285			
Val	Ser	Ser	Thr	Leu	Ser	His	Phe	Phe	Lys	Leu	Leu	Asn	Asn	Gln	Ala
		290				295					300				

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

GAGATAA	ATG	ATG	TTT	TCT	TCA	ATG	TTT	GCT	TCG	TTG	GGG	ACT	CGT	ATC	49	
Met	Met	Phe	Ser	Ser	Met	Phe	Ala	Ser	Leu	Gly	Thr	Arg	Ile			
1				5					10							
ATG	CTG	GTC	GTG	TTA	GCC	GCT	CTT	TTA	GGT	TTA	GGG	GGG	CTT	TTT	ATT	97
Met	Leu	Val	Val	Leu	Ala	Ala	Leu	Leu	Gly	Leu	Gly	Gly	Leu	Phe	Ile	
15				20					25						30	
GGT	TTT	GTA	AAG	GTT	ATG	CAA	AAA	GAT	GTG	TTA	GCG	CAA	CTC	ATG	GAG	145
Gly	Phe	Val	Lys	Val	Met	Gln	Lys	Asp	Val	Leu	Ala	Gln	Leu	Met	Glu	
			35					40						45		
CAT	TTA	GAA	ACC	GGG	CAA	TAC	AAA	AAG	CGT	GAA	AAA	ACG	CTC	GCT	TAC	193
His	Leu	Glu	Thr	Gly	Gln	Tyr	Lys	Lys	Arg	Glu	Lys	Thr	Leu	Ala	Tyr	
			50					55					60			
ATG	ACA	AAA	ATT	ATT	GAA	CAG	GGC	ATT	CAT	GAG	TAT	TAC	AAA	AAT	TTT	241
Met	Thr	Lys	Ile	Ile	Glu	Gln	Gly	Ile	His	Glu	Tyr	Tyr	Lys	Asn	Phe	
		65					70					75				
GAC	AAT	GCT	ACT	GCA	AGA	AAA	ATG	GCG	TTA	GAT	TAT	TTC	AAA	CGC	ATC	289
Asp	Asn	Ala	Thr	Ala	Arg	Lys	Met	Ala	Leu	Asp	Tyr	Phe	Lys	Arg	Ile	
	80					85					90					
AAC	GAC	GAT	AAG	GGC	ATG	ATT	TAT	ATG	GTG	GTG	GTG	GAT	AAA	AAC	GGG	337
Asn	Asp	Asp	Lys	Gly	Met	Ile	Tyr	Met	Val	Val	Val	Asp	Lys	Asn	Gly	
95				100					105						110	
GTG	GTA	TTG	TTT	GAT	CCG	GTC	AAT	CCT	AAA	ACC	GTA	GNC	CAA	TCA	GGG	385
Val	Val	Leu	Phe	Asp	Pro	Val	Asn	Pro	Lys	Thr	Val	Xaa	Gln	Ser	Gly	
			115					120						125		
CTT	GAC	GCT	CAG	AGC	GTT	GAT	GGG	GTG	TAT	TAT	GTT	AGG	GGG	TAT	TTG	433
Leu	Asp	Ala	Gln	Ser	Val	Asp	Gly	Val	Tyr	Tyr	Val	Arg	Gly	Tyr	Leu	
			130				135						140			
GAG	GCG	GCC	AAA	AAA	GGG	GGA	GGC	TAC	ACT	TAT	TAT	AAA	ATG	CCT	AAA	481
Glu	Ala	Ala	Lys	Lys	Gly	Gly	Gly	Tyr	Thr	Tyr	Tyr	Lys	Met	Pro	Lys	
		145				150						155				
TAC	GAT	GGA	GGC	GTA	CCG	GAG	AAA	AAA	TTC	GCC	TAC	TCG	CAT	TAT	GAT	529
Tyr	Asp	Gly	Gly	Val	Pro	Glu	Lys	Lys	Phe	Ala	Tyr	Ser	His	Tyr	Asp	
	160				165						170					
GAA	GTT	TCT	CAA	ATG	GTG	ATC	GCA	ACG	ACT	TCC	TAT	TAC	ACT	GAC	ATT	577
Glu	Val	Ser	Gln	Met	Val	Ile	Ala	Thr	Thr	Ser	Tyr	Tyr	Thr	Asp	Ile	
175				180						185					190	
AAC	ACA	GAA	AAT	AAA	GCG	ATC	AAA	GAA	GGC	GTG	AAT	AAG	GTT	TTT	GAT	625
Asn	Thr	Glu	Asn	Lys	Ala	Ile	Lys	Glu	Gly	Val	Asn	Lys	Val	Phe	Asp	
			195					200					205			
GAA	AAC	ACC	ACG	AAA	TTA	TTC	CTT	TGG	ATA	CTG	ACA	GCG	ACG	ATA	GCG	673
Glu	Asn	Thr	Thr	Lys	Leu	Phe	Leu	Trp	Ile	Leu	Thr	Ala	Thr	Ile	Ala	
			210				215						220			

CTA Leu	GTG Val	GTT Val 225	TTG Leu	ACG Thr	CTC Leu	ATA Ile	TAC Tyr 230	GCT Ala	AAA Lys	TTA Leu	AGG Arg	ATC Ile 235	GTG Val	AAA Lys	CGC Arg	721
ATT Ile	GAT Asp 240	GAA Glu	CTG Leu	GTC Val	CTT Leu	AAA Lys 245	ATC Ile	AAC Asn	GCT Ala	TTT Phe 250	AGC Ser	CGT Arg	GGG Gly	GAT Asp	AAG Lys	769
GAT Asp 255	TTG Leu	AGA Arg	GCC Ala	AAA Lys 260	ATT Ile	GAT Asp	GTG Val	GGT Gly	GAT Asp 265	CGC Arg	AAC Asn	GAT Asp	GAA Glu	ATC Ile	TCG Ser 270	817
CAA Gln	GTG Val	GGC Gly	CGT Arg	GGG Gly 275	ATC Ile	AAT Asn	TTG Leu	TTT Phe 280	GTG Val 280	GAA Glu	AAC Asn	GCC Ala	CGC Arg	TTG Leu 285	ATT Ile	865
ATG Met	GAA Glu	GAG Glu 290	ATT Ile	AAA Lys	GGG Gly	ATT Ile	TCC Ser	ACC Thr 295	CTC Leu	AAT Asn	AAA Lys	ACT Thr 300	TCA Ser	ATG Met	GAT Asp	913
AAA Lys	TTA Leu 305	GTC Val	CAA Gln	ATC Ile	ACG Thr	CAA Gln	GAA Glu 310	ACC Thr	CAA Gln	AAG Lys	AGC Ser 315	ATG Met	AAA Lys	GAT Asp	TCC Ser	961
TCA Ser	ACC Thr 320	ACC Thr	CTA Leu	AAT Asn	TCC Ser	GTG Val 325	AAA Lys	AAT Asn	AAA Lys	GCC Ala 330	ACT Thr	GAT Asp	ATA Ile	GCG Ala	AGC Ser	1009
ATG Met 335	ATG Met	AAT Asn	GCT Ala	TCC Ser 340	ATA Ile	GAG Glu	CAA Gln	TCT Ser	CAA Gln 345	GGG Gly	TTA Leu	AGG Arg	AAG Lys	CGT Arg	TTG Leu 350	1057
ATT Ile	GAA Glu	ACG Thr	CAA Gln 355	GGG Gly	CTG Leu	GTC Val	AAA Lys	GAG Glu	AGC Ser 360	AAG Lys	GAT Asp	GCG Ala	ATC Ile	GGG Gly 365	GAT Asp	1105
TTA Leu	TTT Phe	TCT Ser 370	CAA Gln	ATC Ile	ACA Thr	GAG Glu	AGC Ser	GCG Ala 375	CAC His	ACT Thr	GAA Glu	GAG Glu	GAA Glu 380	CTC Leu	TCT Ser	1153
AGC Ser	AAA Lys	GTG Val 385	GAG Glu	CAG Gln	CTA Leu	AGC Ser	CGT Arg 390	AAC Asn	GCT Ala	GAT Asp	GAT Asp	GTC Val 395	AAA Lys	TCC Ser	ATT Ile	1201
CTG Leu	GAT Asp 400	ATT Ile	ATC Ile	AAT Asn	GAT Asp	ATT Ile 405	GCC Ala	GAT Asp	CAA Gln	ACG Thr 410	AAT Asn	TTA Leu	TTA Leu	GCC Ala	CTA Leu	1249
AAC Asn 415	GCT Ala	GCT Ala	ATT Ile	GAA Glu 420	GCC Ala	GCA Ala	AGG Arg	GCT Ala	GGC Gly 425	GAG Glu	CAT His	GGC Gly	AGA Arg	GGC Gly	TTT Phe 430	1297
GCG Ala	GTG Val	GTG Val	GCT Ala 435	GAT Asp	GAA Glu	GTT Val	AGG Arg	AAT Asn 440	TTA Leu	GCC Ala	GGG Gly	CGC Arg	ACT Thr 445	CAA Gln	AAG Lys	1345
TCT Ser	TTA Leu	GCC Ala	GAA Glu	ATC Ile	AAT Asn	TCC Ser	ACT Thr	ATC Ile	ATG Met	GTG Val	ATT Ile	GTC Val	CAA Gln	GAA Glu	ATC Ile	1393

Leu	Phe	Asp	Pro	Val	Asn	Pro	Lys	Thr	Val	Xaa	Gln	Ser	Gly	Leu	Asp
		115					120					125			
Ala	Gln	Ser	Val	Asp	Gly	Val	Tyr	Tyr	Val	Arg	Gly	Tyr	Leu	Glu	Ala
		130					135					140			
Ala	Lys	Lys	Gly	Gly	Gly	Tyr	Thr	Tyr	Tyr	Lys	Met	Pro	Lys	Tyr	Asp
145					150					155					160
Gly	Gly	Val	Pro	Glu	Lys	Lys	Phe	Ala	Tyr	Ser	His	Tyr	Asp	Glu	Val
				165					170					175	
Ser	Gln	Met	Val	Ile	Ala	Thr	Thr	Ser	Tyr	Tyr	Thr	Asp	Ile	Asn	Thr
			180					185					190		
Glu	Asn	Lys	Ala	Ile	Lys	Glu	Gly	Val	Asn	Lys	Val	Phe	Asp	Glu	Asn
		195					200					205			
Thr	Thr	Lys	Leu	Phe	Leu	Trp	Ile	Leu	Thr	Ala	Thr	Ile	Ala	Leu	Val
		210				215						220			
Val	Leu	Thr	Leu	Ile	Tyr	Ala	Lys	Leu	Arg	Ile	Val	Lys	Arg	Ile	Asp
225					230					235					240
Glu	Leu	Val	Leu	Lys	Ile	Asn	Ala	Phe	Ser	Arg	Gly	Asp	Lys	Asp	Leu
				245					250					255	
Arg	Ala	Lys	Ile	Asp	Val	Gly	Asp	Arg	Asn	Asp	Glu	Ile	Ser	Gln	Val
			260					265					270		
Gly	Arg	Gly	Ile	Asn	Leu	Phe	Val	Glu	Asn	Ala	Arg	Leu	Ile	Met	Glu
		275					280					285			
Glu	Ile	Lys	Gly	Ile	Ser	Thr	Leu	Asn	Lys	Thr	Ser	Met	Asp	Lys	Leu
		290				295					300				
Val	Gln	Ile	Thr	Gln	Glu	Thr	Gln	Lys	Ser	Met	Lys	Asp	Ser	Ser	Thr
305					310					315					320
Thr	Leu	Asn	Ser	Val	Lys	Asn	Lys	Ala	Thr	Asp	Ile	Ala	Ser	Met	Met
				325					330					335	
Asn	Ala	Ser	Ile	Glu	Gln	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Leu	Ile	Glu
			340					345					350		
Thr	Gln	Gly	Leu	Val	Lys	Glu	Ser	Lys	Asp	Ala	Ile	Gly	Asp	Leu	Phe
		355					360					365			
Ser	Gln	Ile	Thr	Glu	Ser	Ala	His	Thr	Glu	Glu	Glu	Leu	Ser	Ser	Lys
		370				375					380				
Val	Glu	Gln	Leu	Ser	Arg	Asn	Ala	Asp	Asp	Val	Lys	Ser	Ile	Leu	Asp
385					390					395					400
Ile	Ile	Asn	Asp	Ile	Ala	Asp	Gln	Thr	Asn	Leu	Leu	Ala	Leu	Asn	Ala
				405					410					415	
Ala	Ile	Glu	Ala	Ala	Arg	Ala	Gly	Glu	His	Gly	Arg	Gly	Phe	Ala	Val
			420					425					430		
Val	Ala	Asp	Glu	Val	Arg	Asn	Leu	Ala	Gly	Arg	Thr	Gln	Lys	Ser	Leu
		435					440					445			
Ala	Glu	Ile	Asn	Ser	Thr	Ile	Met	Val	Ile	Val	Gln	Glu	Ile	Asn	Ala
		450				455					460				
Val	Ser														

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...474
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

CCTTGAGATT GCTCT ATG GAA GCA TTC ATC ATG CTC GCT ATA TCA GTG GCT	51
Met Glu Ala Phe Ile Met Leu Ala Ile Ser Val Ala	
1 5 10	
TTA TTT TTC ACG GAA TTT AGG GTG GTT GAG GAA TCT TTC ATG CTC TTT	99
Leu Phe Phe Thr Glu Phe Arg Val Val Glu Glu Ser Phe Met Leu Phe	
15 20 25	
TGG GTT TCT TGC GTG ATT TGG ACT AAT TTA TCC ATT GAA GTT TTA TTG	147
Trp Val Ser Cys Val Ile Trp Thr Asn Leu Ser Ile Glu Val Leu Leu	
30 35 40	
AGG GTG GAA ATC CCT TTA ATC TCT TCC ATA ATC AAG CGG GCG TTT TCC	195
Arg Val Glu Ile Pro Leu Ile Ser Ser Ile Ile Lys Arg Ala Phe Ser	
45 50 55 60	
ACA AAC AAA TTG ATC CCA CGG CCC ACT TGC GAG ATT TCA TCG TTG CGA	243
Thr Asn Lys Leu Ile Pro Arg Pro Thr Cys Glu Ile Ser Ser Leu Arg	
65 70 75	
TCA CCC ACA TCA ATT TTG GCT CTC AAA TCC TTA TCC CCA CGG CTA AAA	291
Ser Pro Thr Ser Ile Leu Ala Leu Lys Ser Leu Ser Pro Arg Leu Lys	
80 85 90	
GCG TTG ATT TTA AGG ACC AGT TCA TCA ATG CGT TTC ACG ATC CTT AAT	339
Ala Leu Ile Leu Arg Thr Ser Ser Ser Met Arg Phe Thr Ile Leu Asn	
95 100 105	
TTA GCG TAT ATG AGC GTC AAA ACC ACT AGC GCT ATC GTC GCT GTC AGT	387
Leu Ala Tyr Met Ser Val Lys Thr Thr Ser Ala Ile Val Ala Val Ser	
110 115 120	
ATC CAA AGG AAT AAT TTC GTG GTG TTT TCA TCA AAA ACC TTA TTC ACG	435
Ile Gln Arg Asn Asn Phe Val Val Phe Ser Ser Lys Thr Leu Phe Thr	
125 130 135 140	
CCT TCT TTG ATC GCT TTA TTT TCT GTG TTA ATG TCA GTG TAATAGGAAG TC	486
Pro Ser Leu Ile Ala Leu Phe Ser Val Leu Met Ser Val	
145 150	

GTTGCGATCA CCATTGAGA AACTTCATCA TAATGCGAG

525

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

Met Glu Ala Phe Ile Met Leu Ala Ile Ser Val Ala Leu Phe Phe Thr
1 5 10 15
Glu Phe Arg Val Val Glu Glu Ser Phe Met Leu Phe Trp Val Ser Cys
20 25 30
Val Ile Trp Thr Asn Leu Ser Ile Glu Val Leu Leu Arg Val Glu Ile
35 40 45
Pro Leu Ile Ser Ser Ile Ile Lys Arg Ala Phe Ser Thr Asn Lys Leu
50 55 60
Ile Pro Arg Pro Thr Cys Glu Ile Ser Ser Leu Arg Ser Pro Thr Ser
65 70 75 80
Ile Leu Ala Leu Lys Ser Leu Ser Pro Arg Leu Lys Ala Leu Ile Leu
85 90 95
Arg Thr Ser Ser Ser Met Arg Phe Thr Ile Leu Asn Leu Ala Tyr Met
100 105 110
Ser Val Lys Thr Thr Ser Ala Ile Val Ala Val Ser Ile Gln Arg Asn
115 120 125
Asn Phe Val Val Phe Ser Ser Lys Thr Leu Phe Thr Pro Ser Leu Ile
130 135 140
Ala Leu Phe Ser Val Leu Met Ser Val
145 150

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...1164
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

AAATTCAATA AAAAAGGAAA AACC ATG CGC ATG CAA ACC AAA TTA ATC CAT 51
Met Arg Met Gln Thr Lys Leu Ile His
1 5
GGG GGC ATT AGT GAG GAC GCA ACA ACG GGG GCG GTG AGC GTG CCT ATT 99

Gly 10	Gly	Ile	Ser	Glu	Asp 15	Ala	Thr	Thr	Gly	Ala 20	Val	Ser	Val	Pro	Ile 25	
TAT Tyr	CAA Gln	ACT Thr	TCC Ser	ACC Thr 30	TAC Tyr	CGC Arg	CAA Gln	GAC Asp	GCC Ala 35	ATA Ile	GGC Gly	CGC Arg	CAT His	AAG Lys 40	GGC Gly	147
TAT Tyr	GAA Glu	TAC Tyr	TCT Ser 45	CGC Arg	TCA Ser	GGC Gly	AAC Asn	CCC Pro 50	ACG Thr	CGC Arg	TTT Phe	GCT Ala	TTA Leu 55	GAA Glu	GAA Glu	195
CTC Leu	ATC Ile	GCT Ala 60	GAT Asp	TTA Leu	GAA Glu	GGG Gly	GGG Gly 65	GTT Val	AAG Lys	GGG Gly	TTT Phe 70	GCT Ala	TTT Phe	GCC Ala	TCT Ser	243
GGA Gly	TTA Leu 75	GCT Ala	GGA Gly	ATC Ile	CAC His	GCC Ala 80	GTT Val	TTT Phe	TCC Ser	CTC Leu 85	TTG Leu	CAA Gln	TCA Ser	GGC Gly	GAT Asp	291
CAT His 90	GTG Val	TTA Leu	TTG Leu	GGC Gly 95	GAT Asp	GAT Asp	GTT Val	TAT Tyr	GGG Gly 100	GGG Gly	ACT Thr	TTC Phe	CGC Arg	TTG Leu 105	TTT Phe	339
AAT Asn	CAA Gln	GTG Val	CTT Leu 110	GTC Val	AAA Lys	AAC Asn	GGG Gly	CTT Leu 115	TCT Ser	TGC Cys	ACC Thr	ATT Ile	ATA Ile	GAC Asp 120	ACT Thr	387
AGC Ser	GAT Asp	ATA Ile	TCC Ser 125	CAA Gln	ATT Ile	AAA Lys	AAG Lys	GCT Ala 130	ATC Ile	AAG Lys	CCC Pro	AAC Asn	ACC Thr 135	AAA Lys	GCC Ala	435
CTT Leu	TAT Tyr	TTA Leu 140	GAA Glu	ACC Thr	CCT Pro	AGT Ser	AAC Asn 145	CCC Pro	TTG Leu	CTT Leu	AAA Lys 150	ATC Ile	ACG Thr	GAT Asp	TTA Leu	483
GCG Ala 155	CAA Gln	TGC Cys	GCT Ala	AGT Ser	GTC Val	GCT Ala 160	AAA Lys	GAT Asp	CAT His	GGT Gly	TTG Leu 165	CTC Leu	ACT Thr	ATC Ile	GTG Val	531
GAT Asp 170	AAC Asn	ACC Thr	TTT Phe	GCC Ala 175	ACC Thr	CCC Pro	TAT Tyr	TAT Tyr	CAA Gln	AAC Asn 180	CCG Pro	CTT Leu	CTT Leu	TTG Leu 185	GGA Gly	579
GCG Ala	GAC Asp	ATT Ile	GTG Val 190	GCA Ala	CAT His	AGC Ser	GGC Gly	ACC Thr	AAA Lys 195	TAC Tyr	TTA Leu	GGC Gly	GGG Gly	CAT His 200	AGC Ser	627
GAT Asp	GTG Val	GTC Val 205	GCC Ala	GGG Gly	CTT Leu	GTA Val	ACC Thr	ACT Thr 210	AAT Asn	AAT Asn	GAA Glu	GCG Ala	CTA Leu 215	GCC Ala	CAA Gln	675
GAG Glu	ATC Ile	GCT Ala 220	TTT Phe	TTC Phe	CAA Gln	AAC Asn	GCT Ala 225	ATC Ile	GGT Gly	GGG Gly	GTT Val 230	TTA Leu	GGC Gly	CCT Pro	CAA Gln	723
GAC Asp	AGC Ser 235	TGG Trp	CTG Leu	TTG Leu	CAA Gln 240	AGA Arg	GGG Gly 245	ATT Ile	AAA Lys	ACG Thr	CTG Leu 245	GGA Gly	TTG Leu	CGC Arg	ATG Met	771

GAA GCC CAT CAA AAA AAC GCT CTT TGT GTG GCT GAG TTT TTA GAA AAA	819
Glu Ala His Gln Lys Asn Ala Leu Cys Val Ala Glu Phe Leu Glu Lys	
250 255 260 265	
CAC CCT AAA GTG GAA AGG GTT TAT TAC CCG GGC CTT CCC ACT CAC CCT	867
His Pro Lys Val Glu Arg Val Tyr Tyr Pro Gly Leu Pro Thr His Pro	
270 275 280	
AAT TAC GAA CTA GCT AAA AAA CAG ATG CGT GGC TTT AGC GGG ATG CTC	915
Asn Tyr Glu Leu Ala Lys Lys Gln Met Arg Gly Phe Ser Gly Met Leu	
285 290 295	
TCT TTC ACT CTC AAA AAT GAT AGC GAG GCG GTT GCT TTT GTA GAA AGC	963
Ser Phe Thr Leu Lys Asn Asp Ser Glu Ala Val Ala Phe Val Glu Ser	
300 305 310	
CTT AAA CTA TTC ATT TTA GGC GAG AGT TTG GGC GGG GTG GAA AGT TTG	1011
Leu Lys Leu Phe Ile Leu Gly Glu Ser Leu Gly Gly Val Glu Ser Leu	
315 320 325	
GTG GGG ATT CCG GCA TTT ATG ACC CAT GCG TGC ATC CCT AAA ACG CAA	1059
Val Gly Ile Pro Ala Phe Met Thr His Ala Cys Ile Pro Lys Thr Gln	
330 335 340 345	
CGA GAA GCT GCT GGG ATT AGA GAT GGC CTG GTG CGC TTG TCT GTA GGG	1107
Arg Glu Ala Ala Gly Ile Arg Asp Gly Leu Val Arg Leu Ser Val Gly	
350 355 360	
ATT GAG CAT GAA CAG GAT TTG TTA GAA GAT TTA GAG CAA GCG TTC GCT	1155
Ile Glu His Glu Gln Asp Leu Leu Glu Asp Leu Glu Gln Ala Phe Ala	
365 370 375	
AAA ATA GGC TAAAGTTTCA TTACAATTTA TGAATAAAGG AGTTAAAAAC ATGAA	1209
Lys Ile Gly	
380	

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Met Arg Met Gln Thr Lys Leu Ile His Gly Gly Ile Ser Glu Asp Ala	
1 5 10 15	
Thr Thr Gly Ala Val Ser Val Pro Ile Tyr Gln Thr Ser Thr Tyr Arg	
20 25 30	
Gln Asp Ala Ile Gly Arg His Lys Gly Tyr Glu Tyr Ser Arg Ser Gly	
35 40 45	
Asn Pro Thr Arg Phe Ala Leu Glu Glu Leu Ile Ala Asp Leu Glu Gly	
50 55 60	
Gly Val Lys Gly Phe Ala Phe Ala Ser Gly Leu Ala Gly Ile His Ala	

65					70					75					80
Val	Phe	Ser	Leu	Leu	Gln	Ser	Gly	Asp	His	Val	Leu	Leu	Gly	Asp	Asp
				85					90					95	
Val	Tyr	Gly	Gly	Thr	Phe	Arg	Leu	Phe	Asn	Gln	Val	Leu	Val	Lys	Asn
			100					105					110		
Gly	Leu	Ser	Cys	Thr	Ile	Ile	Asp	Thr	Ser	Asp	Ile	Ser	Gln	Ile	Lys
		115					120					125			
Lys	Ala	Ile	Lys	Pro	Asn	Thr	Lys	Ala	Leu	Tyr	Leu	Glu	Thr	Pro	Ser
	130					135					140				
Asn	Pro	Leu	Leu	Lys	Ile	Thr	Asp	Leu	Ala	Gln	Cys	Ala	Ser	Val	Ala
145					150					155					160
Lys	Asp	His	Gly	Leu	Leu	Thr	Ile	Val	Asp	Asn	Thr	Phe	Ala	Thr	Pro
				165					170					175	
Tyr	Tyr	Gln	Asn	Pro	Leu	Leu	Leu	Gly	Ala	Asp	Ile	Val	Ala	His	Ser
			180					185					190		
Gly	Thr	Lys	Tyr	Leu	Gly	Gly	His	Ser	Asp	Val	Val	Ala	Gly	Leu	Val
		195					200					205			
Thr	Thr	Asn	Asn	Glu	Ala	Leu	Ala	Gln	Glu	Ile	Ala	Phe	Phe	Gln	Asn
	210					215					220				
Ala	Ile	Gly	Gly	Val	Leu	Gly	Pro	Gln	Asp	Ser	Trp	Leu	Leu	Gln	Arg
225					230					235					240
Gly	Ile	Lys	Thr	Leu	Gly	Leu	Arg	Met	Glu	Ala	His	Gln	Lys	Asn	Ala
				245					250					255	
Leu	Cys	Val	Ala	Glu	Phe	Leu	Glu	Lys	His	Pro	Lys	Val	Glu	Arg	Val
			260					265					270		
Tyr	Tyr	Pro	Gly	Leu	Pro	Thr	His	Pro	Asn	Tyr	Glu	Leu	Ala	Lys	Lys
		275					280					285			
Gln	Met	Arg	Gly	Phe	Ser	Gly	Met	Leu	Ser	Phe	Thr	Leu	Lys	Asn	Asp
	290					295					300				
Ser	Glu	Ala	Val	Ala	Phe	Val	Glu	Ser	Leu	Lys	Leu	Phe	Ile	Leu	Gly
					310					315					320
Glu	Ser	Leu	Gly	Gly	Val	Glu	Ser	Leu	Val	Gly	Ile	Pro	Ala	Phe	Met
				325					330					335	
Thr	His	Ala	Cys	Ile	Pro	Lys	Thr	Gln	Arg	Glu	Ala	Ala	Gly	Ile	Arg
			340					345					350		
Asp	Gly	Leu	Val	Arg	Leu	Ser	Val	Gly	Ile	Glu	His	Glu	Gln	Asp	Leu
		355					360					365			
Leu	Glu	Asp	Leu	Glu	Gln	Ala	Phe	Ala	Lys	Ile	Gly				
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 912 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 46...873
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

ATTATTA	ACT	TTTTATG	CTA	TAATGCG	GAGG	GTTCTTT	CAT	CAAGA	ATG	GTG	ATT	GAC		57		
												Met Val Ile Asp				
												1				
GAG	ATT	TTT	CAA	ATA	ATG	ATG	TTA	AGA	AGA	ATT	AAA	GTA	GGT	TCT	AAT	105
Glu	Ile	Phe	Gln	Ile	Met	Met	Leu	Arg	Arg	Ile	Lys	Val	Gly	Ser	Asn	
5					10					15					20	
TTG	AAT	AAA	AAA	GAG	AGT	TTG	TTA	GAT	GCG	TTT	GTT	AAA	ACC	TAT	CTG	153
Leu	Asn	Lys	Lys	Glu	Ser	Leu	Leu	Asp	Ala	Phe	Val	Lys	Thr	Tyr	Leu	
				25					30					35		
CAG	ATT	TTA	GAA	CCC	ATT	AGT	TCT	AAA	CGC	TTA	AAA	GAG	TTG	GCG	GAC	201
Gln	Ile	Leu	Glu	Pro	Ile	Ser	Ser	Lys	Arg	Leu	Lys	Glu	Leu	Ala	Asp	
			40					45					50			
TTG	AAA	ATA	TCT	TGC	GCG	ACG	ATC	AGG	AAT	TAT	TTT	CAA	ATC	CTT	TCT	249
Leu	Lys	Ile	Ser	Cys	Ala	Thr	Ile	Arg	Asn	Tyr	Phe	Gln	Ile	Leu	Ser	
		55					60					65				
AAA	GAG	GGC	ATG	CTT	TAT	CAA	GCC	CAT	TCT	AGT	GGC	GCT	AGA	TTG	CCC	297
Lys	Glu	Gly	Met	Leu	Tyr	Gln	Ala	His	Ser	Ser	Gly	Ala	Arg	Leu	Pro	
70						75					80					
ACT	TTT	AAG	GCG	TTT	GAA	AAC	TAT	TGG	CAA	AAG	TCG	TTG	CGC	TTT	GAA	345
Thr	Phe	Lys	Ala	Phe	Glu	Asn	Tyr	Trp	Gln	Lys	Ser	Leu	Arg	Phe	Glu	
85					90					95					100	
ACT	TTA	AAG	GTG	AAT	GAA	AAA	CGC	CTA	AAA	AGC	GCG	AGT	GAA	AAT	TTT	393
Thr	Leu	Lys	Val	Asn	Glu	Lys	Arg	Leu	Lys	Ser	Ala	Ser	Glu	Asn	Phe	
				105					110					115		
GGG	CTT	TTC	ACG	CTG	TTA	AAA	AAA	CCC	AGT	TTG	GAG	CGT	TTA	GAA	AGA	441
Gly	Leu	Phe	Thr	Leu	Leu	Lys	Lys	Pro	Ser	Leu	Glu	Arg	Leu	Glu	Arg	
			120					125					130			
GTC	ATT	GAG	TGC	GAA	AAA	CGC	TTT	TTG	ATT	TTG	GAC	TTT	TTG	GCG	TTT	489
Val	Ile	Glu	Cys	Glu	Lys	Arg	Phe	Leu	Ile	Leu	Asp	Phe	Leu	Ala	Phe	
		135					140					145				
TCT	TGC	GCA	CTG	GGT	TAC	AGC	GTT	AAA	ATG	GAA	AAG	TTT	TTA	TTA	GAG	537
Ser	Cys	Ala	Leu	Gly	Tyr	Ser	Val	Lys	Met	Glu	Lys	Phe	Leu	Leu	Glu	
	150					155					160					
CTT	GTG	GGC	AGA	AGC	GTT	AAA	GAA	GTG	CGC	TCA	ATC	GCT	GCT	TCT	TTC	585
Leu	Val	Gly	Arg	Ser	Val	Lys	Glu	Val	Arg	Ser	Ile	Ala	Ala	Ser	Phe	
165					170					175					180	
AAT	GCG	TTG	AGT	TTG	GCC	AGG	CAA	TTA	GAG	CGT	TTG	GAG	TAT	TCC	AAC	633
Asn	Ala	Leu	Ser	Leu	Ala	Arg	Gln	Leu	Glu	Arg	Leu	Glu	Tyr	Ser	Asn	
				185					190					195		
ACA	CAA	ATC	ACA	CGC	TTT	AAT	CTG	ATG	GGG	TTA	AAA	ACG	CTT	TTA	AAC	681
Thr	Gln	Ile	Thr	Arg	Phe	Asn	Leu	Met	Gly	Leu	Lys	Thr	Leu	Leu	Asn	
			200					205					210			
AGC	CCT	TTA	TTT	TTT	GAC	ATT	TTA	GGG	GGT	AAG	GTT	TTA	GAG	CGT	TTG	729
Ser	Pro	Leu	Phe	Phe	Asp	Ile	Leu	Gly	Gly	Lys	Val	Leu	Glu	Arg	Leu	

215		220		225	
AGT AAG GGT TTG CAT TTT ATA GAG CCT GAT TGC ATG CTA GTA ACA CGC					777
Ser Lys Gly Leu His Phe Ile Glu Pro Asp Cys Met Leu Val Thr Arg					
230		235		240	
CCT GTA GAA TTT CAA AAC AAG CGG ATG CAA CTG CTT TGC GTG GGG AAA					825
Pro Val Glu Phe Gln Asn Lys Arg Met Gln Leu Leu Cys Val Gly Lys					
245		250		255	260
CTA GAA TGC GAT TAT GAA GGG TTT TTT CAA ACG ATT TCT GAG GAG GAA T					874
Leu Glu Cys Asp Tyr Glu Gly Phe Phe Gln Thr Ile Ser Glu Glu Glu					
	265		270		275
AATGAAAGAT GAACACAACC AAGAACACGA TCATTTAA					912

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

Met Val Ile Asp Glu Ile Phe Gln Ile Met Met Leu Arg Arg Ile Lys	
1 5 10 15	
Val Gly Ser Asn Leu Asn Lys Lys Glu Ser Leu Leu Asp Ala Phe Val	
20 25 30	
Lys Thr Tyr Leu Gln Ile Leu Glu Pro Ile Ser Ser Lys Arg Leu Lys	
35 40 45	
Glu Leu Ala Asp Leu Lys Ile Ser Cys Ala Thr Ile Arg Asn Tyr Phe	
50 55 60	
Gln Ile Leu Ser Lys Glu Gly Met Leu Tyr Gln Ala His Ser Ser Gly	
65 70 75 80	
Ala Arg Leu Pro Thr Phe Lys Ala Phe Glu Asn Tyr Trp Gln Lys Ser	
85 90 95	
Leu Arg Phe Glu Thr Leu Lys Val Asn Glu Lys Arg Leu Lys Ser Ala	
100 105 110	
Ser Glu Asn Phe Gly Leu Phe Thr Leu Leu Lys Lys Pro Ser Leu Glu	
115 120 125	
Arg Leu Glu Arg Val Ile Glu Cys Glu Lys Arg Phe Leu Ile Leu Asp	
130 135 140	
Phe Leu Ala Phe Ser Cys Ala Leu Gly Tyr Ser Val Lys Met Glu Lys	
145 150 155 160	
Phe Leu Leu Glu Leu Val Gly Arg Ser Val Lys Glu Val Arg Ser Ile	
165 170 175	
Ala Ala Ser Phe Asn Ala Leu Ser Leu Ala Arg Gln Leu Glu Arg Leu	
180 185 190	
Glu Tyr Ser Asn Thr Gln Ile Thr Arg Phe Asn Leu Met Gly Leu Lys	
195 200 205	
Thr Leu Leu Asn Ser Pro Leu Phe Phe Asp Ile Leu Gly Gly Lys Val	
210 215 220	
Leu Glu Arg Leu Ser Lys Gly Leu His Phe Ile Glu Pro Asp Cys Met	
225 230 235 240	

Leu	Val	Thr	Arg	Pro	Val	Glu	Phe	Gln	Asn	Lys	Arg	Met	Gln	Leu	Leu
				245					250					255	
Cys	Val	Gly	Lys	Leu	Glu	Cys	Asp	Tyr	Glu	Gly	Phe	Phe	Gln	Thr	Ile
			260					265					270		
Ser	Glu	Glu	Glu												
			275												

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...685
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

AGCTCTTTAC TATTTTATTA TCTATCTTTT ATTAAAAAAA CTTGTTATC ATG ATA AAC	58
Met Ile Asn	
1	
ATG AAC ACA CAC ACA AGA GGC ATT GAC AGC AAT CTG ATT CAT TCG CTC	106
Met Asn Thr His Thr Arg Gly Ile Asp Ser Asn Leu Ile His Ser Leu	
5 10 15	
CAA AGC ATT TCA TTA TCC ATG TTT AGA AAG GGT TTT TTT GGG CTT TAT	154
Gln Ser Ile Ser Leu Ser Met Phe Arg Lys Gly Phe Phe Gly Leu Tyr	
20 25 30 35	
CAA GGC TCT ATT TCA GCA CGC ATT GGC GCA AAT CAA TTT GTG ATC AAC	202
Gln Gly Ser Ile Ser Ala Arg Ile Gly Ala Asn Gln Phe Val Ile Asn	
40 45 50	
AAA AGA AAC GCT GTT TTT GAT CAA TTG AAT GAA AAC ACC TTA CTG GTT	250
Lys Arg Asn Ala Val Phe Asp Gln Leu Asn Glu Asn Thr Leu Leu Val	
55 60 65	
TTG CAT GAC AAA ATA GAT TAC CGC TGG AAA GAA GCG AGC TTG GAT TCG	298
Leu His Asp Lys Ile Asp Tyr Arg Trp Lys Glu Ala Ser Leu Asp Ser	
70 75 80	
CCC ATT CAT GCG AGC GTG TAT AGG GAG TTT TTG GAC GCT AAA TTC ATC	346
Pro Ile His Ala Ser Val Tyr Arg Glu Phe Leu Asp Ala Lys Phe Ile	
85 90 95	
GCT TAC GCG CGC CCT CCT TAT AGT TTG GCG TAT TCC TTG CGC CAC AAC	394
Ala Tyr Ala Arg Pro Pro Tyr Ser Leu Ala Tyr Ser Leu Arg His Asn	
100 105 110 115	
CGA TTG CTC CCT AGA GAT TAT TTA GGG TAT CGT TCT TTG GGC GAA GAA	442

Arg	Leu	Leu	Pro	Arg	Asp	Tyr	Leu	Gly	Tyr	Arg	Ser	Leu	Gly	Glu	Glu		
				120					125					130			
ATT	TCC	ATT	TTT	AAC	CCC	AAA	GAC	TAT	GAC	AGC	TGG	CAA	GAA	AGA	GCG	490	
Ile	Ser	Ile	Phe	Asn	Pro	Lys	Asp	Tyr	Asp	Ser	Trp	Gln	Glu	Arg	Ala		
			135					140					145				
GAT	ACA	GAA	ATT	TTA	CGC	CAA	CTG	CAA	GAG	AGC	AAA	AAA	TAT	TTT	GTT	538	
Asp	Thr	Glu	Ile	Leu	Arg	Gln	Leu	Gln	Glu	Ser	Lys	Lys	Tyr	Phe	Val		
		150					155					160					
TTC	ATT	AAG	GGG	TGT	GGG	ATT	TTT	GCC	TAC	CAC	AGA	GAG	CTT	TCT	AAA	586	
Phe	Ile	Lys	Gly	Cys	Gly	Ile	Phe	Ala	Tyr	His		Glu	Leu	Ser	Lys		
	165					170				175							
CTC	ATG	GAA	GTT	TTT	GAT	TTG	ATT	GAA	AAC	TCA	TGC	AAG	GTT	TTA	CGA	634	
Leu	Met	Glu	Val	Phe	Asp	Leu	Ile	Glu	Asn	Ser	Cys	Lys	Val	Leu	Arg		
	180				185					190					195		
TTG	GGC	GAT	TTA	ATG	GAT	TAT	TGC	TAT	AAT	GAT	GAT	CCA	CGA	TTG	AGC	682	
Leu	Gly	Asp	Leu	Met	Asp	Tyr	Cys	Tyr	Asn	Asp	Asp	Pro	Arg	Leu	Ser		
				200					205					210			
GTG	TAAAAAGCTA	AAAAGGATAA	AACATGACCA	TCAAC												720	
Val																	

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Met	Ile	Asn	Met	Asn	Thr	His	Thr	Arg	Gly	Ile	Asp	Ser	Asn	Leu	Ile		
1				5					10					15			
His	Ser	Leu	Gln	Ser	Ile	Ser	Leu	Ser	Met	Phe	Arg	Lys	Gly	Phe	Phe		
			20					25					30				
Gly	Leu	Tyr	Gln	Gly	Ser	Ile	Ser	Ala	Arg	Ile	Gly	Ala	Asn	Gln	Phe		
		35				40					45						
Val	Ile	Asn	Lys	Arg	Asn	Ala	Val	Phe	Asp	Gln	Leu	Asn	Glu	Asn	Thr		
	50				55				60								
Leu	Leu	Val	Leu	His	Asp	Lys	Ile	Asp	Tyr	Arg	Trp	Lys	Glu	Ala	Ser		
65				70				75						80			
Leu	Asp	Ser	Pro	Ile	His	Ala	Ser	Val	Tyr	Arg	Glu	Phe	Leu	Asp	Ala		
			85					90					95				
Lys	Phe	Ile	Ala	Tyr	Ala	Arg	Pro	Pro	Tyr	Ser	Leu	Ala	Tyr	Ser	Leu		
		100				105						110					
Arg	His	Asn	Arg	Leu	Leu	Pro	Arg	Asp	Tyr	Leu	Gly	Tyr	Arg	Ser	Leu		
		115				120						125					
Gly	Glu	Glu	Ile	Ser	Ile	Phe	Asn	Pro	Lys	Asp	Tyr	Asp	Ser	Trp	Gln		
	130				135						140						

Glu Arg Ala Asp Thr Glu Ile Leu Arg Gln Leu Gln Glu Ser Lys Lys
 145 150 155 160
 Tyr Phe Val Phe Ile Lys Gly Cys Gly Ile Phe Ala Tyr His Arg Glu
 165 170 175
 Leu Ser Lys Leu Met Glu Val Phe Asp Leu Ile Glu Asn Ser Cys Lys
 180 185 190
 Val Leu Arg Leu Gly Asp Leu Met Asp Tyr Cys Tyr Asn Asp Asp Pro
 195 200 205
 Arg Leu Ser Val
 210

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 91...2445
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

GGGAGTTTTG TGC	GATATAT CAAGTTTTTC	AAAGAGTTGA ACAATAAAAA	TGTGAATCTG	60
GTTGGGGGCA AGA	ACGCTAG TATTGGTGAA	ATG TTT CAA GAA TTA	GTG CCT ATT	114
	Met Phe Gln Glu Leu Val Pro Ile			
	1	5		
GGT ATT AAA GTG CCT GAT GGC TTT GCG ATC ACC AGC GAA GCG TAT TGG				162
Gly Ile Lys Val Pro Asp Gly Phe Ala Ile Thr Ser Glu Ala Tyr Trp				
10	15	20		
TAT CTT TTA GAG CAA GGA GGG GCT AAA CAA AAA ATC ATA GAG CTT TTA				210
Tyr Leu Leu Glu Gln Gly Gly Ala Lys Gln Lys Ile Ile Glu Leu Leu				
25	30	35	40	
GAA AAT GTT GAT GCC ACC GAA ATT GAT GTG TTA AAA ATC CGC TCC AAA				258
Glu Asn Val Asp Ala Thr Glu Ile Asp Val Leu Lys Ile Arg Ser Lys				
45	50	55		
CAA ATC AGA GAG CTT ATT TTT GGC ACG CCT TTT CCT AGC GAT TTG AGA				306
Gln Ile Arg Glu Leu Ile Phe Gly Thr Pro Phe Pro Ser Asp Leu Arg				
60	65	70		
GAT GAG ATT TTT CAA GCT TAT GAG ATT TTA AGC CAG CAA TAC CAC ATG				354
Asp Glu Ile Phe Gln Ala Tyr Glu Ile Leu Ser Gln Gln Tyr His Met				
75	80	85		
AAA GAA GCC GAT GTG GCT GTA AGG AGT TCC GCT ACT GCA GAA GAT TTG				402
Lys Glu Ala Asp Val Ala Val Arg Ser Ser Ala Thr Ala Glu Asp Leu				
90	95	100		

CCG Pro 105	GAC Asp	GCT Ala	TCT Ser	TTT Phe	GCC Ala 110	GGG Gly	CAG Gln	CAA Gln	GAC Asp	ACT Thr 115	TAT Tyr	TTA Leu	AAC Asn	ATT Ile	AAG Lys 120	450
GGT Gly	AAA Lys	ACC Thr	GAA Glu	TTG Leu 125	ATC Ile	CAC His	TAT Tyr	ATC Ile	AAA Lys 130	TCC Ser	TGT Cys	TTA Leu	GCG Ala	TCG Ser 135	CTT Leu	498
TTT Phe	ACC Thr	GAT Asp	AGA Arg 140	GCG Ala	ATT Ile	AGC Ser	TAT Tyr	AGG Arg 145	GCG Ala	AGT Ser	CGT Arg	GGG Gly 150	TTT Phe	GAT Asp	CAT His	546
TTA Leu	AAA Lys	GTC Val 155	GCG Ala	CTC Leu	AGC Ser	GTG Val	GGG Gly 160	GTG Val	CAA Gln	AAA Lys	ATG Met 165	GTG Val	CGA Arg	GCG Ala	GAT Asp	594
AAA Lys	GGC Gly 170	AGC Ser	GCG Ala	GGC Gly	GTG Val	ATG Met 175	TTT Phe	TCT Ser	ATT Ile	GAC Asp 180	ACC Thr	GAA Glu	ACC Thr	GGT Gly	TTT Phe	642
AAA Lys 185	GAC Asp	GCG Ala	GTG Val	TTT Phe	ATC Ile 190	ACT Thr	TCA Ser	GCG Ala	TGG Trp	GGG Gly 195	TTA Leu	GGC Gly	GAA Glu	AAT Asn	GTG Val 200	690
GTG Val	GGT Gly	GGC Gly	ACG Thr	ATA Ile 205	AAC Asn	CCT Pro	GAT Asp	GAA Glu	TTT Phe 210	TAT Tyr	GTG Val	TTT Phe	AAG Lys	CCC Pro 215	ACT Thr	738
TTA Leu	GAG Glu	CAA Gln	AAC Asn 220	AAA Lys	CGC Arg	CCC Pro	ATT Ile	ATC Ile 225	AAA Lys	CGC Arg	CAA Gln	CTC Leu 230	GGC Gly 235	AAT Asn	AAA Lys	786
ACG Thr	CAA Gln 235	AAA Lys	ATG Met	GTC Val	TAT Tyr	GCC Ala	CCA Pro 240	AGG Arg	GGT Gly	AGC Ser	GAA Glu 245	CAC His 250	CCC Pro	ACC Thr	AGA Arg	834
AAC Asn 250	ATT Ile	AAA Lys	ACC Thr	ACC Thr	AAA Lys	AAA Lys 255	GAA Glu	TGG Trp	CAA Gln	TCC Ser	TTT Phe 260	TCA Ser	TTG Leu	AGC Ser	GAT Asp	882
GAA Glu 265	GAC Asp	GTG Val	CTG Leu	ATT Ile	TTA Leu 270	GCC Ala	AAA Lys	TAC Tyr	GCC Ala	ATT Ile 275	GAA Glu	ATT Ile	GAA Glu	AAA Lys	CAC His 280	930
TAC Tyr	TCT Ser	AAA Lys	GAA Glu	GCC Ala 285	AAA Lys	CAA Gln	TAC Tyr	CGC Arg	CCT Pro 290	ATG Met	GAT Asp	ATA Ile	GAA Glu	TGG Trp 295	GCT Ala	978
AAA Lys	GAT Asp	GGC Gly	GAG Glu 300	AGC Ser	GGG Gly	GAA Glu	ATC Ile	TTT Phe 305	ATC Ile	GTT Val	CAA Gln	GCG Ala	CGC Arg 310	CCA Pro	GAA Glu	1026
ACC Thr	GTT Val 315	CAA Gln	AGC Ser	CAA Gln	AAA Lys	AGT Ser	AAA Lys 320	GAA Glu	GAA Glu	AGT Ser	CAA Gln	GTC Val 325	TTT Phe	GAA Glu	AAA Lys	1074
TTC Phe	AAA Lys	TTC Phe	AAA Lys	AAC Asn	CCT Pro	AAC Asn	GAA Glu	AAG Lys	AAA Lys	GAG Glu	ATT Ile	ATC Ile	TTA Leu	CAA Gln	GGC Gly	1122

330	335	340	
AGA GCG ATT GGG AGT AAA ATT GGC TCA GGA AAA GTG CGC ATC ATC AAT Arg Ala Ile Gly Ser Lys Ile Gly Ser Gly Lys Val Arg Ile Ile Asn 345 350 355 360			1170
GAT TTG GAG CAC ATG AAT TCT TTT AAA GAG GGC GAA ATT TTA GTT ACG Asp Leu Glu His Met Asn Ser Phe Lys Glu Gly Glu Ile Leu Val Thr 365 370 375			1218
GAT AAC ACC GAT CCG GAC TGG GAG CCT TGC ATG AAA AAA GCG AGC GCG Asp Asn Thr Asp Pro Asp Trp Glu Pro Cys Met Lys Lys Ala Ser Ala 380 385 390			1266
GTT ATC ACT AAT CGT GGA GGG CGC ACT TGC CAT GCC GCT ATT GTG GCG Val Ile Thr Asn Arg Gly Gly Arg Thr Cys His Ala Ala Ile Val Ala 395 400 405			1314
AGA GAA ATT GGC GTG CCA GCT ATC GTT GGG GTG AGC GGG GCG ACT GAT Arg Glu Ile Gly Val Pro Ala Ile Val Gly Val Ser Gly Ala Thr Asp 410 415 420			1362
AGC CTT TAT ACC GGC ATG GAA ATC ACG GTT TCT TGC GCT GAG GGC GAA Ser Leu Tyr Thr Gly Met Glu Ile Thr Val Ser Cys Ala Glu Gly Glu 425 430 435 440			1410
GAG GGC TAT GTG TAT GCG GGC ATT TAT GAG CAT GAA ATT GAA AGG GTG Glu Gly Tyr Val Tyr Ala Gly Ile Tyr Glu His Glu Ile Glu Arg Val 445 450 455			1458
GAG CTT TCT AAC ATG CAA GAA ACT CAA ACA AAA ATT TAC ATC AAT ATT Glu Leu Ser Asn Met Gln Glu Thr Gln Thr Lys Ile Tyr Ile Asn Ile 460 465 470			1506
GGA AAC CCT GAA AAA GCC TTT GGC TTT TCT CAA CTC CCT AAT CAC GGC Gly Asn Pro Glu Lys Ala Phe Gly Phe Ser Gln Leu Pro Asn His Gly 475 480 485			1554
GTA GGG CTA GCC AGG ATG GAA ATG ATT ATT TTA AAT CAA ATC AAA GCC Val Gly Leu Ala Arg Met Glu Met Ile Ile Leu Asn Gln Ile Lys Ala 490 495 500			1602
CAC CCT TTA GCT TTA GTG GAT TTG CAC CAC AAA AAA AGC GTG AAA GAA His Pro Leu Ala Leu Val Asp Leu His His Lys Lys Ser Val Lys Glu 505 510 515 520			1650
AAA AAT GAA ATT GAA AAC CTC ATG GCA GGC TAT GCT AAC CCT AAA GAT Lys Asn Glu Ile Glu Asn Leu Met Ala Gly Tyr Ala Asn Pro Lys Asp 525 530 535			1698
TTT TTT GTG AAA AAA ATC GCT GAA GGC ATT GGC ATG ATC AGT GCA GCG Phe Phe Val Lys Lys Ile Ala Glu Gly Ile Gly Met Ile Ser Ala Ala 540 545 550			1746
TTT TAC CCT AAA CCT GTC ATT GTG AGA ACG AGC GAT TTC AAA TCC AAT Phe Tyr Pro Lys Pro Val Ile Val Arg Thr Ser Asp Phe Lys Ser Asn 555 560 565			1794

GAA TAC ATG CGC ATG CTT GGC GGC TCT AGC TAT GAG CCT AAT GAA GAA Glu Tyr Met Arg Met Leu Gly Gly Ser Ser Tyr Glu Pro Asn Glu Glu 570 575 580	1842
AAC CCC ATG CTT GGC TAT AGG GGG GCT AGT CGG TAT TAT TCA GAG AGC Asn Pro Met Leu Gly Tyr Arg Gly Ala Ser Arg Tyr Tyr Ser Glu Ser 585 590 595 600	1890
TAT AAT GAA GCG TTT TCG TGG GAG TGT GAA GCC TTA GCG TTA GTG AGG Tyr Asn Glu Ala Phe Ser Trp Glu Cys Glu Ala Leu Ala Leu Val Arg 605 610 615	1938
GAA GAA ATG GGA TTA ACC AAC ATG AAA GTG ATG ATC CCT TTT TTG CGA Glu Glu Met Gly Leu Thr Asn Met Lys Val Met Ile Pro Phe Leu Arg 620 625 630	1986
ACC ATT GAA GAG GGT AAA AAA GTC CTA GAA ATC TTA AGA AAA AAC AAT Thr Ile Glu Glu Gly Lys Lys Val Leu Glu Ile Leu Arg Lys Asn Asn 635 640 645	2034
TTA GAA TCC GGT AAA AAC GGG CTT GAA ATT TAT ATC ATG TGC GAA TTG Leu Glu Ser Gly Lys Asn Gly Leu Glu Ile Tyr Ile Met Cys Glu Leu 650 655 660	2082
CCG GTG AAT GTC ATT TTG GCT GAT GAT TTC TTG AGC TTG TTT GAT GGC Pro Val Asn Val Ile Leu Ala Asp Asp Phe Leu Ser Leu Phe Asp Gly 665 670 675 680	2130
TTT TCT ATT GGA TCA AAC GAT TTA ACC CAG CTC ACT TTA GGC GTG GAT Phe Ser Ile Gly Ser Asn Asp Leu Thr Gln Leu Thr Leu Gly Val Asp 685 690 695	2178
AGA GAC AGC GAA TTG GTC AGC CAT GTC TTT GAT GAA AGG AAT GAA GCG Arg Asp Ser Glu Leu Val Ser His Val Phe Asp Glu Arg Asn Glu Ala 700 705 710	2226
ATG CTA AAG ATG TTT AAA AAA GCG ATT GAA GCT TGC AAA AGG CAC AAC Met Leu Lys Met Phe Lys Lys Ala Ile Glu Ala Cys Lys Arg His Asn 715 720 725	2274
AAA TAT TGC GGG ATT TGC GGG CAA GCC CCA AGC GAT TAC CCT GAA GTA Lys Tyr Cys Gly Ile Cys Gly Gln Ala Pro Ser Asp Tyr Pro Glu Val 730 735 740	2322
ACA GAG TTT TTA GTC AAA GAG GGC ATC ACT TCC ATT TCT TTA AAC CCT Thr Glu Phe Leu Val Lys Glu Gly Ile Thr Ser Ile Ser Leu Asn Pro 745 750 755 760	2370
GAT AGC GTG ATC CCC ACT TGG AAC GCT GTA GCC AAG TTA GAA AAA GAA Asp Ser Val Ile Pro Thr Trp Asn Ala Val Ala Lys Leu Glu Lys Glu 765 770 775	2418
CTA AAA GAA CAT GGC TTA ACT GAA CAT TGATAATAAA TAAATCAATC TAACTTG Leu Lys Glu His Gly Leu Thr Glu His 780 785	2472
AGTGGATTTT TCGTATTAGT TTCCAT	2498

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

Met	Phe	Gln	Glu	Leu	Val	Pro	Ile	Gly	Ile	Lys	Val	Pro	Asp	Gly	Phe
1				5					10					15	
Ala	Ile	Thr	Ser	Glu	Ala	Tyr	Trp	Tyr	Leu	Leu	Glu	Gln	Gly	Gly	Ala
			20					25					30		
Lys	Gln	Lys	Ile	Ile	Glu	Leu	Leu	Glu	Asn	Val	Asp	Ala	Thr	Glu	Ile
		35					40					45			
Asp	Val	Leu	Lys	Ile	Arg	Ser	Lys	Gln	Ile	Arg	Glu	Leu	Ile	Phe	Gly
		50				55					60				
Thr	Pro	Phe	Pro	Ser	Asp	Leu	Arg	Asp	Glu	Ile	Phe	Gln	Ala	Tyr	Glu
		65			70					75				80	
Ile	Leu	Ser	Gln	Gln	Tyr	His	Met	Lys	Glu	Ala	Asp	Val	Ala	Val	Arg
				85					90					95	
Ser	Ser	Ala	Thr	Ala	Glu	Asp	Leu	Pro	Asp	Ala	Ser	Phe	Ala	Gly	Gln
			100					105					110		
Gln	Asp	Thr	Tyr	Leu	Asn	Ile	Lys	Gly	Lys	Thr	Glu	Leu	Ile	His	Tyr
		115					120					125			
Ile	Lys	Ser	Cys	Leu	Ala	Ser	Leu	Phe	Thr	Asp	Arg	Ala	Ile	Ser	Tyr
	130					135					140				
Arg	Ala	Ser	Arg	Gly	Phe	Asp	His	Leu	Lys	Val	Ala	Leu	Ser	Val	Gly
					150					155					160
Val	Gln	Lys	Met	Val	Arg	Ala	Asp	Lys	Gly	Ser	Ala	Gly	Val	Met	Phe
			165						170					175	
Ser	Ile	Asp	Thr	Glu	Thr	Gly	Phe	Lys	Asp	Ala	Val	Phe	Ile	Thr	Ser
			180					185					190		
Ala	Trp	Gly	Leu	Gly	Glu	Asn	Val	Val	Gly	Gly	Thr	Ile	Asn	Pro	Asp
		195					200					205			
Glu	Phe	Tyr	Val	Phe	Lys	Pro	Thr	Leu	Glu	Gln	Asn	Lys	Arg	Pro	Ile
		210				215						220			
Ile	Lys	Arg	Gln	Leu	Gly	Asn	Lys	Thr	Gln	Lys	Met	Val	Tyr	Ala	Pro
				230						235					240
Arg	Gly	Ser	Glu	His	Pro	Thr	Arg	Asn	Ile	Lys	Thr	Thr	Lys	Lys	Glu
				245					250					255	
Trp	Gln	Ser	Phe	Ser	Leu	Ser	Asp	Glu	Asp	Val	Leu	Ile	Leu	Ala	Lys
			260					265					270		
Tyr	Ala	Ile	Glu	Ile	Glu	Lys	His	Tyr	Ser	Lys	Glu	Ala	Lys	Gln	Tyr
		275					280					285			
Arg	Pro	Met	Asp	Ile	Glu	Trp	Ala	Lys	Asp	Gly	Glu	Ser	Gly	Glu	Ile
		290				295					300				
Phe	Ile	Val	Gln	Ala	Arg	Pro	Glu	Thr	Val	Gln	Ser	Gln	Lys	Ser	Lys
				310						315					320
Glu	Glu	Ser	Gln	Val	Phe	Glu	Lys	Phe	Lys	Phe	Lys	Asn	Pro	Asn	Glu
				325					330					335	
Lys	Lys	Glu	Ile	Ile	Leu	Gln	Gly	Arg	Ala	Ile	Gly	Ser	Lys	Ile	Gly
			340					345					350		
Ser	Gly	Lys	Val	Arg	Ile	Ile	Asn	Asp	Leu	Glu	His	Met	Asn	Ser	Phe
		355					360						365		

Lys	Glu	Gly	Glu	Ile	Leu	Val	Thr	Asp	Asn	Thr	Asp	Pro	Asp	Trp	Glu	
370						375					380					
Pro	Cys	Met	Lys	Lys	Ala	Ser	Ala	Val	Ile	Thr	Asn	Arg	Gly	Gly	Arg	
385					390					395					400	
Thr	Cys	His	Ala	Ala	Ile	Val	Ala	Arg	Glu	Ile	Gly	Val	Pro	Ala	Ile	
				405					410					415		
Val	Gly	Val	Ser	Gly	Ala	Thr	Asp	Ser	Leu	Tyr	Thr	Gly	Met	Glu	Ile	
			420					425					430			
Thr	Val	Ser	Cys	Ala	Glu	Gly	Glu	Glu	Gly	Tyr	Val	Tyr	Ala	Gly	Ile	
		435					440					445				
Tyr	Glu	His	Glu	Ile	Glu	Arg	Val	Glu	Leu	Ser	Asn	Met	Gln	Glu	Thr	
450					455						460					
Gln	Thr	Lys	Ile	Tyr	Ile	Asn	Ile	Gly	Asn	Pro	Glu	Lys	Ala	Phe	Gly	
465					470					475					480	
Phe	Ser	Gln	Leu	Pro	Asn	His	Gly	Val	Gly	Leu	Ala	Arg	Met	Glu	Met	
				485					490					495		
Ile	Ile	Leu	Asn	Gln	Ile	Lys	Ala	His	Pro	Leu	Ala	Leu	Val	Asp	Leu	
			500					505					510			
His	His	Lys	Lys	Ser	Val	Lys	Glu	Lys	Asn	Glu	Ile	Glu	Asn	Leu	Met	
		515					520					525				
Ala	Gly	Tyr	Ala	Asn	Pro	Lys	Asp	Phe	Phe	Val	Lys	Lys	Ile	Ala	Glu	
530						535					540					
Gly	Ile	Gly	Met	Ile	Ser	Ala	Ala	Phe	Tyr	Pro	Lys	Pro	Val	Ile	Val	
545					550					555					560	
Arg	Thr	Ser	Asp	Phe	Lys	Ser	Asn	Glu	Tyr	Met	Arg	Met	Leu	Gly	Gly	
			565						570					575		
Ser	Ser	Tyr	Glu	Pro	Asn	Glu	Glu	Asn	Pro	Met	Leu	Gly	Tyr	Arg	Gly	
			580					585					590			
Ala	Ser	Arg	Tyr	Tyr	Ser	Glu	Ser	Tyr	Asn	Glu	Ala	Phe	Ser	Trp	Glu	
		595					600					605				
Cys	Glu	Ala	Leu	Ala	Leu	Val	Arg	Glu	Glu	Met	Gly	Leu	Thr	Asn	Met	
610						615					620					
Lys	Val	Met	Ile	Pro	Phe	Leu	Arg	Thr	Ile	Glu	Glu	Gly	Lys	Lys	Val	
625					630					635					640	
Leu	Glu	Ile	Leu	Arg	Lys	Asn	Asn	Leu	Glu	Ser	Gly	Lys	Asn	Gly	Leu	
				645					650					655		
Glu	Ile	Tyr	Ile	Met	Cys	Glu	Leu	Pro	Val	Asn	Val	Ile	Leu	Ala	Asp	
			660					665					670			
Asp	Phe	Leu	Ser	Leu	Phe	Asp	Gly	Phe	Ser	Ile	Gly	Ser	Asn	Asp	Leu	
		675					680					685				
Thr	Gln	Leu	Thr	Leu	Gly	Val	Asp	Arg	Asp	Ser	Glu	Leu	Val	Ser	His	
					695						700					
Val	Phe	Asp	Glu	Arg	Asn	Glu	Ala	Met	Leu	Lys	Met	Phe	Lys	Lys	Ala	
705					710						715				720	
Ile	Glu	Ala	Cys	Lys	Arg	His	Asn	Lys	Tyr	Cys	Gly	Ile	Cys	Gly	Gln	
				725					730					735		
Ala	Pro	Ser	Asp	Tyr	Pro	Glu	Val	Thr	Glu	Phe	Leu	Val	Lys	Glu	Gly	
			740					745					750			
Ile	Thr	Ser	Ile	Ser	Leu	Asn	Pro	Asp	Ser	Val	Ile	Pro	Thr	Trp	Asn	
		755					760					765				
Ala	Val	Ala	Lys	Leu	Glu	Lys	Glu	Leu	Lys	Glu	His	Gly	Leu	Thr	Glu	
		770				775					780					
His																
785																

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 565 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 61...483
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GTTATCTTTA ATCAATCAGA TGATAGAATT TATCTTTTAT TTTTGAATTG GGAGCATTTG	60
ATG AAA AAA TTA GCG GTT TCT TTA TTA TTT ACA GGG ACT TTT TTG GGG	108
Met Lys Lys Leu Ala Val Ser Leu Leu Phe Thr Gly Thr Phe Leu Gly	
1 5 10 15	
CTT TTT TTG AAT GCG AGC GAT TTT AAG AGC ATG GAT GAC AAG CAA CTA	156
Leu Phe Leu Asn Ala Ser Asp Phe Lys Ser Met Asp Asp Lys Gln Leu	
20 25 30	
TTA GAG CAA GCA GGG AAA GTT GCT CCT AGC GAA GTC CCT GAG TTT CGC	204
Leu Glu Gln Ala Gly Lys Val Ala Pro Ser Glu Val Pro Glu Phe Arg	
35 40 45	
GCG GAA GTC AAT AAG CGA TTA GCA GTG ATG AAA GAA GAA GAT CGT AAA	252
Ala Glu Val Asn Lys Arg Leu Ala Val Met Lys Glu Glu Asp Arg Lys	
50 55 60	
AAT TAT AAA GCG GAT TTT AAG AAA GCG ATG GAT AAG AAT TTA GCT TCT	300
Asn Tyr Lys Ala Asp Phe Lys Lys Ala Met Asp Lys Asn Leu Ala Ser	
65 70 75 80	
TTA AGC CAA GAA GAT CGC AAC AAG CGT AAA AAA GAA ATT CTT GAA GCG	348
Leu Ser Gln Glu Asp Arg Asn Lys Arg Lys Lys Glu Ile Leu Glu Ala	
85 90 95	
ATT GCT AAC AAA AAG AAA ACA ATG ACC ATG AAA GAA TAT CGT GAA GAA	396
Ile Ala Asn Lys Lys Lys Thr Met Thr Met Lys Glu Tyr Arg Glu Glu	
100 105 110	
GGG TTG GAT TTG CAT GAT TGC GCA TGC GAA GGC CCT TTT CAT GAT CAT	444
Gly Leu Asp Leu His Asp Cys Ala Cys Glu Gly Pro Phe His Asp His	
115 120 125	
GAG AGA AAA AAA GGG AAA AAA CCA AGC CAT CAT AAG CAT TAGCGCTTAG GG	495
Glu Arg Lys Lys Gly Lys Lys Pro Ser His His Lys His	
130 135 140	
TGTGCTAACT TTTTGTGATT TTTGTGAAAC CACGCCGTAA GTCCCTAGCT TTTGGCTGTG	555
GGGATTAAGG	565

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Met	Lys	Lys	Leu	Ala	Val	Ser	Leu	Leu	Phe	Thr	Gly	Thr	Phe	Leu	Gly
1				5					10					15	
Leu	Phe	Leu	Asn	Ala	Ser	Asp	Phe	Lys	Ser	Met	Asp	Asp	Lys	Gln	Leu
			20					25					30		
Leu	Glu	Gln	Ala	Gly	Lys	Val	Ala	Pro	Ser	Glu	Val	Pro	Glu	Phe	Arg
		35					40					45			
Ala	Glu	Val	Asn	Lys	Arg	Leu	Ala	Val	Met	Lys	Glu	Glu	Asp	Arg	Lys
		50				55					60				
Asn	Tyr	Lys	Ala	Asp	Phe	Lys	Lys	Ala	Met	Asp	Lys	Asn	Leu	Ala	Ser
65					70					75				80	
Leu	Ser	Gln	Glu	Asp	Arg	Asn	Lys	Arg	Lys	Lys	Glu	Ile	Leu	Glu	Ala
				85					90					95	
Ile	Ala	Asn	Lys	Lys	Lys	Thr	Met	Thr	Met	Lys	Glu	Tyr	Arg	Glu	Glu
			100					105					110		
Gly	Leu	Asp	Leu	His	Asp	Cys	Ala	Cys	Glu	Gly	Pro	Phe	His	Asp	His
		115					120					125			
Glu	Arg	Lys	Lys	Gly	Lys	Lys	Pro	Ser	His	His	Lys	His			
		130				135					140				

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 558 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...506
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GGGTGCATGG	GCCTCAAAAA	GTCGCTATCA	TTCTCTACTA	AAGGATAAGA	ATG GAA	56
					Met Glu	
					1	
AAA TTA GAA GTA GGG CAA TTA GCC CCT GAT TTT AGA TTG AAA AAC AGC						104
Lys Leu Glu Val Gly Gln Leu Ala Pro Asp Phe Arg Leu Lys Asn Ser						
	5		10		15	
GAT GGC GTG GAA ATT TCT TTA AAA GAT TTG CTC CAT AAA AAA GTG GTG						152
Asp Gly Val Glu Ile Ser Leu Lys Asp Leu Leu His Lys Lys Val Val						
	20		25		30	

CTG TAT TTC TAC CCT AAA GAC AAC ACC CCC GGA TGC ACT CTA GAA GCC	200
Leu Tyr Phe Tyr Pro Lys Asp Asn Thr Pro Gly Cys Thr Leu Glu Ala	
35 40 45 50	
AAA GAC TTT AGC GCT CTA TTT AGT GAA TTT GAA AAG AAA AAC GCT GTT	248
Lys Asp Phe Ser Ala Leu Phe Ser Glu Phe Glu Lys Lys Asn Ala Val	
55 60 65	
GTC GTA GGC ATA AGC CCT GAT AAC GCG CAA TCG CAT CAA AAA TTT ATC	296
Val Val Gly Ile Ser Pro Asp Asn Ala Gln Ser His Gln Lys Phe Ile	
70 75 80	
AGC CAA TGC TCT TTG AAT GTG ATT TTG CTC TGC GAT GAA GAT AAA AAA	344
Ser Gln Cys Ser Leu Asn Val Ile Leu Leu Cys Asp Glu Asp Lys Lys	
85 90 95	
GCC GCC AAT CTT TAC AAA GCT TAT GGC AAA CGC ATG CTT TAT GGG AAG	392
Ala Ala Asn Leu Tyr Lys Ala Tyr Gly Lys Arg Met Leu Tyr Gly Lys	
100 105 110	
GAG CAT TTG GGG ATT ATC CGC TCC ACC TTC ATT ATC AAC ACG CAA GGC	440
Glu His Leu Gly Ile Ile Arg Ser Thr Phe Ile Ile Asn Thr Gln Gly	
115 120 125 130	
GTT TTA GAA AAA TGT TTC TAC AAT GTC AAA GCG AAA GGC CAT GCT CAA	488
Val Leu Glu Lys Cys Phe Tyr Asn Val Lys Ala Lys Gly His Ala Gln	
135 140 145	
AAG GTT TTA GAG AGT TTG TAGTTTAACT TTCTAACTTT CGCCCATTTT AATTTGAG	544
Lys Val Leu Glu Ser Leu	
150	
ATTTTTTAGC CATT	558

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

Met Glu Lys Leu Glu Val Gly Gln Leu Ala Pro Asp Phe Arg Leu Lys	
1 5 10 15	
Asn Ser Asp Gly Val Glu Ile Ser Leu Lys Asp Leu Leu His Lys Lys	
20 25 30	
Val Val Leu Tyr Phe Tyr Pro Lys Asp Asn Thr Pro Gly Cys Thr Leu	
35 40 45	
Glu Ala Lys Asp Phe Ser Ala Leu Phe Ser Glu Phe Glu Lys Lys Asn	
50 55 60	
Ala Val Val Val Gly Ile Ser Pro Asp Asn Ala Gln Ser His Gln Lys	
65 70 75 80	
Phe Ile Ser Gln Cys Ser Leu Asn Val Ile Leu Leu Cys Asp Glu Asp	
85 90 95	

Lys Lys Ala Ala Asn Leu Tyr Lys Ala Tyr Gly Lys Arg Met Leu Tyr
100 105 110
Gly Lys Glu His Leu Gly Ile Ile Arg Ser Thr Phe Ile Ile Asn Thr
115 120 125
Gln Gly Val Leu Glu Lys Cys Phe Tyr Asn Val Lys Ala Lys Gly His
130 135 140
Ala Gln Lys Val Leu Glu Ser Leu
145 150

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...651
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

ACTTAGAAGG GGTGATTT ATG AGT AAA GAG CTT ATT TTA AAG CGC ATT AAA	51
Met Ser Lys Glu Leu Ile Leu Lys Arg Ile Lys	
1 5 10	
GAA GCC AGA GCC AAG CAT GCC ATT CAG GGA GCG AAC CCT ATT TAT AGG	99
Glu Ala Arg Ala Lys His Ala Ile Gln Gly Ala Asn Pro Ile Tyr Arg	
15 20 25	
AAT ATC ATT AAA GTG GAG TTT GAG GAC TTG GTG GAA GAA TAC AAG CAT	147
Asn Ile Ile Lys Val Glu Phe Glu Asp Leu Val Glu Glu Tyr Lys His	
30 35 40	
TTC CAA GTG TTG AAT AAA GCT GAA GTC ATT GAA AGC GCT AAA GAA AAT	195
Phe Gln Val Leu Asn Lys Ala Glu Val Ile Glu Ser Ala Lys Glu Asn	
45 50 55	
TTA GAG CAA GCC ATT TTA AAG GCT TTA GAA AAT TTT AAA AGC AAA AAA	243
Leu Glu Gln Ala Ile Leu Lys Ala Leu Glu Asn Phe Lys Ser Lys Lys	
60 65 70 75	
ATC TTA CAC TCC ACA GAT TTG AAT TTG AAT TTT GAA GCG TTT AAG GAT	291
Ile Leu His Ser Thr Asp Leu Asn Leu Asn Phe Glu Ala Phe Lys Asp	
80 85 90	
TTT ACT TTA CAG CCT TAT GAT AAA GAA ATT GAA GCG ATG CGT GAA GAG	339
Phe Thr Leu Gln Pro Tyr Asp Lys Glu Ile Glu Ala Met Arg Glu Glu	
95 100 105	
TTG TTT GAG ATT GAT ACG GCT TTA TTG CAT GGG GTT TGT GGG ATT TCA	387
Leu Phe Glu Ile Asp Thr Ala Leu Leu His Gly Val Cys Gly Ile Ser	
110 115 120	

AGC TTG GGC ATG ATT GGG GCG GTC TCT TCG CAT GCA AGC CCG CGA TTG	435
Ser Leu Gly Met Ile Gly Ala Val Ser Ser His Ala Ser Pro Arg Leu	
125 130 135	
CTT TCG CTC ATC ACC CTT AAT TGC ATC ATC TTA TTG AAA AAA GAA TCC	483
Leu Ser Leu Ile Thr Leu Asn Cys Ile Ile Leu Leu Lys Lys Glu Ser	
140 145 150 155	
ATT GTG CGC AAT TTG AGT GAA GGC ATG CAA GCT TTA AAA AAC CAA AGC	531
Ile Val Arg Asn Leu Ser Glu Gly Met Gln Ala Leu Lys Asn Gln Ser	
160 165 170	
CAA AAC GGT GCA TTA CCC ACA AAC ATG CTC CTT ATT GGC GGG CCT AGC	579
Gln Asn Gly Ala Leu Pro Thr Asn Met Leu Leu Ile Gly Gly Pro Ser	
175 180 185	
CGG ACA GCT GAC ATT GAA TTA AAA ACC GTT TTT GGG GTG CAT GGG CCT	627
Arg Thr Ala Asp Ile Glu Leu Lys Thr Val Phe Gly Val His Gly Pro	
190 195 200	
CAA AAA GTC GCT ATC ATT CTC TAC TAAAGGATAA GAATGGAAAA ATTAGAAGTA	681
Gln Lys Val Ala Ile Ile Leu Tyr	
205 210	
GGGCAATTAG CCCCTGATT	700

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

Met Ser Lys Glu Leu Ile Leu Lys Arg Ile Lys Glu Ala Arg Ala Lys	
1 5 10 15	
His Ala Ile Gln Gly Ala Asn Pro Ile Tyr Arg Asn Ile Ile Lys Val	
20 25 30	
Glu Phe Glu Asp Leu Val Glu Glu Tyr Lys His Phe Gln Val Leu Asn	
35 40 45	
Lys Ala Glu Val Ile Glu Ser Ala Lys Glu Asn Leu Glu Gln Ala Ile	
50 55 60	
Leu Lys Ala Leu Glu Asn Phe Lys Ser Lys Lys Ile Leu His Ser Thr	
65 70 75 80	
Asp Leu Asn Leu Asn Phe Glu Ala Phe Lys Asp Phe Thr Leu Gln Pro	
85 90 95	
Tyr Asp Lys Glu Ile Glu Ala Met Arg Glu Glu Leu Phe Glu Ile Asp	
100 105 110	
Thr Ala Leu Leu His Gly Val Cys Gly Ile Ser Ser Leu Gly Met Ile	
115 120 125	
Gly Ala Val Ser Ser His Ala Ser Pro Arg Leu Leu Ser Leu Ile Thr	
130 135 140	
Leu Asn Cys Ile Ile Leu Leu Lys Lys Glu Ser Ile Val Arg Asn Leu	
145 150 155 160	

Ser	Glu	Gly	Met	Gln	Ala	Leu	Lys	Asn	Gln	Ser	Gln	Asn	Gly	Ala	Leu
			165					170					175		
Pro	Thr	Asn	Met	Leu	Leu	Ile	Gly	Gly	Pro	Ser	Arg	Thr	Ala	Asp	Ile
		180					185					190			
Glu	Leu	Lys	Thr	Val	Phe	Gly	Val	His	Gly	Pro	Gln	Lys	Val	Ala	Ile
		195				200					205				
Ile	Leu	Tyr													
	210														

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...531
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

TATTCCAATA ACGACTACCC TATTATTTTG CCTAGCGGTT CATGCACAGG G ATG ATG	57
Met Met	
1	
CGG CAT GAT TAT TTG GAA TTG TTT GAA GGG CAT GCG GAA TTC AAC ATG	105
Arg His Asp Tyr Leu Glu Leu Phe Glu Gly His Ala Glu Phe Asn Met	
5 10 15	
GTT AAA GAT TTT TGC TCT AGG GTG TAT GAA TTG AGC GAA TTT TTG GAT	153
Val Lys Asp Phe Cys Ser Arg Val Tyr Glu Leu Ser Glu Phe Leu Asp	
20 25 30	
AAA AAA TTG CAA GTC AAA TAT GAA GAT AAG GGC GAA CCC CTT AAA ATC	201
Lys Lys Leu Gln Val Lys Tyr Glu Asp Lys Gly Glu Pro Leu Lys Ile	
35 40 45 50	
ACA TGG CAT TCT AAT TGC CAT GCC TTA AGG GTG GCT AAA GTG ATT GAC	249
Thr Trp His Ser Asn Cys His Ala Leu Arg Val Ala Lys Val Ile Asp	
55 60 65	
TCG GCG AAA AAC CTC ATC AGA CAG CTT AAA AAT GTG GAA CTC ATT GAA	297
Ser Ala Lys Asn Leu Ile Arg Gln Leu Lys Asn Val Glu Leu Ile Glu	
70 75 80	
TTG GAA AAA GAA GAA GAA TGC TGC GGG TTT GGG GGG ACT TTT TCG GTT	345
Leu Glu Lys Glu Glu Glu Cys Cys Gly Phe Gly Gly Thr Phe Ser Val	
85 90 95	
AAA GAG CCT GAA ATT TCA GCG GTT ATG GTT AAA GAA AAG ATT AAA AAC	393
Lys Glu Pro Glu Ile Ser Ala Val Met Val Lys Glu Lys Ile Lys Asn	
100 105 110	

ATA GAA AGC CGT CAA GTG GAT GTG ATT GTT TCA GCG GAT GCT GGG TGT 441
 Ile Glu Ser Arg Gln Val Asp Val Ile Val Ser Ala Asp Ala Gly Cys
 115 120 125 130

TTG ATG AAT ATC AGC ACC GCT ATG CAA AAA ATG GGC TCT TTG ACA AAA 489
 Leu Met Asn Ile Ser Thr Ala Met Gln Lys Met Gly Ser Leu Thr Lys
 135 140 145

CCC ATG CAT TTT TAT GAC TTT TTA GCC TCA AGA CTT GGG CTT TAACATTAA 540
 Pro Met His Phe Tyr Asp Phe Leu Ala Ser Arg Leu Gly Leu
 150 155 160

AGAATTATTT TAAGGAATGA TCATGGAAAA A 571

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

Met Met Arg His Asp Tyr Leu Glu Leu Phe Glu Gly His Ala Glu Phe
 1 5 10 15
 Asn Met Val Lys Asp Phe Cys Ser Arg Val Tyr Glu Leu Ser Glu Phe
 20 25 30
 Leu Asp Lys Lys Leu Gln Val Lys Tyr Glu Asp Lys Gly Glu Pro Leu
 35 40 45
 Lys Ile Thr Trp His Ser Asn Cys His Ala Leu Arg Val Ala Lys Val
 50 55 60
 Ile Asp Ser Ala Lys Asn Leu Ile Arg Gln Leu Lys Asn Val Glu Leu
 65 70 75 80
 Ile Glu Leu Glu Lys Glu Glu Glu Cys Cys Gly Phe Gly Gly Thr Phe
 85 90 95
 Ser Val Lys Glu Pro Glu Ile Ser Ala Val Met Val Lys Glu Lys Ile
 100 105 110
 Lys Asn Ile Glu Ser Arg Gln Val Asp Val Ile Val Ser Ala Asp Ala
 115 120 125
 Gly Cys Leu Met Asn Ile Ser Thr Ala Met Gln Lys Met Gly Ser Leu
 130 135 140
 Thr Lys Pro Met His Phe Tyr Asp Phe Leu Ala Ser Arg Leu Gly Leu
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 70...714
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

AACCTGCAAA CCCACCTTAA AAGGCTCAAA AGAAGTGAGT TTGTGGGCCA AAAAAAGGAA	60
TTAGAGGGC ATG GGG AGG TTT TCT TTA AAA GAA ATT TTA ATG CTC AGC CTT	111
Met Gly Arg Phe Ser Leu Lys Glu Ile Leu Met Leu Ser Leu	
1 5 10	
ACC TTA TTG GCT TTA CTG GGT TGG ATT TTT GGC AAA CCT TTA GGC TTG	159
Thr Leu Leu Ala Leu Leu Gly Trp Ile Phe Gly Lys Pro Leu Gly Leu	
15 20 25 30	
CAT GCG AGT GCG ACG GCT TTG ATT GTC ATG GTT TTA ATG GCG TTT TGT	207
His Ala Ser Ala Thr Ala Leu Ile Val Met Val Leu Met Ala Phe Cys	
35 40 45	
AAG ATT GTA AGC TAT GAA GAC ATC ATT AAA AAC AAG AGC GCG TTC AAT	255
Lys Ile Val Ser Tyr Glu Asp Ile Ile Lys Asn Lys Ser Ala Phe Asn	
50 55 60	
ATT TTT TTA TTG CTT GGA TCG CTG CTC ACG ATG GCT GGC GGG CTT AAA	303
Ile Phe Leu Leu Leu Gly Ser Leu Leu Thr Met Ala Gly Gly Leu Lys	
65 70 75	
AAT GTA GGG TTT TTA AAT TTT ATC GGC AAT GCG GCT CAA AAT TTT TTA	351
Asn Val Gly Phe Leu Asn Phe Ile Gly Asn Ala Ala Gln Asn Phe Leu	
80 85 90	
GAG CAT GCT CAC TTG GAT CCG TTA ATA GCG GTC TTG TTT ATT GTA GCC	399
Glu His Ala His Leu Asp Pro Leu Ile Ala Val Leu Phe Ile Val Ala	
95 100 105 110	
CTC TTT TAT CTG TCG CAT TAT TTT TTC GCA AGC ATC ACC GCT CAT GTG	447
Leu Phe Tyr Leu Ser His Tyr Phe Phe Ala Ser Ile Thr Ala His Val	
115 120 125	
AGC GCG TTA TTC GCG CTT TTT GTA GGG ATT GGT TCG CAC ATT CAA GGG	495
Ser Ala Leu Phe Ala Leu Phe Val Gly Ile Gly Ser His Ile Gln Gly	
130 135 140	
GTC AAT TTG CAA GAA TTG AGC TTG TTT TTA ATG TTT TCT TTA GGG ATT	543
Val Asn Leu Gln Glu Leu Ser Leu Phe Leu Met Phe Ser Leu Gly Ile	
145 150 155	
ATG GGG ATT TTA ACG CCC TAT GGC ACA GGC CCA TCC ACC ATT TAT TAC	591
Met Gly Ile Leu Thr Pro Tyr Gly Thr Gly Pro Ser Thr Ile Tyr Tyr	
160 165 170	
GGG AGC GGG TAT ATT CAA AGC AAG GAT TTT TGG AAA TGG GGG TTT ATT	639
Gly Ser Gly Tyr Ile Gln Ser Lys Asp Phe Trp Lys Trp Gly Phe Ile	
175 180 185 190	
TTT GGC TTT TTG TAT TTA ATC GTG TTT TTA AGC GTG TGC ACA CCT TGG	687
Phe Gly Phe Leu Tyr Leu Ile Val Phe Leu Ser Val Cys Thr Pro Trp	

195	200	205	
GTC AAA TTC ATC GCT TAT AGG TGG TTG TAGCTGGAAA CTTTACACAA CGCCCTT	741		
Val Lys Phe Ile Ala Tyr Arg Trp Leu			
210	215		

TTAAAATGGT ATGAAGAA 759

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

Met	Gly	Arg	Phe	Ser	Leu	Lys	Glu	Ile	Leu	Met	Leu	Ser	Leu	Thr	Leu
1				5					10					15	
Leu	Ala	Leu	Leu	Gly	Trp	Ile	Phe	Gly	Lys	Pro	Leu	Gly	Leu	His	Ala
			20					25					30		
Ser	Ala	Thr	Ala	Leu	Ile	Val	Met	Val	Leu	Met	Ala	Phe	Cys	Lys	Ile
		35					40					45			
Val	Ser	Tyr	Glu	Asp	Ile	Ile	Lys	Asn	Lys	Ser	Ala	Phe	Asn	Ile	Phe
		50				55					60				
Leu	Leu	Leu	Gly	Ser	Leu	Thr	Met	Ala	Gly	Gly	Leu	Lys	Asn	Val	
65					70				75					80	
Gly	Phe	Leu	Asn	Phe	Ile	Gly	Asn	Ala	Ala	Gln	Asn	Phe	Leu	Glu	His
				85					90					95	
Ala	His	Leu	Asp	Pro	Leu	Ile	Ala	Val	Leu	Phe	Ile	Val	Ala	Leu	Phe
			100					105					110		
Tyr	Leu	Ser	His	Tyr	Phe	Phe	Ala	Ser	Ile	Thr	Ala	His	Val	Ser	Ala
		115					120					125			
Leu	Phe	Ala	Leu	Phe	Val	Gly	Ile	Gly	Ser	His	Ile	Gln	Gly	Val	Asn
	130					135					140				
Leu	Gln	Glu	Leu	Ser	Leu	Phe	Leu	Met	Phe	Ser	Leu	Gly	Ile	Met	Gly
145					150					155				160	
Ile	Leu	Thr	Pro	Tyr	Gly	Thr	Gly	Pro	Ser	Thr	Ile	Tyr	Tyr	Gly	Ser
			165						170					175	
Gly	Tyr	Ile	Gln	Ser	Lys	Asp	Phe	Trp	Lys	Trp	Gly	Phe	Ile	Phe	Gly
		180					185						190		
Phe	Leu	Tyr	Leu	Ile	Val	Phe	Leu	Ser	Val	Cys	Thr	Pro	Trp	Val	Lys
	195						200					205			
Phe	Ile	Ala	Tyr	Arg	Trp	Leu									
210						215									

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...309
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

AAGGGGGGAT TTATATCGGT AAAGAGTTGT TTAAGC	ATG GCT AGT GGC CTT TTT	54
	Met Ala Ser Gly Leu Phe	
	1 5	
GAA AAC GAT GGA ATC AAA GAC AAC AAA GCG CGA GAT TTT TTC TAT AGC		102
Glu Asn Asp Gly Ile Lys Asp Asn Lys Ala Arg Asp Phe Phe Tyr Ser		
	10 15 20	
CAT AGC TCC CTA ATT GTC TTT TTC CTT TTA CTG CTT GGG TTT GGG TAT		150
His Ser Ser Leu Ile Val Phe Phe Leu Leu Leu Leu Gly Phe Gly Tyr		
	25 30 35	
TAT TTA GGG AAG TTG CTT TTT GGG GGC TCT TCT TTA GAA GTT TAT TTG		198
Tyr Leu Gly Lys Leu Leu Phe Gly Gly Ser Ser Leu Glu Val Tyr Leu		
	40 45 50	
GAT TTA AGA GAC AAG CAT GAA CGA TTG CAG CAA GAA ATC ACC GAA TTG		246
Asp Leu Arg Asp Lys His Glu Arg Leu Gln Gln Glu Ile Thr Glu Leu		
	55 60 65 70	
CAA AGC AAG AAT GTG CGC TTG CAA AAG CGT TTG TTT GAG TTG AAG GAA		294
Gln Ser Lys Asn Val Arg Leu Gln Lys Arg Leu Phe Glu Leu Lys Glu		
	75 80 85	
TTA CGG CCT AGA GAT TAGATTTAAG GAAAATGGTA GTGTTAAAAA AGATGATAGG T		350
Leu Arg Pro Arg Asp		
	90	
TTGGTG		357

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

Met Ala Ser Gly Leu Phe Glu Asn Asp Gly Ile Lys Asp Asn Lys Ala	
1 5 10 15	
Arg Asp Phe Phe Tyr Ser His Ser Ser Leu Ile Val Phe Phe Leu Leu	
	20 25 30
Leu Leu Gly Phe Gly Tyr Tyr Leu Gly Lys Leu Leu Phe Gly Gly Ser	
	35 40 45
Ser Leu Glu Val Tyr Leu Asp Leu Arg Asp Lys His Glu Arg Leu Gln	

50						55						60					
Gln	Glu	Ile	Thr	Glu	Leu	Gln	Ser	Lys	Asn	Val	Arg	Leu	Gln	Lys	Arg		
65					70					75					80		
Leu	Phe	Glu	Leu	Lys	Glu	Leu	Arg	Pro	Arg	Asp							
				85					90								

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...675
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

ATG	ATA	GAA	GTT	TTA	ATG	ATA	GAA	GAT	GAT	ATA	GAA	TTA	GCC	GAG	TTT		48
Met	Ile	Glu	Val	Leu	Met	Ile	Glu	Asp	Asp	Ile	Glu	Leu	Ala	Glu	Phe		
1				5					10					15			
TTG	AGC	GAG	TTT	TTG	CTC	CAA	CAT	GGC	ATT	CAT	GTA	ACC	AAT	TAC	GAT		96
Leu	Ser	Glu	Phe	Leu	Leu	Gln	His	Gly	Ile	His	Val	Thr	Asn	Tyr	Asp		
			20					25					30				
GAG	CCA	TAT	ACC	GGC	ATT	AGT	GCG	GCT	AAC	ACA	CAA	AAT	TAT	GAT	TTG		144
Glu	Pro	Tyr	Thr	Gly	Ile	Ser	Ala	Ala	Asn	Thr	Gln	Asn	Tyr	Asp	Leu		
		35					40					45					
TTG	TTG	TTG	GAT	TTG	ACT	TTG	CCT	AAT	TTA	GAC	GGG	CTT	GAA	GTG	TGT		192
Leu	Leu	Leu	Asp	Leu	Thr	Leu	Pro	Asn	Leu	Asp	Gly	Leu	Glu	Val	Cys		
	50					55					60						
AGG	CGC	ATC	TCC	AAA	CAA	AAA	CAT	ATC	CCT	ATT	ATT	ATT	TCT	TCA	GCG		240
Arg	Arg	Ile	Ser	Lys	Gln	Lys	His	Ile	Pro	Ile	Ile	Ile	Ser	Ser	Ala		
65				70					75						80		
AGA	AGT	GAT	GTG	GAA	GAT	AAG	ATT	AAA	GCA	CTA	GAT	TAT	GGG	GCT	GAT		288
Arg	Ser	Asp	Val	Glu	Asp	Lys	Ile	Lys	Ala	Leu	Asp	Tyr	Gly	Ala	Asp		
			85					90					95				
GAT	TAC	CTC	CCT	AAA	CCC	TAT	GAT	CCT	AAA	GAA	TTA	TTA	GCT	CGC	ATC		336
Asp	Tyr	Leu	Pro	Lys	Pro	Tyr	Asp	Pro	Lys	Glu	Leu	Leu	Ala	Arg	Ile		
			100					105					110				
CAA	TCG	CTA	CTC	AGG	CGT	TCT	CAT	AAA	AAA	GAA	GAA	GTG	AGT	GAG	CCA		384
Gln	Ser	Leu	Leu	Arg	Arg	Ser	His	Lys	Lys	Glu	Glu	Val	Ser	Glu	Pro		
		115					120					125					
GGC	GAT	GCG	AAT	ATC	TTT	AGG	GTG	GAT	AAG	GAT	AGC	CGA	GAA	GTG	TAT		432
Gly	Asp	Ala	Asn	Ile	Phe	Arg	Val	Asp	Lys	Asp	Ser	Arg	Glu	Val	Tyr		

130	135	140	
ATG CAT GAA AAA AAG CTG GAC TTA ACT AGG GCT GAA TAT GAA ATC CTT			480
Met His Glu Lys Lys Leu Asp Leu Thr Arg Ala Glu Tyr Glu Ile Leu			
145	150	155	160
TCG CTT CTC ATT AGC AAA AAA GGT TAT GTG TTT AGC CGT GAA AGC ATT			528
Ser Leu Leu Ile Ser Lys Lys Gly Tyr Val Phe Ser Arg Glu Ser Ile			
	165	170	175
GCG ATT GAG AGC GAG AGC ATC AAC CCT GAA AGC TCT AAT AAA AGC ATT			576
Ala Ile Glu Ser Glu Ser Ile Asn Pro Glu Ser Ser Asn Lys Ser Ile			
	180	185	190
GAT GTG ATC ATT GGC CGT TTG CGA TCT AAG ATT GAA AAA AAT CCT AAA			624
Asp Val Ile Ile Gly Arg Leu Arg Ser Lys Ile Glu Lys Asn Pro Lys			
	195	200	205
CAA CCG CAA TAC ATC ATC TCT GTT AGA GGG ATT GGT TAT AAA TTA GAA			672
Gln Pro Gln Tyr Ile Ile Ser Val Arg Gly Ile Gly Tyr Lys Leu Glu			
	210	215	220
TAC TGA			678
Tyr			
225			

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

Met	Ile	Glu	Val	Leu	Met	Ile	Glu	Asp	Asp	Ile	Glu	Leu	Ala	Glu	Phe
1				5					10					15	
Leu	Ser	Glu	Phe	Leu	Leu	Gln	His	Gly	Ile	His	Val	Thr	Asn	Tyr	Asp
		20						25					30		
Glu	Pro	Tyr	Thr	Gly	Ile	Ser	Ala	Ala	Asn	Thr	Gln	Asn	Tyr	Asp	Leu
		35					40					45			
Leu	Leu	Leu	Asp	Leu	Thr	Leu	Pro	Asn	Leu	Asp	Gly	Leu	Glu	Val	Cys
	50					55					60				
Arg	Arg	Ile	Ser	Lys	Gln	Lys	His	Ile	Pro	Ile	Ile	Ile	Ser	Ser	Ala
	65				70					75					80
Arg	Ser	Asp	Val	Glu	Asp	Lys	Ile	Lys	Ala	Leu	Asp	Tyr	Gly	Ala	Asp
			85						90					95	
Asp	Tyr	Leu	Pro	Lys	Pro	Tyr	Asp	Pro	Lys	Glu	Leu	Leu	Ala	Arg	Ile
		100						105					110		
Gln	Ser	Leu	Leu	Arg	Arg	Ser	His	Lys	Lys	Glu	Glu	Val	Ser	Glu	Pro
		115					120					125			
Gly	Asp	Ala	Asn	Ile	Phe	Arg	Val	Asp	Lys	Asp	Ser	Arg	Glu	Val	Tyr
	130					135					140				
Met	His	Glu	Lys	Lys	Leu	Asp	Leu	Thr	Arg	Ala	Glu	Tyr	Glu	Ile	Leu

145		150		155		160									
Ser	Leu	Leu	Ile	Ser	Lys	Lys	Gly	Tyr	Val	Phe	Ser	Arg	Glu	Ser	Ile
		165				170								175	
Ala	Ile	Glu	Ser	Glu	Ser	Ile	Asn	Pro	Glu	Ser	Ser	Asn	Lys	Ser	Ile
		180				185							190		
Asp	Val	Ile	Ile	Gly	Arg	Leu	Arg	Ser	Lys	Ile	Glu	Lys	Asn	Pro	Lys
		195				200						205			
Gln	Pro	Gln	Tyr	Ile	Ile	Ser	Val	Arg	Gly	Ile	Gly	Tyr	Lys	Leu	Glu
	210					215					220				
Tyr															
225															

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 72...1082
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

AAGTCTATGC	CACGATCAAT	GGTTTCCCTT	TCAATTCACA	GCTCAAACCTT	TTAGAAGAAC	60
ATATTGATAA	A ATG GCA GAA TTA GAG CCG GAC GCT TTT ATT ATC GCT GCG	110				
	Met Ala Glu Leu Glu Pro Asp Ala Phe Ile Ile Ala Ala					
	1 5 10					
CCT GGT GTG GTG AAA CTC GCT TTA AAA ATC GCC CCG CAT ATC CCT ATC	158					
Pro Gly Val Val Lys Leu Ala Leu Lys Ile Ala Pro His Ile Pro Ile						
15 20 25						
CAT TTA TCC ACG CAA GCG AAT GTC TTA AAT TTG CTA GAT GCA CAA GTG	206					
His Leu Ser Thr Gln Ala Asn Val Leu Asn Leu Leu Asp Ala Gln Val						
30 35 40 45						
TTT TAT GAT TTA GGG GTT AAA CGC ATC GTG TGC GCG AGG GAA TTG AGC	254					
Phe Tyr Asp Leu Gly Val Lys Arg Ile Val Cys Ala Arg Glu Leu Ser						
50 55 60						
CTG AAT GAT GCG ATT GAG ATT AAA AAA GCC TTA CCT AAT TTA GAA TTA	302					
Leu Asn Asp Ala Ile Glu Ile Lys Lys Ala Leu Pro Asn Leu Glu Leu						
65 70 75						
GAA ATC TTT GTG CAT GGG AGC ATG TGC TTT GCC TTT TCA GGG CGC TGC	350					
Glu Ile Phe Val His Gly Ser Met Cys Phe Ala Phe Ser Gly Arg Cys						
80 85 90						
TTG ATT TCG GCC TTA CAA AAG GGG CGC GTG CCT AAT AGA GGG AGT TGC	398					
Leu Ile Ser Ala Leu Gln Lys Gly Arg Val Pro Asn Arg Gly Ser Cys						
95 100 105						

GC Ala 110	CGC Asn	AAT Asp	GAT Cys	TGC Arg	CGG Phe 115	TTT Asp	GAT Tyr	TAT Glu	GAA Tyr	TAT Tyr 120	TAC Val	GTG Lys	AAA Asn	AAC Pro	CCT Asp 125	GAT Asp	446
AAT Asn	GGC Gly	GTG Val	ATG Met	ATG Met 130	AGA Arg	CTG Leu	GTT Val	GAA Glu	GAA Glu 135	GAG Glu	GGC Gly	GTA Val	GGC Gly	ACG Thr 140	CAT His	494	
ATT Ile	TTT Phe	AAC Asn	GCT Ala 145	AAG Lys	GAT Asp	TTG Leu	AAC Asn	CTC Leu 150	TCT Ser	GGC Gly	CAT His	ATC Ile	GCT Ala 155	GAA Glu	ATT Ile	542	
TTA Leu	AGT Ser	TCC Ser 160	AAC Asn	GCC Ala	ATT Ile	AGC Ser	GCG Ala 165	CTT Leu	AAG Lys	ATT Ile	GAA Glu	GGG Gly 170	CGC Arg	ACC Thr	AAG Lys	590	
TCC Ser	AGT Ser 175	TAC Tyr	TAC Tyr	GCC Ala	GCG Ala	CAA Gln 180	ACC Thr	ACG Thr	CGC Arg	ATC Ile	TAT Tyr 185	CGT Arg	TTA Leu	GCG Ala	GTT Val	638	
GAT Asp 190	GAT Asp	TTT Phe	TAC Tyr	CAT His	AAC Asn 195	ACC Thr	TTA Leu	AAG Lys	CCG Pro	AGT Ser 200	TTT Phe	TAT Tyr	GCC Ala	AGC Ser	GAA Glu 205	686	
TTG Leu	AAC Asn	ACG Thr	CTT Leu	AAA Lys 210	AAC Asn	AGG Arg	GGT Gly	TTT Phe	ACG Thr 215	GAC Asp	GGC Gly	TAT Tyr	TTG Leu	ATG Met 220	CGA Arg	734	
AGG Arg	CCT Pro	TTT Phe	GAA Glu 225	AGG Arg	TTG Leu	GAT Asp	ACT Thr	CAA Gln 230	AAC Asn	CAC His	CAA Gln	ACA Thr	GCC Ala 235	ATT Ile	AGC Ser	782	
GAA Glu	GGG Gly	GAT Asp 240	TTT Phe	CAA Gln	GTC Val	AAT Asn	GGC Gly 245	GAA Glu	ATA Ile	ACC Thr	GAA Glu	GAC Asp 250	GGG Gly	CGT Arg	TTT Phe	830	
TTT Phe 255	GCA Ala	TGC Cys	AAA Lys	TTC Phe	ACC Thr	ACT Thr 260	ACC Thr	ACT Thr	AAC Asn	ACC Thr 265	GCT Ala	TAT Tyr	GAA Glu	ATC Ile	ATC Ile	878	
GCT Ala 270	CCC Pro	AAA Lys	AAT Asn	GCG Ala	GCT Ala 275	ATC Ile	ACG Thr	CCC Pro	ATA Ile	GTC Val 280	AAT Asn	GAA Glu	ATT Ile	GGC Gly	AAG Lys 285	926	
ATT Ile	TAC Tyr	ACC Thr	TTT Phe	GAA Glu 290	AAA Lys	CGC Arg	TCT Ser	TAT Tyr	TTA Leu 295	GTG Val	CTG Leu	TAT Tyr	AAA Lys	ATC Ile 300	CTT Leu	974	
TTA Leu	GAA Glu	AAT Asn	AAC Asn 305	ACC Thr	GAG Glu	CTA Leu	GAA Glu	ACT Thr 310	ATC Ile	CAT His	AGC Ser	GGG Gly	AAC Asn 315	GTG Val	AAT Asn	1022	
TTA Leu	GTG Val	CGA Arg 320	CTG Leu	CCC Pro	GCA Ala	CCC Pro	TTA Leu 325	CCG Pro	GCT Ala	TTT Phe	AGT Ser	TTT Phe 330	TTA Leu	CGC Arg	ACC Thr	1070	
CAA Gln	GTC Val	AGA Arg	GTC Val	TAAAAATGGC			GTTTAGAGAT			TAGGTATTGA			AAATGATTAA			GAGAA	1127

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

```

Met Ala Glu Leu Glu Pro Asp Ala Phe Ile Ile Ala Ala Pro Gly Val
 1          5          10          15
Val Lys Leu Ala Leu Lys Ile Ala Pro His Ile Pro Ile His Leu Ser
 20          25          30
Thr Gln Ala Asn Val Leu Asn Leu Asp Ala Gln Val Phe Tyr Asp
 35          40          45
Leu Gly Val Lys Arg Ile Val Cys Ala Arg Glu Leu Ser Leu Asn Asp
 50          55          60
Ala Ile Glu Ile Lys Lys Ala Leu Pro Asn Leu Glu Leu Glu Ile Phe
 65          70          75          80
Val His Gly Ser Met Cys Phe Ala Phe Ser Gly Arg Cys Leu Ile Ser
 85          90          95
Ala Leu Gln Lys Gly Arg Val Pro Asn Arg Gly Ser Cys Ala Asn Asp
100          105          110
Cys Arg Phe Asp Tyr Glu Tyr Tyr Val Lys Asn Pro Asp Asn Gly Val
115          120          125
Met Met Arg Leu Val Glu Glu Glu Gly Val Gly Thr His Ile Phe Asn
130          135          140
Ala Lys Asp Leu Asn Leu Ser Gly His Ile Ala Glu Ile Leu Ser Ser
145          150          155          160
Asn Ala Ile Ser Ala Leu Lys Ile Glu Gly Arg Thr Lys Ser Ser Tyr
165          170          175
Tyr Ala Ala Gln Thr Thr Arg Ile Tyr Arg Leu Ala Val Asp Asp Phe
180          185          190
Tyr His Asn Thr Leu Lys Pro Ser Phe Tyr Ala Ser Glu Leu Asn Thr
195          200          205
Leu Lys Asn Arg Gly Phe Thr Asp Gly Tyr Leu Met Arg Arg Pro Phe
210          215          220
Glu Arg Leu Asp Thr Gln Asn His Gln Thr Ala Ile Ser Glu Gly Asp
225          230          235          240
Phe Gln Val Asn Gly Glu Ile Thr Glu Asp Gly Arg Phe Phe Ala Cys
245          250          255
Lys Phe Thr Thr Thr Thr Asn Thr Ala Tyr Glu Ile Ile Ala Pro Lys
260          265          270
Asn Ala Ala Ile Thr Pro Ile Val Asn Glu Ile Gly Lys Ile Tyr Thr
275          280          285
Phe Glu Lys Arg Ser Tyr Leu Val Leu Tyr Lys Ile Leu Leu Glu Asn
290          295          300
Asn Thr Glu Leu Glu Thr Ile His Ser Gly Asn Val Asn Leu Val Arg
305          310          315          320
Leu Pro Ala Pro Leu Pro Ala Phe Ser Phe Leu Arg Thr Gln Val Arg
325          330          335

```

Val

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1038
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

ATTAAGGAGA AATAAGAA ATG TTA CAA CCC CCT AAA ATT GTC GCT GAA TTG	51
Met Leu Gln Pro Pro Lys Ile Val Ala Glu Leu	
1 5 10	
AGC GCT AAT CAT AAC CAG GAT TTA AAC CTA GCC AAA GAA AGC CTT CAT	99
Ser Ala Asn His Asn Gln Asp Leu Asn Leu Ala Lys Glu Ser Leu His	
15 20 25	
GCC ATT AAG GAA AGC GGT GCG GAT TTT GTC AAG CTC CAA ACC TAC ACG	147
Ala Ile Lys Glu Ser Gly Ala Asp Phe Val Lys Leu Gln Thr Tyr Thr	
30 35 40	
CCA AGC TGC ATG ACT TTA AAC TCT AAA GAA GAT CCT TTC ATC ATT CAA	195
Pro Ser Cys Met Thr Leu Asn Ser Lys Glu Asp Pro Phe Ile Ile Gln	
45 50 55	
GGC ACT TTA TGG GAT AAA GAA AAT TTG TAT GAA TTG TAT CAA AAG GCT	243
Gly Thr Leu Trp Asp Lys Glu Asn Leu Tyr Glu Leu Tyr Gln Lys Ala	
60 65 70 75	
TCT ACC CCC CTA GAA TGG CAT GCT GAA TTG TTT GAG TTG GCT AGA AAG	291
Ser Thr Pro Leu Glu Trp His Ala Glu Leu Phe Glu Leu Ala Arg Lys	
80 85 90	
CTT GAT TTA GGC ATT TTT AGC TCG CCT TTT AGT TCA CAA GCT TTA GAG	339
Leu Asp Leu Gly Ile Phe Ser Ser Pro Phe Ser Ser Gln Ala Leu Glu	
95 100 105	
CTT TTA GAG AGC CTA AAT TGC CCC ATG TAT AAA ATC GCT AGT TTT GAA	387
Leu Leu Glu Ser Leu Asn Cys Pro Met Tyr Lys Ile Ala Ser Phe Glu	
110 115 120	
ATC GTT GAT TTG GAC TTG ATT GAA AAG GCC GCT CGC ACA CAA AAG CCC	435
Ile Val Asp Leu Asp Leu Ile Glu Lys Ala Ala Arg Thr Gln Lys Pro	
125 130 135	
ATT ATC CTT TCT AGC GGT ATC GCT ACA CAC ACC GAA TTG CAA GAC GCT	483

[illegible]

(2) INFORMATION FOR SEQ ID NO:490:

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Met	Leu	Gln	Pro	Pro	Lys	Ile	Val	Ala	Glu	Leu	Ser	Ala	Asn	His	Asn
1				5					10					15	
Gln	Asp	Leu	Asn	Leu	Ala	Lys	Glu	Ser	Leu	His	Ala	Ile	Lys	Glu	Ser
			20					25					30		
Gly	Ala	Asp	Phe	Val	Lys	Leu	Gln	Thr	Tyr	Thr	Pro	Ser	Cys	Met	Thr
			35				40					45			
Leu	Asn	Ser	Lys	Glu	Asp	Pro	Phe	Ile	Ile	Gln	Gly	Thr	Leu	Trp	Asp
	50					55					60				
Lys	Glu	Asn	Leu	Tyr	Glu	Leu	Tyr	Gln	Lys	Ala	Ser	Thr	Pro	Leu	Glu
65					70					75					80
Trp	His	Ala	Glu	Leu	Phe	Glu	Leu	Ala	Arg	Lys	Leu	Asp	Leu	Gly	Ile
				85					90					95	
Phe	Ser	Ser	Pro	Phe	Ser	Ser	Gln	Ala	Leu	Glu	Leu	Leu	Glu	Ser	Leu
			100					105					110		
Asn	Cys	Pro	Met	Tyr	Lys	Ile	Ala	Ser	Phe	Glu	Ile	Val	Asp	Leu	Asp
		115					120					125			
Leu	Ile	Glu	Lys	Ala	Ala	Arg	Thr	Gln	Lys	Pro	Ile	Ile	Leu	Ser	Ser
	130					135					140				
Gly	Ile	Ala	Thr	His	Thr	Glu	Leu	Gln	Asp	Ala	Ile	Ser	Leu	Cys	Arg
145					150					155					160
Arg	Val	Asn	Asn	Phe	Asp	Ile	Thr	Leu	Leu	Lys	Cys	Val	Ser	Ala	Tyr
				165					170					175	
Pro	Ser	Lys	Ile	Glu	Asp	Ala	Asn	Leu	Leu	Ser	Met	Val	Lys	Leu	Gly
			180					185					190		
Glu	Ile	Phe	Gly	Val	Lys	Phe	Gly	Leu	Ser	Asp	His	Thr	Ile	Gly	Ser
		195					200					205			
Leu	Cys	Pro	Ile	Leu	Ala	Thr	Thr	Leu	Gly	Ala	Ser	Met	Ile	Glu	Lys
	210					215				220					
His	Phe	Ile	Leu	Asn	Lys	Ser	Leu	Gln	Thr	Pro	Asp	Ser	Ala	Phe	Ser
225					230					235					240
Met	Asp	Phe	Asn	Gly	Phe	Lys	Ser	Met	Val	Glu	Ala	Ile	Lys	Gln	Ser
				245					250					255	
Val	Leu	Ala	Leu	Gly	Glu	Glu	Glu	Pro	Arg	Ile	Asn	Pro	Lys	Thr	Leu
			260					265					270		
Glu	Lys	Arg	Arg	Phe	Phe	Ala	Arg	Ser	Leu	Phe	Val	Ile	Lys	Asp	Ile
			275				280					285			
Gln	Lys	Gly	Glu	Ala	Leu	Thr	Glu	Asn	Asn	Ile	Lys	Ala	Leu	Arg	Pro
	290					295					300				
Asn	Leu	Gly	Leu	His	Pro	Lys	Phe	Tyr	Lys	Glu	Ile	Leu	Gly	Gln	Lys
305					310					315					320
Ala	Ser	Lys	Phe	Leu	Lys	Ala	Asn	Thr	Pro	Leu	Ser	Ala	Asp	Asp	Ile
				325					330					335	
Glu	Arg	Ser	Leu												
			340												

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 31...1197

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GTGAATGAGC GTTTGGAGGT GCTGTTGGAA	ATG GTT TTG ATG CGG TTT GAA GAG	54
	Met Val Leu Met Arg Phe Glu Glu	
	1 5	
CCC GAT CCT GGA AGA GCT ATC AGA ACC TTT CAG AGC GTG AAT GAC AGA		102
Pro Asp Pro Gly Arg Ala Ile Arg Thr Phe Gln Ser Val Asn Asp Arg		
10 15 20		
GGC GTG CCT CTC CTC TTG CTA GAC AAA CTA AAA TCC CTT CTC ATC TAT		150
Gly Val Pro Leu Leu Leu Asp Lys Leu Lys Ser Leu Leu Ile Tyr		
25 30 35 40		
TAC TCC AAC ATT TTT TGC GAT GGG AAA AGG GGG CTA GAC CAA TTT ATC		198
Tyr Ser Asn Ile Phe Cys Asp Gly Lys Arg Gly Leu Asp Gln Phe Ile		
45 50 55		
ATC GAT CAT TTT GGG GAG ATC TTT AAG ATC TTT GCC AAG ATT AAA AAG		246
Ile Asp His Phe Gly Glu Ile Phe Lys Ile Phe Ala Lys Ile Lys Lys		
60 65 70		
AGC GAC CAC ATC TCC AGC GTT GGA GGC TTT GAT GAA GGC GAT ATC TTC		294
Ser Asp His Ile Ser Ser Val Gly Gly Phe Asp Glu Gly Asp Ile Phe		
75 80 85		
CGC TAC CAC GCA GGG AGC CAA AAA TTT GAT GGA ATC GAG TTT TTA GGG		342
Arg Tyr His Ala Gly Ser Gln Lys Phe Asp Gly Ile Glu Phe Leu Gly		
90 95 100		
CAC TAC GAA GCA AGC ACG GAC AAA ACC TAC GAG AAA CTC AAA GAT GAA		390
His Tyr Glu Ala Ser Thr Asp Lys Thr Tyr Glu Lys Leu Lys Asp Glu		
105 110 115 120		
CTA AAA AAA ATC AAA AAA AGC AAA TTG AAA AGT TTC ATC CAA TCC TAT		438
Leu Lys Lys Ile Lys Lys Ser Lys Leu Lys Ser Phe Ile Gln Ser Tyr		
125 130 135		
GTC AGC GAT TTG AAA AAT TTC TAT CAG GCT TTT CTT GAT CTA TTG AGC		486
Val Ser Asp Leu Lys Asn Phe Tyr Gln Ala Phe Leu Asp Leu Leu Ser		
140 145 150		
GAG ATT GAC ACC AAC CCA ACC ACC TTT AAG GTC ATG CTC ATC AAC AAG		534
Glu Ile Asp Thr Asn Pro Thr Thr Phe Lys Val Met Leu Ile Asn Lys		
155 160 165		
ATC GAC TCG TCT TTT TTC AAT TCG CTC ATC CGC CTG AAA ATC AAC AAC		582
Ile Asp Ser Ser Phe Phe Asn Ser Leu Ile Arg Leu Lys Ile Asn Asn		

170				175				180								
GAA Glu 185	CTA Leu	GAC Asp	GAT Asp	GAA Glu	ACG Thr 190	CTG Leu	AAA Lys	CTC Leu	TTT Phe	GCC Ala 195	AAA Lys	ACC Thr	GAT Asp	ATT Ile	GTG Val 200	630
CTT Leu	TTC Phe	AAA Lys	GCT Ala	ACT Thr 205	AGA Arg	GAT Asp	AGG Arg	CCA Pro	GGA Gly 210	ACG Thr	GAC Asp	AAC Asn	CTG Leu	ATT Ile 215	AAT Asn	678
GCG Ala	TAT Tyr	CTT Leu	AAA Lys 220	AAG Lys	GGC Gly	AAA Lys	GAG Glu	GGA Gly 225	TTG Leu	AAG Lys	AGC Ser	GAG Glu	ATG Met 230	ATT Ile	GCT Ala	726
CAA Gln	TGC Cys	AGA Arg 235	AAT Asn	GAT Asp	ATA Ile	GGG Gly	CTG Leu 240	GCT Ala	TTT Phe	TGG Trp	CAG Gln	TCT Ser 245	GTA Val	AAC Asn	AAC Asn	774
GCA Ala 250	TCC Ser	AAC Asn	TCA Ser	TCA Ser	TGC Cys	TTC Phe 255	CAC His	TAT Tyr	ATC Ile	TTC Phe	TTT Phe 260	GAA Glu	AAG Lys	AAC Asn	TGC Cys	822
CAG Gln 265	GAG Glu	ATG Met	GGT Gly	CTT Leu	GCC Ala 270	GAT Asp	CTC Leu	AAA Lys	AAA Lys	TTG Leu 275	ATC Ile	CCT Pro	AGG Arg	AAG Lys	CAA Gln 280	870
TTC Phe	TCC Ser	CAA Gln	GAA Glu	AAA Lys 285	GAA Glu	CAC His	ATC Ile	ATC Ile	CCC Pro 290	ATC Ile	AAT Asn	TTA Leu	TTA Leu	AAA Lys 295	CAG Gln	918
GAA Glu	TCC Ser	AAC Asn	AAT Asn 300	AAG Lys	ATC Ile	AGA Arg	GAT Asp	CTT Leu 305	GGT Gly	TTT Phe	GAA Glu	GAC Asp	AAA Lys 310	AAA Lys	GAT Asp	966
CTT Leu	GAA Glu 315	GAC Asp	TAC Tyr	ATT Ile	GAC Asp	ACA Thr	TAC Tyr 320	GGC Gly	AAC Asn	CTC Leu	ATC Ile	TCC Ser 325	CTG Leu	GAA Glu	AAA Lys	1014
TCG Ser 330	CTC Leu	AAT Asn	CGT Arg	AAG Lys	GCA Ala	AGC Ser	GAT Asp 335	AAG Lys	GAT Asp	CTG Leu	TAT Tyr 340	GGA Gly	AAA Lys	GAT Asp	GAA Glu	1062
ATC Ile 345	TAT Tyr	AAA Lys	AGT Ser	AGT Ser	GAG Glu 350	ATC Ile	CCT Pro	TTC Phe	AAC Asn	AGG Arg 355	CGC Arg	TTT Phe	GAT Asp	ACA Thr	AAA Lys 360	1110
AAC Asn	TTC Phe	AAT Asn	AAG Lys	AAG Lys 365	GCA Ala	TTG Leu	GTA Val	AAA Lys	AGA Arg 370	AAT Asn	GAA Glu	GAA Glu	ATG Met	CGA Arg 375	GAA Glu	1158
TGG Trp	CTG Leu	ATC Ile	GAC Asp 380	ACC Thr	TTT Phe	TTT Phe	AAG Lys	GAT Asp 385	TTC Phe	GCC Ala	GCC Ala	CAC His	TAAAGAGAGT	GA		1209
GATTAAAAGA GAGTGATCGC ACTCA															1234	

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

Met	Val	Leu	Met	Arg	Phe	Glu	Glu	Pro	Asp	Pro	Gly	Arg	Ala	Ile	Arg
1			5					10						15	
Thr	Phe	Gln	Ser	Val	Asn	Asp	Arg	Gly	Val	Pro	Leu	Leu	Leu	Leu	Asp
			20					25					30		
Lys	Leu	Lys	Ser	Leu	Leu	Ile	Tyr	Tyr	Ser	Asn	Ile	Phe	Cys	Asp	Gly
		35					40					45			
Lys	Arg	Gly	Leu	Asp	Gln	Phe	Ile	Ile	Asp	His	Phe	Gly	Glu	Ile	Phe
	50					55					60				
Lys	Ile	Phe	Ala	Lys	Ile	Lys	Lys	Ser	Asp	His	Ile	Ser	Ser	Val	Gly
65					70					75					80
Gly	Phe	Asp	Glu	Gly	Asp	Ile	Phe	Arg	Tyr	His	Ala	Gly	Ser	Gln	Lys
			85					90						95	
Phe	Asp	Gly	Ile	Glu	Phe	Leu	Gly	His	Tyr	Glu	Ala	Ser	Thr	Asp	Lys
			100					105						110	
Thr	Tyr	Glu	Lys	Leu	Lys	Asp	Glu	Leu	Lys	Lys	Ile	Lys	Lys	Ser	Lys
			115				120						125		
Leu	Lys	Ser	Phe	Ile	Gln	Ser	Tyr	Val	Ser	Asp	Leu	Lys	Asn	Phe	Tyr
			130			135					140				
Gln	Ala	Phe	Leu	Asp	Leu	Leu	Ser	Glu	Ile	Asp	Thr	Asn	Pro	Thr	Thr
145					150					155					160
Phe	Lys	Val	Met	Leu	Ile	Asn	Lys	Ile	Asp	Ser	Ser	Phe	Phe	Asn	Ser
			165						170					175	
Leu	Ile	Arg	Leu	Lys	Ile	Asn	Asn	Glu	Leu	Asp	Asp	Glu	Thr	Leu	Lys
			180					185						190	
Leu	Phe	Ala	Lys	Thr	Asp	Ile	Val	Leu	Phe	Lys	Ala	Thr	Arg	Asp	Arg
			195				200					205			
Pro	Gly	Thr	Asp	Asn	Leu	Ile	Asn	Ala	Tyr	Leu	Lys	Lys	Gly	Lys	Glu
			210			215						220			
Gly	Leu	Lys	Ser	Glu	Met	Ile	Ala	Gln	Cys	Arg	Asn	Asp	Ile	Gly	Leu
225					230					235					240
Ala	Phe	Trp	Gln	Ser	Val	Asn	Asn	Ala	Ser	Asn	Ser	Ser	Cys	Phe	His
			245						250					255	
Tyr	Ile	Phe	Phe	Glu	Lys	Asn	Cys	Gln	Glu	Met	Gly	Leu	Ala	Asp	Leu
			260					265						270	
Lys	Lys	Leu	Ile	Pro	Arg	Lys	Gln	Phe	Ser	Gln	Glu	Lys	Glu	His	Ile
		275					280						285		
Ile	Pro	Ile	Asn	Leu	Leu	Lys	Gln	Glu	Ser	Asn	Asn	Lys	Ile	Arg	Asp
			290			295						300			
Leu	Gly	Phe	Glu	Asp	Lys	Lys	Asp	Leu	Glu	Asp	Tyr	Ile	Asp	Thr	Tyr
305					310					315					320
Gly	Asn	Leu	Ile	Ser	Leu	Glu	Lys	Ser	Leu	Asn	Arg	Lys	Ala	Ser	Asp
			325						330					335	
Lys	Asp	Leu	Tyr	Gly	Lys	Asp	Glu	Ile	Tyr	Lys	Ser	Ser	Glu	Ile	Pro
			340				345						350		
Phe	Asn	Arg	Arg	Phe	Asp	Thr	Lys	Asn	Phe	Asn	Lys	Lys	Ala	Leu	Val
		355					360						365		
Lys	Arg	Asn	Glu	Glu	Met	Arg	Glu	Trp	Leu	Ile	Asp	Thr	Phe	Phe	Lys
			370			375						380			

Asp Phe Ala Ala His
385

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...840
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

TTATAAAGGA AAATC ATG GGA TTT TTA AAA GGT AAA AAA GGG CTT ATT GTA	51
Met Gly Phe Leu Lys Gly Lys Lys Gly Leu Ile Val	
1 5 10	
GGG GTG GCG AAC AAT AAA TCC ATC GCT TAT GGG ATC GCT CAA TCT TGT	99
Gly Val Ala Asn Asn Lys Ser Ile Ala Tyr Gly Ile Ala Gln Ser Cys	
15 20 25	
TTC AAT CAA GGG GCT ACT TTG GCT TTC ACT TAT TTG AAT GAG AGT TTA	147
Phe Asn Gln Gly Ala Thr Leu Ala Phe Thr Tyr Leu Asn Glu Ser Leu	
30 35 40	
GAA AAG CGC GTA AGG CCT ATC GCG CAG GAA TTG AAT AGC CCC TAT GTG	195
Glu Lys Arg Val Arg Pro Ile Ala Gln Glu Leu Asn Ser Pro Tyr Val	
45 50 55 60	
TAT GAA TTG GAT GTG AGC AAA GAA GAG CAT TTC AAG TCG CTA TAC AAT	243
Tyr Glu Leu Asp Val Ser Lys Glu Glu His Phe Lys Ser Leu Tyr Asn	
65 70 75	
AGC GTT AAA AAG GAT TTA GGC TCA TTG GAT TTT ATT GTT CAT AGC GTG	291
Ser Val Lys Lys Asp Leu Gly Ser Leu Asp Phe Ile Val His Ser Val	
80 85 90	
GCC TTT GCC CCT AAA GAG GCT TTA GAG GGG AGC TTG TTG GAA ACT TCT	339
Ala Phe Ala Pro Lys Glu Ala Leu Glu Gly Ser Leu Leu Glu Thr Ser	
95 100 105	
AAA AGC GCG TTT AAC ACC GCT ATG GAA ATT TCT GTT TAT TCT TTA ATA	387
Lys Ser Ala Phe Asn Thr Ala Met Glu Ile Ser Val Tyr Ser Leu Ile	
110 115 120	
GAG CTG ACA AAC ACC CTA AAA CCT TTA TTG AAT AAC GGA GCG TCT GTT	435
Glu Leu Thr Asn Thr Leu Lys Pro Leu Leu Asn Asn Gly Ala Ser Val	
125 130 135 140	
TTG ACT CTA AGC TAT TTG GGT AGC ACC AAA TAC ATG GCG CAT TAC AAT	483

[illegible]

65		70		75		80
Asp	Leu	Gly	Ser	Leu	Asp	Phe
		85		90		95
Lys	Glu	Ala	Leu	Glu	Gly	Ser
		100		105		110
Asn	Thr	Ala	Met	Glu	Ile	Ser
		115		120		125
Thr	Leu	Lys	Pro	Leu	Leu	Asn
		130		135		140
Tyr	Leu	Gly	Ser	Thr	Lys	Tyr
		145		150		155
Ala	Lys	Ala	Ala	Leu	Glu	Ser
		165		170		175
Gly	Lys	His	His	Ile	Arg	Val
		180		185		190
Thr	Leu	Ala	Ser	Ser	Gly	Ile
		195		200		205
Asn	Glu	Ile	Asn	Ala	Pro	Leu
		210		215		220
Gly	Asn	Ala	Gly	Met	Tyr	Leu
		225		230		235
Gly	Glu	Val	His	Phe	Val	Asp
		245		250		255
Ala	Val	Glu	Glu	Lys	Asp	Asn
		260		265		270
Lys	Glu	Gln				
		275				

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...1688
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

TGGAGGTTAG	TAATTTTAAA	GGGTAAAATA	AA	ATG	GAA	AAT	CAT	TCG	CAT	GCC	53
				Met	Glu	Asn	His	Ser	His	Ala	
				1				5			
AAT	ACG	CAT	ACC	GAT	ACG	CGC	ACC	GAT	GAT	AAA	AGC
Asn	Thr	His	Thr	Asp	Thr	Arg	Thr	Asp	Asp	Lys	Ser
		10				15				20	
CGC	TTG	TTG	GGG	TTA	ATA	GGG	GGA	GCG	TTA	ATC	GCG
Arg	Leu	Leu	Gly	Leu	Ile	Gly	Gly	Ala	Leu	Ile	Ala
		25				30				35	
											149

TAT Tyr 40	GCG Ala	CTC Leu	AAT Asn	TCT Ser	CAA Gln 45	ATG Met	CCT Pro	CAT His	ATT Ile	GTA Val 50	GAA Glu	GAA Glu	ATC Ile	CCC Pro	AAG Lys 55	197
CTC Leu	AGT Ser	TCT Ser	TTG Leu	AAT Asn 60	TAT Tyr	AAG Lys	GCG Ala	ATG Met	CCT Pro 65	GTT Val	GTG Val	GCA Ala	GGG Gly	GTG Val 70	GCT Ala	245
GTT Val	TTA Leu	ATG Met	GGG Gly 75	ATA Ile	TGG Trp	TGG Trp	ATG Met	ACT Thr 80	GAA Glu	GCC Ala	ATT Ile	GAC Asp	TTG Leu 85	CCC Pro	GCA Ala	293
ACC Thr	GCG Ala	CTT Leu 90	TTA Leu	CCT Pro	TTG Leu	GTG Val	CTT Leu 95	TTT Phe	AGC Ser	GTC Val	TTT Phe	AGC Ser 100	GTG Val	GAT Asp	CAA Gln	341
TTC Phe 105	GCT Ala	AGC Ser	GTC Val	AGC Ser	TCT Ser 110	TCT Ser	TAC Tyr	GCA Ala	TCG Ser	CCG Pro	ATC Ile 115	ATC Ile	TTT Phe	CTT Leu	TTT Phe	389
ATG Met 120	GGA Gly	GGG Gly	TTT Phe	ATT Ile	TTA Leu 125	GCC Ala	CTA Leu	AGC Ser	ATG Met	CAA Gln 130	AAA Lys	TGG Trp	AAT Asn	TTG Leu	CAC His 135	437
ACG Thr	CGC Arg	ATC Ile	GCT Ala	TTA Leu 140	AGC Ser	ATT Ile	ATT Ile	TTA Leu	TTA Leu 145	GTA Val	GGC Gly	ACA Thr	AGC Ser	CCT Pro 150	AGG Arg	485
AGG Arg	TTG Leu	ATT Ile	TTA Leu 155	GGT Gly	TTC Phe	ATG Met	ATG Met	GCT Ala 160	ACA Thr	GGC Gly	TTT Phe	CTG Leu	TCT Ser 165	ATG Met	TGG Trp	533
GTG Val	AGC Ser	AAT Asn 170	ACC Thr	GCA Ala	ACG Thr	GCG Ala	GTG Val 175	ATG Met	ATG Met	CTC Leu	CCT Pro	GTT Val 180	GGC Gly	ATG Met	AGC Ser	581
GTT Val 185	TTG Leu	CAA Gln	TTA Leu	GTC Val	GCT Ala	AAA Lys 190	CTG Leu	GTG Val	GGC Gly	AAA Lys	GAA Glu 195	GAC Asp	GCC Ala	TCT Ser	AAT Asn	629
TCA Ser 200	TGG Trp	CAT His	CAA Gln	AAA Lys	GAA Glu 205	GAA Glu	ATC Ile	ACC Thr	AAA Lys	GCG Ala 210	CAT His	GGG Gly	GGT Gly	ATT Ile	ATG Met 215	677
AGT Ser	AAT Asn	ATC Ile	GTG Val	CAT His 220	AAG Lys	GGT Gly	AAA Lys	GAT Asp	ATT Ile 225	ACT Thr	CAA Gln	GTC Val	ATT Ile	CAA Gln 230	GAA Glu	725
AAG Lys	ACT Thr	ACT Thr	ATC Ile 235	TAT Tyr	CGC Arg	ACG Thr	AAT Asn	TTC Phe 240	AGT Ser	ATT Ile	TGC Cys	TTG Leu	ATG Met 245	CTT Leu	GGC Gly	773
ATC Ile	GCT Ala	TAT Tyr 250	GCG Ala	GCT Ala	TCT Ser	ATT Ile	GGC Gly 255	TCT Ser	TTA Leu	GGC Gly	ACT Thr	TTG Leu 260	ATT Ile	GGC Gly	ACG Thr	821
CCG Pro	CCT Pro	AAC Asn	GCT Ala	TTA Leu	TTG Leu	GCC Ala	GGC Gly	TAT Tyr	ATG Met	AAA Lys	ACC Thr	GCT Ala	TTC Phe	AAT Asn	ATT Ile	869

265				270				275								
GAA Glu 280	ATT Ile	GAT Asp	TTC Phe	GCT Ala	CAG Gln 285	TGG Trp	ATG Met	GTG Val	TTT Phe	GGG Gly 290	ACG Thr	CCG Pro	TTA Leu	GCC Ala	TTT Phe 295	917
ATC Ile	ATG Met	CTC Leu	ATT Ile	TTA Leu 300	GCG Ala	TGG Trp	CTC Leu	TTG Leu	CTC Leu 305	ACT Thr	TAT Tyr	GTG Val	ATT Ile	TTC Phe 310	CCT Pro	965
TTA Leu	AAG Lys	ATT Ile	AAA Lys 315	GAA Glu	ATC Ile	CCA Pro	GGG Gly	GGT Gly 320	AAG Lys	GAA Glu	GTC Val	ATT Ile	AGG Arg 325	GTA Val	GAG Glu	1013
TTA Leu	AAA Lys	AAA Lys 330	TTA Leu	GGC Gly	CGT Arg	TTG Leu	AGT Ser 335	CAG Gln	GCG Ala	GAA Glu	ATC Ile	TCT Ser 340	GTG Val	GGG Gly	ATT Ile	1061
ATT Ile	TTT Phe 345	ATT Ile	TTA Leu	GCG Ala	TCT Ser	TTA Leu 350	GGG Gly	TGG Trp	ATT Ile	TTT Phe	TTA Leu 355	GGC Gly	GTA Val	ATG Met	TTA Leu	1109
AAA Lys 360	TCT Ser	TGG Trp	GGC Gly	GTT Val	AAG Lys 365	ATA Ile	GAT Asp	AAA Lys	ATT Ile	GAT Asp 370	TCA Ser	GTG Val	ATC Ile	GCT Ala	ATG Met 375	1157
GGG Gly	GTT Val	TCT Ser	GCG Ala	CTT Leu 380	TTA Leu	TTC Phe	ATT Ile	TTG Leu	CCC Pro 385	GCT Ala	AAC Asn	CAT His	CAG Gln	GGC Gly 390	GAT Asp	1205
AGG Arg	CTC Leu	ATT Ile	GAT Asp 395	TGG Trp	GGT Gly	GTT Val	GCT Ala	AAA Lys 400	AAA Lys	CTC Leu	CCT Pro	TGG Trp	GAT Asp 405	GTG Val	TTG Leu	1253
CTT Leu	TTA Leu	TTT Phe 410	GGC Gly	GGC Gly	GGG Gly	TTA Leu	GCC Ala 415	TTG Leu	AGC Ser	GCG Ala	CAA Gln	TTT Phe 420	TCT Ser	AAA Lys	ACC Thr	1301
GGG Gly 425	TTG Leu	AGT Ser	TTG Leu	TGG Trp	ATC Ile	GGG Gly 430	CAT His	TTA Leu	GTC Val	TCT Ser	GGC Gly 435	TTT Phe	TCG Ser	CAT His	TTA Leu	1349
CCG Pro 440	ATT Ile	TTA Leu	TTC Phe	ATC Ile	ATT Ile 445	GTC Val	ATG Met	GTT Val	ACT Thr	TTA Leu 450	ATG Met	GTC Val	ATT Ile	TTC Phe	TTA Leu 455	1397
ACC Thr	GAA Glu	ATC Ile	ACT Thr	TCT Ser 460	AAC Asn	ACC Thr	GCC Ala	ACC Thr	GCT Ala 465	GCC Ala	GCA Ala	TTT Phe	TTA Leu	CCG Pro 470	GTG Val	1445
ATT Ile	GGA Gly	GGG Gly	GTT Val 475	GCG Ala	ATG Met	GGC Gly	ATG Met	GGT Gly 480	TAT Tyr	GAA Glu	AAC Asn	CAT His	CAG Gln 485	AGC Ser	TTG Leu	1493
TTA Leu	TTG Leu	ACC Thr 490	ATT Ile	CCT Pro	GTA Val	GCC Ala	TTG Leu 495	AGT Ser	GCG Ala	ACT Thr	TGC Cys 500	GCG Ala	TTC Phe	ATG Met	CTC Leu	1541

CCT GTG GTC ACC CCA CCG AAT GCA ATA GCT TAT GGC TCT GGG TAT GTT	1589
Pro Val Val Thr Pro Pro Asn Ala Ile Ala Tyr Gly Ser Gly Tyr Val	
505 510 515	

AAA ATA ACG GAC ATG ATT AAA GCC GGT TTG TGG CTT AAT CTG GTA GGA	1637
Lys Ile Thr Asp Met Ile Lys Ala Gly Leu Trp Leu Asn Leu Val Gly	
520 525 530 535	

GTT GTT TTG ATT AGC ACG TTT AGC TAT TTT TTG GTT TCG TTA ATA TTT	1685
Val Val Leu Ile Ser Thr Phe Ser Tyr Phe Leu Val Ser Leu Ile Phe	
540 545 550	

AAT TGATTAAGGA AAAAAGTGAA AGAAGAGTTA TTAAAGAAA AATCTCGTTA CATTAC	1744
Asn	

AGGGTTTGTT TTAATC	1760
-------------------	------

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

Met	Glu	Asn	His	Ser	His	Ala	Asn	Thr	His	Thr	Asp	Thr	Arg	Thr	Asp
1				5				10						15	
Asp	Lys	Ser	Thr	Lys	Ile	Val	Arg	Leu	Gly	Leu	Ile	Gly	Gly	Ala	
			20					25					30		
Leu	Ile	Ala	Leu	Val	Ile	Tyr	Tyr	Ala	Leu	Asn	Ser	Gln	Met	Pro	His
		35					40					45			
Ile	Val	Glu	Glu	Ile	Pro	Lys	Leu	Ser	Ser	Leu	Asn	Tyr	Lys	Ala	Met
		50				55					60				
Pro	Val	Val	Ala	Gly	Val	Ala	Val	Leu	Met	Gly	Ile	Trp	Trp	Met	Thr
65					70					75				80	
Glu	Ala	Ile	Asp	Leu	Pro	Ala	Thr	Ala	Leu	Leu	Pro	Leu	Val	Leu	Phe
				85					90					95	
Ser	Val	Phe	Ser	Val	Asp	Gln	Phe	Ala	Ser	Val	Ser	Ser	Ser	Tyr	Ala
			100					105					110		
Ser	Pro	Ile	Ile	Phe	Leu	Phe	Met	Gly	Gly	Phe	Ile	Leu	Ala	Leu	Ser
		115					120					125			
Met	Gln	Lys	Trp	Asn	Leu	His	Thr	Arg	Ile	Ala	Leu	Ser	Ile	Ile	Leu
		130				135					140				
Leu	Val	Gly	Thr	Ser	Pro	Arg	Arg	Leu	Ile	Leu	Gly	Phe	Met	Met	Ala
145					150					155					160
Thr	Gly	Phe	Leu	Ser	Met	Trp	Val	Ser	Asn	Thr	Ala	Thr	Ala	Val	Met
				165					170					175	
Met	Leu	Pro	Val	Gly	Met	Ser	Val	Leu	Gln	Leu	Val	Ala	Lys	Leu	Val
			180					185					190		
Gly	Lys	Glu	Asp	Ala	Ser	Asn	Ser	Trp	His	Gln	Lys	Glu	Glu	Ile	Thr
		195					200					205			
Lys	Ala	His	Gly	Gly	Ile	Met	Ser	Asn	Ile	Val	His	Lys	Gly	Lys	Asp
		210				215					220				

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GGTGGCGGCG TATTTTAACG GCGTCCTAT AGAATGCGCT CTTATTAGCG CC ATG GTC 58
Met Val
1

ATG GCT AGT GTT ATC GCT TAT CAA AAA GCG CAC CAT AGC GAA GCC ATT 106
Met Ala Ser Val Ile Ala Tyr Gln Lys Ala His His Ser Glu Ala Ile
5 10 15

TTA CCC TTT TTG TAT CCG GGC GTT GGG TTT TTT GCG CTT TTT GGG GTT 154
Leu Pro Phe Leu Tyr Pro Gly Val Gly Phe Phe Ala Leu Phe Gly Val
20 25 30

TAT AAG GAT TTT GGT GCA GTA GCG ATC ATT TGG CTT TTA GTC GTG GTG 202
Tyr Lys Asp Phe Gly Ala Val Ala Ile Ile Trp Leu Leu Val Val Val
35 40 45 50

GTT GCA AGC GAT GTG GGG GCG TTT TTT GGA GGC AAG CTT TTA GGC AAA 250
Val Ala Ser Asp Val Gly Ala Phe Phe Gly Gly Lys Leu Leu Gly Lys
55 60 65

ACC CCT TTC ACG CCC ACT TCG CCG AAT AAA ACC TTA GAG GGC GCG TTG 298
Thr Pro Phe Thr Pro Thr Ser Pro Asn Lys Thr Leu Glu Gly Ala Leu
70 75 80

ATT GGC GTG GTT TTG GCG AGC GTT TTA GGA TCG TTT GTG GGC ATG GGG 346
Ile Gly Val Val Leu Ala Ser Val Leu Gly Ser Phe Val Gly Met Gly
85 90 95

AAA TTG AGC GGA GGC TTT TTT ATG GCG CTC TTT TTT AGT TTT TTA ATC 394
Lys Leu Ser Gly Gly Phe Phe Met Ala Leu Phe Phe Ser Phe Leu Ile
100 105 110

GCT CTT GTG GCG GTG TTT GGG GAT TTG TAT GAA AGC TAT TTG AAA AGA 442
Ala Leu Val Ala Val Phe Gly Asp Leu Tyr Glu Ser Tyr Leu Lys Arg
115 120 125 130

AAG GTC GGT ATC AAA GAT AGC GGT AAG ATT TTA CCC GGG CAT GGG GGC 490
Lys Val Gly Ile Lys Asp Ser Gly Lys Ile Leu Pro Gly His Gly Gly
135 140 145

GTT TTA GAC CGG TTG GAT TCC ATG CTT TTT GGG GCT TTA GGC TTG CAT 538
Val Leu Asp Arg Leu Asp Ser Met Leu Phe Gly Ala Leu Gly Leu His
150 155 160

GCG CTG TTG TAT TTT TTA GAA ATT TGG AAA GAA ACG GCG GTG TTT TTA 586
Ala Leu Leu Tyr Phe Leu Glu Ile Trp Lys Glu Thr Ala Val Phe Leu
165 170 175

GGG GAT TGAATGGTTG TTTTAGGAAG CACCGGCTCT ATTGGGAAAA ACGCCCTAAA AA 644
Gly Asp
180

TCGCAAAAAA ATTTGGC 661

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Met Val Met Ala Ser Val Ile Ala Tyr Gln Lys Ala His His Ser Glu
1 5 10 15
Ala Ile Leu Pro Phe Leu Tyr Pro Gly Val Gly Phe Phe Ala Leu Phe
20 25 30
Gly Val Tyr Lys Asp Phe Gly Ala Val Ala Ile Ile Trp Leu Leu Val
35 40 45
Val Val Val Ala Ser Asp Val Gly Ala Phe Phe Gly Gly Lys Leu Leu
50 55 60
Gly Lys Thr Pro Phe Thr Pro Thr Ser Pro Asn Lys Thr Leu Glu Gly
65 70 75 80
Ala Leu Ile Gly Val Val Leu Ala Ser Val Leu Gly Ser Phe Val Gly
85 90 95
Met Gly Lys Leu Ser Gly Gly Phe Phe Met Ala Leu Phe Phe Ser Phe
100 105 110
Leu Ile Ala Leu Val Ala Val Phe Gly Asp Leu Tyr Glu Ser Tyr Leu
115 120 125
Lys Arg Lys Val Gly Ile Lys Asp Ser Gly Lys Ile Leu Pro Gly His
130 135 140
Gly Gly Val Leu Asp Arg Leu Asp Ser Met Leu Phe Gly Ala Leu Gly
145 150 155 160
Leu His Ala Leu Leu Tyr Phe Leu Glu Ile Trp Lys Glu Thr Ala Val
165 170 175
Phe Leu Gly Asp
180

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 12...1115
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

TAGGGGATTG A ATG GTT GTT TTA GGA AGC ACC GGC TCT ATT GGG AAA AAC 50
Met Val Val Leu Gly Ser Thr Gly Ser Ile Gly Lys Asn
1 5 10
GCC CTA AAA ATC GCA AAA AAA TTT GGC ATA GAA ATA GAG GCC TTA AGC 98

Ala 15	Leu	Lys	Ile	Ala	Lys	Lys 20	Phe	Gly	Ile	Glu	Ile 25	Glu	Ala	Leu	Ser	
TGT Cys 30	GGG Gly	AAA Lys	AAT Asn	ATC Ile	GCT Ala 35	TTA Leu	ATC Ile	AAT Asn	GAA Glu	CAA Gln 40	ATC Ile	CAA Gln	GTT Val	TTC Phe	AAA Lys 45	146
CCC Pro	AAG Lys	AAA Lys	GTG Val	GCG Ala 50	ATT Ile	TTA Leu	GAT Asp	CCT Pro	AGC Ser 55	GAT Asp	TTG Leu	AAT Asn	GAT Asp	TTA Leu 60	GAG Glu	194
CCT Pro	TTG Leu	GGT Gly	GCG Ala 65	GAA Glu	GTG Val	TTT Phe	GTG Val	GGG Gly 70	TTA Leu	GAG Glu	GGC Gly	ATT Ile 75	GAT Asp	GCG Ala	ATG Met	242
ATA Ile	GAA Glu	GAG Glu 80	TGC Cys	ACC Thr	TCA Ser	AAT Asn	TTA Leu 85	GTC Val	CTT Leu	AAC Asn	GCC Ala	ATT Ile 90	GTG Val	GGC Gly	GTG Val	290
GCA Ala 95	GGA Gly	TTG Leu	AAA Lys	GCG Ala	AGC Ser	TTT Phe 100	AAA Lys	AGC Ser	TTA Leu	CAA Gln	AGG Arg 105	AAT Asn	AAA Lys	AAA Lys	CTG Leu	338
GCC Ala 110	CTA Leu	GCG Ala	AAT Asn	AAA Lys	GAA Glu 115	AGC Ser	TTA Leu	GTG Val	AGC Ser	GCG Ala 120	GGG Gly	CAT His	TTA Leu	TTA Leu	GAC Asp 125	386
ATT Ile	TCA Ser	CAA Gln	ATC Ile 130	ACG Thr	CCC Pro	ATT Ile	GAT Asp	AGC Ser	GAG Glu 135	CAT His	TTT Phe	GGT Gly	TTG Leu	TGG Trp 140	GCG Ala	434
TTG Leu	TTG Leu	CAA Gln 145	AAC Asn	AAG Lys	ACT Thr	TTA Leu	AAG Lys	CCT Pro 150	AAA Lys	TCC Ser	TTA Leu	ATC Ile 155	ATT Ile	AGC Ser	GCG Ala	482
AGT Ser	GGG Gly	GGG Gly 160	GCT Ala	TTC Phe	AGG Arg	GAC Asp	ACG Thr 165	CCT Pro	TTA Leu	GAA Glu	TTT Phe 170	ATT Ile	CCT Pro	ATT Ile	CAA Gln	530
AAC Asn 175	GCG Ala	CAA Gln	AAT Asn	GCG Ala	CTC Leu	AAG Lys 180	CAC His	CCT Pro	AAT Asn	TGG Trp	AGC Ser 185	ATG Met	GGA Gly	TCT Ser	AAA Lys	578
ATC Ile 190	ACC Thr	ATT Ile	GAT Asp	TCA Ser	GCG Ala 195	AGC Ser	ATG Met	GTC Val	AAT Asn	AAG Lys 200	CTT Leu	TTT Phe	GAA Glu	ATC Ile	CTA Leu 205	626
GAA Glu	ACT Thr	TAT Tyr	TGG Trp	CTT Leu 210	TTT Phe	GGC Gly	GCG Ala	TCT Ser	TTA Leu 215	AAG Lys	ATT Ile	GAT Asp	GCG Ala	CTG Leu 220	ATT Ile	674
GAA Glu	AGG Arg	AGT Ser	TCT Ser 225	ATC Ile	GTG Val	CAT His	GCT Ala	TTG Leu 230	GTG Val	GAG Glu	TTT Phe	GAA Glu	GAC Asp 235	AAC Asn	TCT Ser	722
ATC Ile	ATC Ile	GCG Ala 240	CAT His	TTA Leu	GCG Ala	AGC Ser	GCA Ala 245	GAT Asp	ATG Met	CAA Gln	TTA Leu	CCC Pro 250	ATA Ile	AGC Ser	TAT Tyr	770

GCG Ala	ATC Ile	GAT Asp	CCG Pro	AAG Lys	TTG Leu	GCC Ala	TCT Ser	TTG Leu	AGC Ser	GCG Ala	TCT Ser	ATC Ile	AAG Lys	CCC Pro	TTA Leu	818
255						260					265					
GAT Asp	CTA Leu	TAC Tyr	GCT Ala	TTA Leu	AGC Ser	GCG Ala	ATT Ile	AAA Lys	TTT Phe	GAA Glu	CCC Pro	ATT Ile	AGC Ser	ATG Met	GAG Glu	866
270					275					280					285	
CGC Arg	TAC Tyr	ACT Thr	TTG Leu	TGG Trp	TGT Cys	TAT Tyr	AAA Lys	GAC Asp	TTA Leu	CTG Leu	CTA Leu	GAA Glu	AAC Asn	CCT Pro	AAG Lys	914
				290					295					300		
CTT Leu	GGC Gly	GTG Val	GTG Val	CTG Leu	AAT Asn	GCG Ala	AGC Ser	AAT Asn	GAA Glu	GTG Val	GCG Ala	ATG Met	GAG Glu	AAG Lys	TTT Phe	962
			305					310					315			
TTA Leu	AAC Asn	AAA Lys	GAG Glu	ATC Ile	GCT Ala	TTT Phe	GGT Gly	GGC Gly	CTT Leu	ATC Ile	CAA Gln	ACC Thr	ATT Ile	TCT Ser	CAA Gln	1010
		320					325					330				
GCC Ala	TTA Leu	GAA Glu	TCA Ser	TAC Tyr	GAT Asp	AAA Lys	ATG Met	CCT Pro	TTC Phe	AAG Lys	CTC Leu	TCT Ser	AGT Ser	TTA Leu	GAA Glu	1058
	335					340					345					
GAA Glu	GTG Val	CTG Leu	GAA Glu	TTA Leu	GAC Asp	AAA Lys	GAA Glu	GTT Val	AGG Arg	GAG Glu	CGT Arg	TTT Phe	AAA Lys	AAT Asn	GTA Val	1106
350					355					360					365	
GCG Ala	GGA Gly	GTG Val	TAGTATAATA			AGATTTTGCT			TCTAATAGCG			TTTTATTTCAT			AT	1157

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

Met 1	Val	Val	Leu	Gly 5	Ser	Thr	Gly	Ser	Ile 10	Gly	Lys	Asn	Ala	Leu 15	Lys
Ile	Ala	Lys	Lys 20	Phe	Gly	Ile	Glu	Ile 25	Glu	Ala	Leu	Ser	Cys 30	Gly	Lys
Asn	Ile	Ala 35	Leu	Ile	Asn	Glu	Gln 40	Ile	Gln	Val	Phe	Lys 45	Pro	Lys	Lys
Val	Ala 50	Ile	Leu	Asp	Pro	Ser 55	Asp	Leu	Asn	Asp	Leu 60	Glu	Pro	Leu	Gly
Ala 65	Glu	Val	Phe	Val 70	Gly	Leu	Glu	Gly	Ile 75	Asp	Ala	Met	Ile	Glu 80	Glu
Cys	Thr	Ser	Asn 85	Leu	Val	Leu	Asn	Ala 90	Ile	Val	Gly	Val	Ala 95	Gly	Leu
Lys	Ala	Ser	Phe	Lys	Ser	Leu	Gln	Arg	Asn	Lys	Lys	Leu	Ala	Leu	Ala

15							20					25					
ACG	CAT	TTA	GGG	GTC	ATC	ACC	GAA	GAG	CAG	GCT	AAA	GCC	AAA	AAC	GCT	147	
Thr	His	Leu	Gly	Val	Ile	Thr	Glu	Glu	Gln	Ala	Lys	Ala	Lys	Asn	Ala		
			30					35					40				
AAG	CTC	ATT	GTG	GCG	GAT	TAT	GGC	GCA	GAG	GCA	TGC	GGT	GAT	GCG	GTG	195	
Lys	Leu	Ile	Val	Ala	Asp	Tyr	Gly	Ala	Glu	Ala	Cys	Gly	Asp	Ala	Val		
		45					50					55					
AGG	TTG	TAT	TGG	CTT	GTA	GAT	GAA	AGC	ACG	GAT	AGA	ATT	GTT	GAC	GCG	243	
Arg	Leu	Tyr	Trp	Leu	Val	Asp	Glu	Ser	Thr	Asp	Arg	Ile	Val	Asp	Ala		
	60					65					70						
AAG	TTT	AAA	AGC	TTT	GGT	TGC	GGA	ACA	GCG	ATC	GCA	AGC	TCA	GAC	ATG	291	
Lys	Phe	Lys	Ser	Phe	Gly	Cys	Gly	Thr	Ala	Ile	Ala	Ser	Ser	Asp	Met		
	75				80					85					90		
ATG	GTA	GAG	TTG	TGC	TTG	AAT	AAA	AGA	GTC	CAA	GAT	GCG	GTA	AAA	ATC	339	
Met	Val	Glu	Leu	Cys	Leu	Asn	Lys	Arg	Val	Gln	Asp	Ala	Val	Lys	Ile		
				95					100					105			
ACG	AAT	TTA	GAT	GTG	GAA	AGA	GGC	TTG	AGA	GAC	GAT	CCG	GAC	ACG	CCG	387	
Thr	Asn	Leu	Asp	Val	Glu	Arg	Gly	Leu	Arg	Asp	Asp	Pro	Asp	Thr	Pro		
			110					115					120				
GCG	GTG	CCT	GGG	CAA	AAA	ATG	CAC	TGC	TCG	GTG	ATG	GCG	TAT	GAT	GTG	435	
Ala	Val	Pro	Gly	Gln	Lys	Met	His	Cys	Ser	Val	Met	Ala	Tyr	Asp	Val		
		125					130					135					
ATC	AAA	AAA	GCT	GCC	GGC	ATG	TAT	TTG	GGG	AAA	AAC	GCT	GAA	GAT	TTT	483	
Ile	Lys	Lys	Ala	Ala	Gly	Met	Tyr	Leu	Gly	Lys	Asn	Ala	Glu	Asp	Phe		
	140					145					150						
GAA	GAA	GAA	ATC	ATC	GTG	TGC	GAG	TGC	GCT	AGG	GTG	AGT	TTA	GGT	ACG	531	
Glu	Glu	Glu	Ile	Ile	Val	Cys	Glu	Cys	Ala	Arg	Val	Ser	Leu	Gly	Thr		
	155				160					165					170		
ATT	AAA	GAA	GTG	ATT	AAG	CTC	AAT	GAT	TTA	AAA	AGC	GTT	GAA	GAA	ATC	579	
Ile	Lys	Glu	Val	Ile	Lys	Leu	Asn	Asp	Leu	Lys	Ser	Val	Glu	Glu	Ile		
				175					180					185			
ACT	AAC	TAC	ACC	AAA	GCC	GGT	GCT	TTT	TGT	AAA	AGC	TGT	GTG	AGG	CCT	627	
Thr	Asn	Tyr	Thr	Lys	Ala	Gly	Ala	Phe	Cys	Lys	Ser	Cys	Val	Arg	Pro		
			190					195					200				
GGA	GGG	CAT	GAA	AAA	AGG	GAT	TAT	TAC	TTG	GTG	GAT	ATT	CTT	AAA	GAA	675	
Gly	Gly	His	Glu	Lys	Arg	Asp	Tyr	Tyr	Leu	Val	Asp	Ile	Leu	Lys	Glu		
		205					210					215					
GTG	CGC	GAA	GAA	ATG	GAA	GCT	GAA	AAA	CTT	AAA	GCG	ACC	GCT	AAT	AAA	723	
Val	Arg	Glu	Glu	Met	Glu	Ala	Glu	Lys	Leu	Lys	Ala	Thr	Ala	Asn	Lys		
	220					225					230						
TCC	CAA	AGC	GGA	GAA	TTG	GCT	TTC	AGG	GAA	ATG	ACT	ATG	GTT	CAA	AAG	771	
Ser	Gln	Ser	Gly	Glu	Leu	Ala	Phe	Arg	Glu	Met	Thr	Met	Val	Gln	Lys		
	235				240					245					250		

Gly	Ala	Phe	Cys	Lys	Ser	Cys	Val	Arg	Pro	Gly	Gly	His	Glu	Lys	Arg
	195						200					205			
Asp	Tyr	Tyr	Leu	Val	Asp	Ile	Leu	Lys	Glu	Val	Arg	Glu	Glu	Met	Glu
	210					215					220				
Ala	Glu	Lys	Leu	Lys	Ala	Thr	Ala	Asn	Lys	Ser	Gln	Ser	Gly	Glu	Leu
	225				230					235					240
Ala	Phe	Arg	Glu	Met	Thr	Met	Val	Gln	Lys	Ile	Lys	Ala	Val	Asp	Lys
				245					250					255	
Val	Ile	Asp	Glu	Asn	Ile	Arg	Pro	Met	Leu	Met	Met	Asp	Gly	Gly	Asp
		260					265					270			
Leu	Glu	Ile	Leu	Asp	Ile	Lys	Glu	Ser	Asp	Asp	Tyr	Ile	Asp	Val	Tyr
	275					280						285			
Ile	Arg	Tyr	Met	Gly	Ala	Cys	Asp	Gly	Cys	Met	Ser	Ala	Thr	Thr	Gly
	290					295					300				
Thr	Leu	Phe	Ala	Ile	Glu	Asn	Ala	Leu	Gln	Glu	Leu	Leu	Asp	Arg	Ser
	305				310					315					320
Ile	Arg	Val	Leu	Pro	Ile										
					325										

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...375
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

TAGAGCTTGA	TTTTTTTA	ATG	TTA	ATA	ATG	GAT	TGG	AAA	TTA	AAA	GTG	GTG			51	
		Met	Leu	Ile	Met	Asp	Trp	Lys	Leu	Lys	Val	Val				
		1				5					10					
AAA	GAA	ATC	ATC	ACC	ATT	ACC	GCC	ACA	ACC	GCC	ACA	ATG	GGG	ATC	TTA	99
Lys	Glu	Ile	Ile	Thr	Ile	Thr	Ala	Thr	Thr	Ala	Thr	Met	Gly	Ile	Leu	
		15					20					25				
ACC	ACA	TAT	TCA	TTA	AAC	ACT	AAT	ATG	AGC	ACC	ATT	AAA	GAA	AAG	CCG	147
Thr	Thr	Tyr	Ser	Leu	Asn	Thr	Asn	Met	Ser	Thr	Ile	Lys	Glu	Lys	Pro	
		30				35					40					
GCA	AAA	AAA	GTA	GAA	AGC	CTT	GTT	TTA	GCC	CCG	GAT	TTT	GCG	TTA	ATG	195
Ala	Lys	Lys	Val	Glu	Ser	Leu	Val	Leu	Ala	Pro	Asp	Phe	Ala	Leu	Met	
	45					50					55					
ATA	GAC	TGC	CCC	ACT	AAA	GCG	CAC	CCT	GTC	ATT	CCC	CCC	AAA	AGC	CCT	243
Ile	Asp	Cys	Pro	Thr	Lys	Ala	His	Pro	Val	Ile	Pro	Pro	Lys	Ser	Pro	
	60				65				70						75	
GAG	ATG	ATA	TTC	CCC	AAG	CCT	TGC	GCT	TTA	GTT	TCT	TTA	TTT	TTA	TCG	291

Glu Met Ile Phe Pro Lys Pro Cys Ala Leu Val Ser Leu Phe Leu Ser
80 85 90

CTC ACG CCG TCT TTT AAA ATC ACA TCT AAA GTT TTA GCC GTC AAT AAG 339
Leu Thr Pro Ser Phe Lys Ile Thr Ser Lys Val Leu Ala Val Asn Lys
95 100 105

CTT TCT ATC GTT CCC ACT AGT GCT AAA GAA AGA GCG TAAGGCAACA ACTCTA 391
Leu Ser Ile Val Pro Thr Ser Ala Lys Glu Arg Ala
110 115

TCATTATTTT AAAATCCAAA TTT 414

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

Met Leu Ile Met Asp Trp Lys Leu Lys Val Val Lys Glu Ile Ile Thr
1 5 10 15
Ile Thr Ala Thr Thr Ala Thr Met Gly Ile Leu Thr Thr Tyr Ser Leu
20 25 30
Asn Thr Asn Met Ser Thr Ile Lys Glu Lys Pro Ala Lys Lys Val Glu
35 40 45
Ser Leu Val Leu Ala Pro Asp Phe Ala Leu Met Ile Asp Cys Pro Thr
50 55 60
Lys Ala His Pro Val Ile Pro Pro Lys Ser Pro Glu Met Ile Phe Pro
65 70 75 80
Lys Pro Cys Ala Leu Val Ser Leu Phe Leu Ser Leu Thr Pro Ser Phe
85 90 95
Lys Ile Thr Ser Lys Val Leu Ala Val Asn Lys Leu Ser Ile Val Pro
100 105 110
Thr Ser Ala Lys Glu Arg Ala
115

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...660
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

TATAAGGTTG CTCTC ATG AAA AAA CCC TAT AGG AAG ATT TCT GAT TAT GCG	51
Met Lys Lys Pro Tyr Arg Lys Ile Ser Asp Tyr Ala	
1 5 10	
ATC GTG GGT GGT TTG AGC GCG TTA GTG ATG GTG AGC ATT GTG GGG TGT	99
Ile Val Gly Gly Leu Ser Ala Leu Val Met Val Ser Ile Val Gly Cys	
15 20 25	
AAG AGC AAT GCT GAT GAC AAA CCA AAA GAG CAA AGC TCT TTA AGT CAA	147
Lys Ser Asn Ala Asp Asp Lys Pro Lys Glu Gln Ser Ser Leu Ser Gln	
30 35 40	
AGC GTT CAA AAA GGC GCG TTT GTG ATT TTA GAA GAG CAA AAG GAT AAA	195
Ser Val Gln Lys Gly Ala Phe Val Ile Leu Glu Glu Gln Lys Asp Lys	
45 50 55 60	
TCT TAC AAG GTT GTT GAA GAA TAC CCC AGC TCA AGA ACC CAC ATT ATA	243
Ser Tyr Lys Val Val Glu Glu Tyr Pro Ser Ser Arg Thr His Ile Ile	
65 70 75	
GTG CGC GAT TTG CAA GGC AAT GAA CGC GTG TTA AGC AAT GAA GAG ATT	291
Val Arg Asp Leu Gln Gly Asn Glu Arg Val Leu Ser Asn Glu Glu Ile	
80 85 90	
CAA AAG CTC ATC AAA GAA GAA GAA GCT AAA ATT GAT AAC GGC ACG AGC	339
Gln Lys Leu Ile Lys Glu Glu Glu Ala Lys Ile Asp Asn Gly Thr Ser	
95 100 105	
AAG CTT GTC CAG CCT AAT AAT GGA GGG AGT AAT GAA GGC TCA GGC TTT	387
Lys Leu Val Gln Pro Asn Asn Gly Gly Ser Asn Glu Gly Ser Gly Phe	
110 115 120	
GGC TTG GGG AGC GCG ATT TTA GGG AGC GCG GCG GGG GCG ATT TTA GGG	435
Gly Leu Gly Ser Ala Ile Leu Gly Ser Ala Ala Gly Ala Ile Leu Gly	
125 130 135 140	
AGT TAT ATT GGT AAT AAG CTT TTC AAT AAC CCT AAT TAC CAG CAA AAC	483
Ser Tyr Ile Gly Asn Lys Leu Phe Asn Asn Pro Asn Tyr Gln Gln Asn	
145 150 155	
GCC CAA CGG ACC TAC AAA TCC CCA CAA GCT TAC CAA CGC TCT CAA AAT	531
Ala Gln Arg Thr Tyr Lys Ser Pro Gln Ala Tyr Gln Arg Ser Gln Asn	
160 165 170	
TCC TTT TCT AAA AGT GCG CCC AGT GCT TCA AGC ATG GGC GGA GCG AGT	579
Ser Phe Ser Lys Ser Ala Pro Ser Ala Ser Ser Met Gly Gly Ala Ser	
175 180 185	
AAG GGA CAG AGC GGG TTT TTT GGC TCT AGT AGG CCT ACT AGT TCA CCG	627
Lys Gly Gln Ser Gly Phe Phe Gly Ser Ser Arg Pro Thr Ser Ser Pro	
190 195 200	
GCG GTA AGC TCT GGG ACA AGG GGC TTT AAC TCA TAATTTAATT GATTCAAGGC	680
Ala Val Ser Ser Gly Thr Arg Gly Phe Asn Ser	
205 210 215	

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

```

Met Lys Lys Pro Tyr Arg Lys Ile Ser Asp Tyr Ala Ile Val Gly Gly
 1           5           10           15
Leu Ser Ala Leu Val Met Val Ser Ile Val Gly Cys Lys Ser Asn Ala
 20           25           30
Asp Asp Lys Pro Lys Glu Gln Ser Ser Leu Ser Gln Ser Val Gln Lys
 35           40           45
Gly Ala Phe Val Ile Leu Glu Gln Lys Asp Lys Ser Tyr Lys Val
 50           55           60
Val Glu Glu Tyr Pro Ser Arg Thr His Ile Ile Val Arg Asp Leu
 65           70           75           80
Gln Gly Asn Glu Arg Val Leu Ser Asn Glu Glu Ile Gln Lys Leu Ile
 85           90           95
Lys Glu Glu Glu Ala Lys Ile Asp Asn Gly Thr Ser Lys Leu Val Gln
100          105          110
Pro Asn Asn Gly Gly Ser Asn Glu Gly Ser Gly Phe Gly Leu Gly Ser
115          120          125
Ala Ile Leu Gly Ser Ala Ala Gly Ala Ile Leu Gly Ser Tyr Ile Gly
130          135          140
Asn Lys Leu Phe Asn Asn Pro Asn Tyr Gln Gln Asn Ala Gln Arg Thr
145          150          155          160
Tyr Lys Ser Pro Gln Ala Tyr Gln Arg Ser Gln Asn Ser Phe Ser Lys
165          170          175
Ser Ala Pro Ser Ala Ser Ser Met Gly Gly Ala Ser Lys Gly Gln Ser
180          185          190
Gly Phe Phe Gly Ser Ser Arg Pro Thr Ser Ser Pro Ala Val Ser Ser
195          200          205
Gly Thr Arg Gly Phe Asn Ser
210          215

```

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...1362
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

TTATAGGACT TTTTA ATG GAG TTA GAA ACT CAT TTG TCA AAA TAT TTC ACC	51
Met Glu Leu Glu Thr His Leu Ser Lys Tyr Phe Thr	
1 5 10	
CTA GCC TTT ACG CAT AAA AGC ATG AGC TTA GAA ATG CGA GAA AAA CTC	99
Leu Ala Phe Thr His Lys Ser Met Ser Leu Glu Met Arg Glu Lys Leu	
15 20 25	
GCT ATT AAT TCG AAT GCA ACG CTT AAA GAA TTT TTA CAA ACC ATT AAA	147
Ala Ile Asn Ser Asn Ala Thr Leu Lys Glu Phe Leu Gln Thr Ile Lys	
30 35 40	
AAC CAT TGC CCT AAC ATC AAA GAG TGC ATG GTG TTA TCC ACA TGC AAT	195
Asn His Cys Pro Asn Ile Lys Glu Cys Met Val Leu Ser Thr Cys Asn	
45 50 55 60	
CGC TTT GAA ATC TAT GCG AGC CTA AAA CAC GGC GCT AAT ACT AAT GAA	243
Arg Phe Glu Ile Tyr Ala Ser Leu Lys His Gly Ala Asn Thr Asn Glu	
65 70 75	
CAA AAA AAC GCA CTA TTA AAG ATT TTG GCT CAA AAT AAA AAA ATG AGC	291
Gln Lys Asn Ala Leu Leu Lys Ile Leu Ala Gln Asn Lys Lys Met Ser	
80 85 90	
GTG TCT GAT TTA GAA AAA TGC GTT TTA ATG AAC ACT GAT GAA AGC GCA	339
Val Ser Asp Leu Glu Lys Cys Val Leu Met Asn Thr Asp Glu Ser Ala	
95 100 105	
GTC CAT CAT GTC TTT AGC GTG TGC AGC AGT TTG GAT AGC TTG GTG GTT	387
Val His His Val Phe Ser Val Cys Ser Ser Leu Asp Ser Leu Val Val	
110 115 120	
GGG GAA ACT CAA ATC ACA GGG CAG ATG AAA AAC GCT TAT AAA TTC GCT	435
Gly Glu Thr Gln Ile Thr Gly Gln Met Lys Asn Ala Tyr Lys Phe Ala	
125 130 135 140	
TTT GAA GAG AAA TTT TGC TCT AAA GAT TTA ACC CGA TTG CTC CAT TTT	483
Phe Glu Glu Lys Phe Cys Ser Lys Asp Leu Thr Arg Leu Leu His Phe	
145 150 155	
GCT TTC AAA TGC GCC GCT AAA GTG CGC AAT TTA ACC GGC ATT TCC AAG	531
Ala Phe Lys Cys Ala Ala Lys Val Arg Asn Leu Thr Gly Ile Ser Lys	
160 165 170	
CAA GGG GTT TCC ATC TCT TCA GTG GCG GTC AAA GAA GCG CTT AAT ATT	579
Gln Gly Val Ser Ile Ser Ser Val Ala Val Lys Glu Ala Leu Asn Ile	
175 180 185	
TTT GAA AAA GAA AGG ATT AAG GAT AAA AAA GCC CTT GTG ATA GGG CTT	627
Phe Glu Lys Glu Arg Ile Lys Asp Lys Lys Ala Leu Val Ile Gly Leu	
190 195 200	
GGC GAG ATG GCT CAA TTA GTC ATC AAG CAC CTT TTA AAC AAG CAA TTT	675
Gly Glu Met Ala Gln Leu Val Ile Lys His Leu Leu Asn Lys Gln Phe	
205 210 215 220	

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

```

Met Glu Leu Glu Thr His Leu Ser Lys Tyr Phe Thr Leu Ala Phe Thr
 1           5           10           15
His Lys Ser Met Ser Leu Glu Met Arg Glu Lys Leu Ala Ile Asn Ser
 20           25           30
Asn Ala Thr Leu Lys Glu Phe Leu Gln Thr Ile Lys Asn His Cys Pro
 35           40           45
Asn Ile Lys Glu Cys Met Val Leu Ser Thr Cys Asn Arg Phe Glu Ile
 50           55           60
Tyr Ala Ser Leu Lys His Gly Ala Asn Thr Asn Glu Gln Lys Asn Ala
 65           70           75           80
Leu Leu Lys Ile Leu Ala Gln Asn Lys Lys Met Ser Val Ser Asp Leu
 85           90           95
Glu Lys Cys Val Leu Met Asn Thr Asp Glu Ser Ala Val His His Val
100           105           110
Phe Ser Val Cys Ser Ser Leu Asp Ser Leu Val Val Gly Glu Thr Gln
115           120           125
Ile Thr Gly Gln Met Lys Asn Ala Tyr Lys Phe Ala Phe Glu Glu Lys
130           135           140
Phe Cys Ser Lys Asp Leu Thr Arg Leu Leu His Phe Ala Phe Lys Cys
145           150           155           160
Ala Ala Lys Val Arg Asn Leu Thr Gly Ile Ser Lys Gln Gly Val Ser
165           170           175
Ile Ser Ser Val Ala Val Lys Glu Ala Leu Asn Ile Phe Glu Lys Glu
180           185           190
Arg Ile Lys Asp Lys Lys Ala Leu Val Ile Gly Leu Gly Glu Met Ala
195           200           205
Gln Leu Val Ile Lys His Leu Leu Asn Lys Gln Phe Glu Ala Leu Ile
210           215           220
Leu Gly Arg Asn Ala Ala Lys Phe Glu Asp Phe Ile Lys Glu Leu Glu
225           230           235           240
Glu Pro Lys Lys Val Ser Phe Gln Asn Ile Glu Asn Leu Asn Ala Tyr
245           250           255
Ile Asn Glu Tyr Glu Leu Leu Phe Cys Ala Thr Ser Ser Pro His Phe
260           265           270
Ile Val Gln Asn Arg Met Leu Lys Glu Thr Ile Phe Arg Arg Phe Trp
275           280           285
Phe Asp Leu Ala Val Pro Arg Asn Ile Glu Lys Pro Val Leu Asp Asn
290           295           300
Ile Phe Leu Tyr Ser Val Asp Asp Leu Glu Pro Met Val Arg Glu Asn
305           310           315           320
Val Glu Asn Arg Gln Glu Ser Arg Met Arg Ala Tyr Glu Ile Val Gly
325           330           335

```

Leu Ala Thr Met Glu Phe Tyr Gln Trp Ile Gln Ser Leu Glu Val Glu
 340 345 350
 Pro Val Ile Lys Asp Leu Arg Glu Leu Ala Arg Ile Ser Ala Gln Lys
 355 360 365
 Glu Leu Gln Lys Ala Leu Lys Lys Arg Tyr Val Pro Lys Glu Tyr Glu
 370 375 380
 Asn Asn Ile Glu Lys Ile Leu His Asn Ala Phe Asn Thr Phe Leu His
 385 390 395 400
 Asn Pro Thr Ile Ala Leu Lys Lys Asn Ala Gln Lys Glu Glu Ser Asp
 405 410 415
 Val Leu Val Gly Ala Ile Lys Asn Leu Phe Asn Leu Asp Lys Ser Asn
 420 425 430
 Ala Asn His Ala Gln Asn Leu Asn Leu Tyr Lys Cys Glu Tyr Tyr Glu
 435 440 445
 Glu

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...1125
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

AAAACCCAAA CGCCGTTAAA ATATTTAAAA AGGAAATTC ATG CCC ATT GAT TTG	54
Met Pro Ile Asp Leu	
1 5	
AAC GAA CAT TTA AAA AAG AAA AAT TCT CAA AGA GAA ACC CCC ACG CCT	102
Asn Glu His Leu Lys Lys Lys Asn Ser Gln Arg Glu Thr Pro Thr Pro	
10 15 20	
AAT ACG CCT AAT AAT GGG GGG CGT TTC ATC CCG CCG TCT AAT TCT TTT	150
Asn Thr Pro Asn Asn Gly Gly Arg Phe Ile Pro Pro Ser Asn Ser Phe	
25 30 35	
AAT TCT AAA AAA CTA TCG GTT TTA ATT GTC ATT GTC CTT TTA GGC GTT	198
Asn Ser Lys Lys Leu Ser Val Leu Ile Val Ile Val Leu Leu Gly Val	
40 45 50	
ATC GCT TTT TTG GCC AAG CCT TTT GAA GTG ATT AGC TCA GGA GAA ATT	246
Ile Ala Phe Leu Ala Lys Pro Phe Glu Val Ile Ser Ser Gly Glu Ile	
55 60 65	
GGC ATT AAA ATC ACC GCC GGG AAA TAC GAA CCC ACC CCC TTA CAG CCA	294
Gly Ile Lys Ile Thr Ala Gly Lys Tyr Glu Pro Thr Pro Leu Gln Pro	
70 75 80 85	

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

Met	Pro	Ile	Asp	Leu	Asn	Glu	His	Leu	Lys	Lys	Lys	Asn	Ser	Gln	Arg	1	5	10	15
Glu	Thr	Pro	Thr	Pro	Asn	Thr	Pro	Asn	Asn	Gly	Gly	Arg	Phe	Ile	Pro	20	25	30	
Pro	Ser	Asn	Ser	Phe	Asn	Ser	Lys	Lys	Leu	Ser	Val	Leu	Ile	Val	Ile	35	40	45	
Val	Leu	Leu	Gly	Val	Ile	Ala	Phe	Leu	Ala	Lys	Pro	Phe	Glu	Val	Ile	50	55	60	
Ser	Ser	Gly	Glu	Ile	Gly	Ile	Lys	Ile	Thr	Ala	Gly	Lys	Tyr	Glu	Pro	65	70	75	80
Thr	Pro	Leu	Gln	Pro	Gly	Ile	His	Phe	Phe	Val	Pro	Ile	Ile	Gln	Asp	85	90	95	
Ile	Leu	Ile	Val	Asp	Thr	Arg	Ile	Arg	Asn	Ile	Asn	Phe	Ser	Arg	Thr	100	105	110	
Glu	Asp	Met	Gly	Val	Ala	Gly	Lys	Asn	Gln	Gly	Ile	Phe	Arg	Asn	Asp	115	120	125	
Ala	Ile	Asn	Val	Met	Asp	Ser	Arg	Gly	Leu	Thr	Val	Ser	Ile	Glu	Leu	130	135	140	
Thr	Val	Gln	Tyr	Arg	Leu	Asn	Pro	Gln	Thr	Thr	Pro	Gln	Thr	Ile	Ala	145	150	155	160
Thr	Tyr	Gly	Leu	Ser	Trp	Glu	Gln	Lys	Ile	Ile	Asn	Pro	Val	Val	Arg	165	170	175	
Asp	Val	Val	Arg	Ser	Val	Val	Gly	Arg	Tyr	Pro	Ala	Glu	Asp	Leu	Pro	180	185	190	
Ile	Lys	Arg	Asn	Glu	Ile	Ala	Ala	Leu	Ile	Asn	Ser	Gly	Ile	Asn	Lys	195	200	205	
Glu	Val	Ser	Lys	Leu	Pro	Asn	Thr	Pro	Val	Glu	Leu	Ser	Ser	Ile	Gln	210	215	220	
Leu	Arg	Glu	Ile	Val	Leu	Pro	Ala	Lys	Ile	Lys	Glu	Gln	Ile	Glu	Lys	225	230	235	240
Val	Gln	Ile	Ala	Arg	Gln	Glu	Ser	Glu	Arg	Val	Lys	Tyr	Glu	Val	Glu	245	250	255	
Arg	Ser	Lys	Gln	Glu	Ala	Gln	Lys	Gln	Ala	Ala	Leu	Ala	Lys	Gly	Glu	260	265	270	
Ala	Asp	Ala	Asn	Arg	Ile	Lys	Ala	Gln	Gly	Val	Ala	Asp	Ala	Ile	Val	275	280	285	
Ile	Glu	Ala	Lys	Ala	Lys	Ser	Gln	Ala	Asn	Leu	Ser	Ile	Ser	Gln	Ser	290	295	300	
Leu	Ser	Asp	Lys	Leu	Leu	Arg	Leu	Arg	Gln	Ile	Glu	Val	Gln	Gly	Gln	305	310	315	320
Phe	Asn	Glu	Ala	Leu	Lys	Thr	Asn	Asn	Asn	Ala	Gln	Ile	Met	Leu	Thr	325	330	335	
Pro	Gly	Gly	Ala	Val	Pro	Asn	Ile	Trp	Ile	Asp	Thr	Lys	Ser	Lys	Val	340	345	350	
Lys	Ser	Ser	Ile	Ala	Glu	Thr	Lys	Glu	Pro							355	360		

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 23...559
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GACTAAAGAG CCTTAAAAAC GC ATG GCA TCT CTT GCC TTT ATC CAA GCT TTT	52
Met Ala Ser Leu Ala Phe Ile Gln Ala Phe	
1 5 10	
TTG GAG TCT TTT AAG GGA TTT TTA AGT CAA GCG ACT CTA ATC AGC GTT	100
Leu Glu Ser Phe Lys Gly Phe Leu Ser Gln Ala Thr Leu Ile Ser Val	
15 20 25	
TTA ATA GCG AGC GTT TTA ATC CTT TTT TGC GCG ATT TTG CTC CTT TTG	148
Leu Ile Ala Ser Val Leu Ile Leu Phe Cys Ala Ile Leu Leu Leu Leu	
30 35 40	
GCT CTG CTT TTG AGA AAC CGC TTA GCT AGC TAT ATA GCA ACA GCA GCT	196
Ala Leu Leu Leu Arg Asn Arg Leu Ala Ser Tyr Ile Ala Thr Ala Ala	
45 50 55	
TTT TTG GGT GCG TTT TTA AGC ATG CCT TTT GTT TTG AAC ATT TTA CTC	244
Phe Leu Gly Ala Phe Leu Ser Met Pro Phe Val Leu Asn Ile Leu Leu	
60 65 70	
ACT CAA GCG ATT TAC CCC ATA GAA ACA CGC ATC TTA CAC GCT AAC CCT	292
Thr Gln Ala Ile Tyr Pro Ile Glu Thr Arg Ile Leu His Ala Asn Pro	
75 80 85 90	
TTA AGT TAC AGC AAC GCC TTT TCT TTG CAA GTG GGA GTC AAA AAC CAT	340
Leu Ser Tyr Ser Asn Ala Phe Ser Leu Gln Val Gly Val Lys Asn His	
95 100 105	
TCC AAA TTT ACT CTA AAC AAA TGC GTT TTA CGC CTA GAA GTG CTT AAA	388
Ser Lys Phe Thr Leu Asn Lys Cys Val Leu Arg Leu Glu Val Leu Lys	
110 115 120	
AAC CCT CAC AAT TTT GTA GAA GAG CAT GCT TTT AAA TGG TTT GTC AAA	436
Asn Pro His Asn Phe Val Glu Glu His Ala Phe Lys Trp Phe Val Lys	
125 130 135	
AAA AGC TAT GAA AAA ATT TTT AAA GAA AAG ATT TTG CCC AAA GAA TCT	484
Lys Ser Tyr Glu Lys Ile Phe Lys Glu Lys Ile Leu Pro Lys Glu Ser	
140 145 150	

AAG GTC TTT TCA TTC TTT ATT GAC AAC TAC CCT TAT TCA AAA ACG GCC 532
 Lys Val Phe Ser Phe Phe Ile Asp Asn Tyr Pro Tyr Ser Lys Thr Ala
 155 160 165 170

CCT TAT CAA GTT TCT TTG TTT TGT TTA TAAAAAATA AAAGATAACG CCCAAGA 586
 Pro Tyr Gln Val Ser Leu Phe Cys Leu
 175

TAACATTTCAT TAAAAAGCGA TTAAAAACGC TTAAAGGCAT AGAT 630

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

Met Ala Ser Leu Ala Phe Ile Gln Ala Phe Leu Glu Ser Phe Lys Gly
 1 5 10 15
 Phe Leu Ser Gln Ala Thr Leu Ile Ser Val Leu Ile Ala Ser Val Leu
 20 25 30
 Ile Leu Phe Cys Ala Ile Leu Leu Leu Leu Ala Leu Leu Leu Arg Asn
 35 40 45
 Arg Leu Ala Ser Tyr Ile Ala Thr Ala Ala Phe Leu Gly Ala Phe Leu
 50 55 60
 Ser Met Pro Phe Val Leu Asn Ile Leu Leu Thr Gln Ala Ile Tyr Pro
 65 70 75 80
 Ile Glu Thr Arg Ile Leu His Ala Asn Pro Leu Ser Tyr Ser Asn Ala
 85 90 95
 Phe Ser Leu Gln Val Gly Val Lys Asn His Ser Lys Phe Thr Leu Asn
 100 105 110
 Lys Cys Val Leu Arg Leu Glu Val Leu Lys Asn Pro His Asn Phe Val
 115 120 125
 Glu Glu His Ala Phe Lys Trp Phe Val Lys Lys Ser Tyr Glu Lys Ile
 130 135 140
 Phe Lys Glu Lys Ile Leu Pro Lys Glu Ser Lys Val Phe Ser Phe Phe
 145 150 155 160
 Ile Asp Asn Tyr Pro Tyr Ser Lys Thr Ala Pro Tyr Gln Val Ser Leu
 165 170 175
 Phe Cys Leu

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 47...1273
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

AAAGAATGAT CTTAAAAGGG CAAACCACAT TTATTAAGGA GAATGC ATG CAA GAA	55
Met Gln Glu	
1	
ATC ATA GGA GCG TCT TTA GTT TTT TTG TGC AAT GAA AAG TGC GAA GTG	103
Ile Ile Gly Ala Ser Leu Val Phe Leu Cys Asn Glu Lys Cys Glu Val	
5 10 15	
TTA GAA GAT TAT GGC GTA GTC TTT GAT GAA AAG ATT GTT GAA ATA GGC	151
Leu Glu Asp Tyr Gly Val Val Phe Asp Glu Lys Ile Val Glu Ile Gly	
20 25 30 35	
GAT TAT CAA AGT TTA ACG CTT AAA TAC CCT CAC TTA AAG GCG CAG TTT	199
Asp Tyr Gln Ser Leu Thr Leu Lys Tyr Pro His Leu Lys Ala Gln Phe	
40 45 50	
TTT GAA AAT TCC GTT CTG TTG CCC GCT TTT ATC AAC GCG CAC ACC CAT	247
Phe Glu Asn Ser Val Leu Leu Pro Ala Phe Ile Asn Ala His Thr His	
55 60 65	
TTT GAA TTT TCC AAC AAC AAG GCG AGT TTT GAT TAC GGG AGT TTT TCT	295
Phe Glu Phe Ser Asn Asn Lys Ala Ser Phe Asp Tyr Gly Ser Phe Ser	
70 75 80	
GGC TGG TTA GGG AGC GTG TTA AAC AAT GGG GGG GCG ATT TTA GAA AAT	343
Gly Trp Leu Gly Ser Val Leu Asn Asn Gly Gly Ala Ile Leu Glu Asn	
85 90 95	
TGC CAA GGG GCT ATT CAA AAC GCT ATC AGC ACG CAA TTA AAA AGC GGG	391
Cys Gln Gly Ala Ile Gln Asn Ala Ile Ser Thr Gln Leu Lys Ser Gly	
100 105 110 115	
GTG GGG AGC GTG GGA GCG ATT TCT AAC CAC CTG ATA GAA GTT AAT TTG	439
Val Gly Ser Val Gly Ala Ile Ser Asn His Leu Ile Glu Val Asn Leu	
120 125 130	
TTA AAA GAA AGC CCT TTG AAT GCT GTC GTG TTT TTA GAG TTT TTA GGG	487
Leu Lys Glu Ser Pro Leu Asn Ala Val Val Phe Leu Glu Phe Leu Gly	
135 140 145	
AGC AGT TAT TCT TTA GAA AAA TTA AAA GCG TTT GAG GCC AAA TTT AAG	535
Ser Ser Tyr Ser Leu Glu Lys Leu Lys Ala Phe Glu Ala Lys Phe Lys	
150 155 160	
GAA TTA AAA GAT TTA GAA GAT AAA AAA CTT AAA GCG GCT CTC GCT GTG	583
Glu Leu Lys Asp Leu Glu Asp Lys Lys Leu Lys Ala Ala Leu Ala Val	
165 170 175	
CAT GCC CCT TAT TCG GTC CAA AAA GAC ATG GCT TTG AGC GTC ATC CAA	631
His Ala Pro Tyr Ser Val Gln Lys Asp Met Ala Leu Ser Val Ile Gln	
180 185 190 195	

TTA GCC AAA GAT TCA CAA AGC CTG CTT TCT ACG CAT TTT TTA GAA TCG Leu Ala Lys Asp Ser Gln Ser Leu Leu Ser Thr His Phe Leu Glu Ser 200 205 210	679
CTT GAA GAA TTA GAA TGG GTA GAA AAC TCT AAA GGG TGG TTT GAA AAT Leu Glu Glu Leu Glu Trp Val Glu Asn Ser Lys Gly Trp Phe Glu Asn 215 220 225	727
TTT TAC CAG CAT TTT TTA AAG GAG TCT CAT TTC AAA TCG CTC TAT AAG Phe Tyr Gln His Phe Leu Lys Glu Ser His Phe Lys Ser Leu Tyr Lys 230 235 240	775
GGC GCG AAC GAT TAC ATT GAC ATG TTT AAA GAC ACG CAC ACT TTA TTC Gly Ala Asn Asp Tyr Ile Asp Met Phe Lys Asp Thr His Thr Leu Phe 245 250 255	823
GTG CAT AAC CAG TTC GCT TCT TTA GAA GCG TTA AAA AGG ATT AAA TCT Val His Asn Gln Phe Ala Ser Leu Glu Ala Leu Lys Arg Ile Lys Ser 260 265 270 275	871
CAA GTC AAA AAC GCT TTT TTA ATC ACA TGC CCC TTT TCT AAC CGC CTA Gln Val Lys Asn Ala Phe Leu Ile Thr Cys Pro Phe Ser Asn Arg Leu 280 285 290	919
TTG AGC GGG CAA GCG TTG GAT TTA GAA AGA ACT AAA GAA GCC GGT TTG Leu Ser Gly Gln Ala Leu Asp Leu Glu Arg Thr Lys Glu Ala Gly Leu 295 300 305	967
AGC GTG AGC GTG GCC ACT GAT GGC TTG AGT TCT AAC ATT TCG CTG AGC Ser Val Ser Val Ala Thr Asp Gly Leu Ser Ser Asn Ile Ser Leu Ser 310 315 320	1015
CTT TTA GAC GAA TTA AGA GCG TTT TTG CTC ACC CAT AAC ATG CCG TTA Leu Leu Asp Glu Leu Arg Ala Phe Leu Leu Thr His Asn Met Pro Leu 325 330 335	1063
TTA GAA TTA GCT AAA ATA GCC CTT TTA GGG GCG ACT AGG CAT GGG GCT Leu Glu Leu Ala Lys Ile Ala Leu Leu Gly Ala Thr Arg His Gly Ala 340 345 350 355	1111
AAA GCT TTA GCT TTG AAT AAT GGC GAG ATA GAA GCC AAC AAA AGG GCG Lys Ala Leu Ala Leu Asn Asn Gly Glu Ile Glu Ala Asn Lys Arg Ala 360 365 370	1159
GAT TTG AGC GTG TTT GGT TTT AAT GAA AAA TTC ACT AAA GAG CAA GCG Asp Leu Ser Val Phe Gly Phe Asn Glu Lys Phe Thr Lys Glu Gln Ala 375 380 385	1207
ATT TTG CAA TTT TTA TTG CAT GCT AAA GAA GTG GAG TGC TTG TTT TTA Ile Leu Gln Phe Leu Leu His Ala Lys Glu Val Glu Cys Leu Phe Leu 390 395 400	1255
GGG GGG AAA AGG GTG ATC TAATTTGTTT TAAAGACAGA ATGCGTTAAA ATGAGAAA Gly Gly Lys Arg Val Ile 405	1311
TCTAAATCAA TTAAGGAAAG AGTCAATGAA ACTAGTTTT	1350

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

Met	Gln	Glu	Ile	Ile	Gly	Ala	Ser	Leu	Val	Phe	Leu	Cys	Asn	Glu	Lys
1				5					10					15	
Cys	Glu	Val	Leu	Glu	Asp	Tyr	Gly	Val	Val	Phe	Asp	Glu	Lys	Ile	Val
			20					25					30		
Glu	Ile	Gly	Asp	Tyr	Gln	Ser	Leu	Thr	Leu	Lys	Tyr	Pro	His	Leu	Lys
		35					40					45			
Ala	Gln	Phe	Phe	Glu	Asn	Ser	Val	Leu	Leu	Pro	Ala	Phe	Ile	Asn	Ala
							55				60				
His	Thr	His	Phe	Glu	Phe	Ser	Asn	Asn	Lys	Ala	Ser	Phe	Asp	Tyr	Gly
65					70				75						80
Ser	Phe	Ser	Gly	Trp	Leu	Gly	Ser	Val	Leu	Asn	Asn	Gly	Gly	Ala	Ile
				85				90						95	
Leu	Glu	Asn	Cys	Gln	Gly	Ala	Ile	Gln	Asn	Ala	Ile	Ser	Thr	Gln	Leu
			100					105					110		
Lys	Ser	Gly	Val	Gly	Ser	Val	Gly	Ala	Ile	Ser	Asn	His	Leu	Ile	Glu
		115					120					125			
Val	Asn	Leu	Leu	Lys	Glu	Ser	Pro	Leu	Asn	Ala	Val	Val	Phe	Leu	Glu
		130					135					140			
Phe	Leu	Gly	Ser	Ser	Tyr	Ser	Leu	Glu	Lys	Leu	Lys	Ala	Phe	Glu	Ala
145					150					155					160
Lys	Phe	Lys	Glu	Leu	Lys	Asp	Leu	Glu	Asp	Lys	Lys	Leu	Lys	Ala	Ala
				165					170					175	
Leu	Ala	Val	His	Ala	Pro	Tyr	Ser	Val	Gln	Lys	Asp	Met	Ala	Leu	Ser
			180					185					190		
Val	Ile	Gln	Leu	Ala	Lys	Asp	Ser	Gln	Ser	Leu	Leu	Ser	Thr	His	Phe
		195					200						205		
Leu	Glu	Ser	Leu	Glu	Glu	Leu	Glu	Trp	Val	Glu	Asn	Ser	Lys	Gly	Trp
		210					215					220			
Phe	Glu	Asn	Phe	Tyr	Gln	His	Phe	Leu	Lys	Glu	Ser	His	Phe	Lys	Ser
225					230					235					240
Leu	Tyr	Lys	Gly	Ala	Asn	Asp	Tyr	Ile	Asp	Met	Phe	Lys	Asp	Thr	His
				245					250					255	
Thr	Leu	Phe	Val	His	Asn	Gln	Phe	Ala	Ser	Leu	Glu	Ala	Leu	Lys	Arg
			260					265					270		
Ile	Lys	Ser	Gln	Val	Lys	Asn	Ala	Phe	Leu	Ile	Thr	Cys	Pro	Phe	Ser
		275					280					285			
Asn	Arg	Leu	Leu	Ser	Gly	Gln	Ala	Leu	Asp	Leu	Glu	Arg	Thr	Lys	Glu
		290					295					300			
Ala	Gly	Leu	Ser	Val	Ser	Val	Ala	Thr	Asp	Gly	Leu	Ser	Ser	Asn	Ile
					310					315					320
Ser	Leu	Ser	Leu	Leu	Asp	Glu	Leu	Arg	Ala	Phe	Leu	Leu	Thr	His	Asn
				325					330					335	
Met	Pro	Leu	Leu	Glu	Leu	Ala	Lys	Ile	Ala	Leu	Leu	Gly	Ala	Thr	Arg
				340				345					350		
His	Gly	Ala	Lys	Ala	Leu	Ala	Leu	Asn	Asn	Gly	Glu	Ile	Glu	Ala	Asn
		355					360					365			

Ala	Phe	Glu	Phe	Phe 125	Glu	Lys	Lys	Ala	Gln 130	Ile	Arg	Ser	Leu	Leu 135	Asn	
ATC Ile	TCT Ser	ATA Ile	GGG Gly 140	TGC Cys	GAT Asp	AAG Lys	AAA Lys	TGC Cys 145	GCT Ala	TAT Tyr	TGC Cys	ATC Ile	GTC Val 150	CCG Pro	CAC His	486
ACT Thr	AGG Arg	GGG Gly 155	AAA Lys	GAA Glu	ATT Ile	TCT Ser	ATC Ile 160	CCT Pro	ATG Met	GAT Asp	TTG Leu 165	ATT Ile	TTA Leu	AAA Lys	GAA Glu	534
GCT Ala	GAG Glu 170	AAA Lys	TTA Leu	GCG Ala	AAT Asn	AAC Asn 175	GGC Gly	ACC Thr	AAA Lys	GAG Glu 180	CTT Leu 180	ATG Met	CTT Leu	TTA Leu	GGG Gly	582
CAG Gln 185	AAT Asn	GTG Val	AAT Asn	AAT Asn	TAC Tyr 190	GGC Gly	GCG Ala	CGT Arg	TTC Phe 195	AGC Ser	AGC Ser	GAG Glu	CAT His	GCG Ala	AAA Lys 200	630
GTG Val	GAT Asp	TTT Phe	AGC Ser 205	GAT Asp	TTG Leu	TTG Leu	GAT Asp	AAA Lys 210	TTG Leu	AGC Ser	GAA Glu	ATC Ile	CAG Gln 215	GGG Gly	ATT Ile	678
GAA Glu	AGG Arg	ATA Ile 220	CGA Arg	TTC Phe	ACT Thr	TCG Ser	CCT Pro	CAC His 225	CCC Pro	TTG Leu	CAC His	ATG Met 230	AAT Asn 230	GAT Asp	GGA Gly	726
TTT Phe	TTA Leu 235	GAG Glu	CGT Arg	TTT Phe	GCC Ala	AAA Lys 240	AAC Asn	CCT Pro	AAA Lys	GTG Val	TGC Cys 245	AAG Lys 245	AGT Ser	ATC Ile	CAC His	774
ATG Met	CCT Pro 250	TTA Leu	CAG Gln	AGC Ser	GGA Gly 255	TCT Ser 255	AGC Ser	GCG Ala	GTG Val	TTA Leu 260	AAG Lys 260	ATG Met	ATG Met	CGA Arg	AGG Arg	822
GGT Gly 265	TAT Tyr	AGT Ser	AAG Lys	GAG Glu	TGG Trp 270	TTT Phe	TTA Leu	AAT Asn	AGG Arg 275	GTG Val 275	GAG Glu	AGG Arg	TTA Leu	AAA Lys	GCT Ala 280	870
TTA Leu	GTG Val	CCT Pro	GAA Glu 285	GTG Val 285	GGC Gly	ATT Ile	AGC Ser	ACG Thr 290	GAT Asp 290	ATT Ile	ATC Ile	GTA Val	GGC Gly 295	TTC Phe 295	CCT Pro	918
AAT Asn	GAG Glu	AGC Ser 300	GAT Asp	AAG Lys	GAT Asp	TTT Phe	GAA Glu	GAC Asp 305	ACA Thr	ATG Met	GAG Glu	GTG Val 310	CTA Leu 310	GAA Glu	AAA Lys	966
GTG Val	CGC Arg 315	TTT Phe	GAC Asp	ACG Thr	CTC Leu	TAT Tyr 320	AGT Ser	TTC Phe	ATT Ile	TAT Tyr	TCC Ser 325	CCA Pro 325	CGC Arg	CCT Pro	TTC Phe	1014
ACT Thr	GAA Glu 330	GCG Ala	GGA Gly	GCT Ala	TGG Trp 335	AAG Lys 335	GAA Glu	AGA Arg	GTG Val 340	CCG Pro 340	TTA Leu 340	GAA Glu	GTT Val	TCA Ser	TCT Ser	1062
TCA Ser 345	AGG Arg	TTG Leu	GAG Glu	AGG Arg 350	TTG Leu 350	CAA Gln	AAC Asn	AGG Arg	CAC His 355	AAA Lys 355	GAA Glu	ATT Ile	TTA Leu	GAA Glu	GAA Glu 360	1110

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

```

Met Ala Lys Ile Thr Thr Val Ile Asp Ile Gly Ser Asn Ser Val Arg
 1           5           10           15
Leu Ala Val Phe Lys Lys Thr Ser Gln Phe Gly Phe Tyr Leu Leu Phe
 20           25           30
Glu Thr Lys Ser Lys Val Arg Ile Ser Glu Gly Cys Tyr Ala Phe Asn
 35           40           45
Gly Ile Leu Gln Glu Ile Pro Met Gln Arg Ala Val Lys Ala Leu Ser
 50           55           60
Glu Phe Lys Glu Ile Ala Leu Lys Tyr Lys Ser Lys Lys Ile Leu Cys
 65           70           75           80
Val Ala Thr Ser Ala Val Arg Asp Ala Pro Asn Arg Leu Glu Phe Val
 85           90           95
Ala Arg Val Lys Lys Ala Cys Gly Leu Gln Ile Lys Ile Ile Asp Gly
100           105           110
Gln Lys Glu Ala Leu Tyr Gly Gly Ile Ala Cys Ala Asn Leu Leu His
115           120           125
Lys Asn Ser Gly Ile Thr Ile Asp Ile Gly Gly Gly Ser Thr Glu Cys
130           135           140
Ala Leu Ile Glu Lys Gly Lys Ile Lys Asp Leu Ile Ser Leu Asp Val
145           150           155           160
Gly Thr Ile Arg Ile Lys Glu Met Phe Leu Asp Lys Asp Leu Glu Val
165           170           175
Lys Leu Ala Lys Ala Phe Ile Gln Lys Glu Val Ser Lys Leu Pro Phe
180           185           190
Lys His Lys Asn Ala Phe Gly Val Gly Gly Thr Ile Arg Ala Leu Ser
195           200           205
Lys Val Leu Met Lys Arg Phe Cys Tyr Pro Ile Asp Ser Leu His Gly
210           215           220
Tyr Glu Ile Asp Ala His Lys Asn Leu Ala Phe Ile Glu Lys Ile Val
225           230           235           240
Met Leu Lys Glu Asp Gln Leu Arg Leu Leu Gly Val Asn Glu Glu Arg
245           250           255
Leu Asp Ser Ile Arg Ser Gly Ala Leu Ile Leu Ser Val Val Leu Glu
260           265           270
His Leu Lys Thr Ser Leu Met Ile Thr Ser Gly Val Gly Val Arg Glu
275           280           285
Gly Val Phe Leu Ser Asp Leu Leu Arg His His Tyr His Lys Phe Pro
290           295           300
Pro Asn Ile Asn Pro Ser Leu Ile Ser Leu Lys Asp Arg Phe Leu Pro
305           310           315           320
His Glu Lys His Ser Gln Lys Val Lys Lys Glu Cys Val Lys Leu Phe
325           330           335
Glu Ala Leu Ser Pro Leu His Lys Ile Asp Glu Lys Tyr Leu Phe His
340           345           350

```

Leu Lys Ile Ala Gly Glu Leu Ala Ser Met Gly Lys Ile Leu Ser Val
 355 360 365
 Tyr Leu Ala His Lys His Ser Ala Tyr Phe Ile Leu Asn Ala Leu Ser
 370 375 380
 Tyr Gly Phe Ser His Gln Asp Arg Ala Ile Ile Cys Leu Leu Ala Gln
 385 390 395 400
 Phe Ser His Lys Lys Ile Pro Lys Asp Asn Ala Ile Ala His Met Ser
 405 410 415
 Ala Met Met Pro Ser Leu Leu Thr Leu Gln Trp Leu Ser Phe Ile Leu
 420 425 430
 Ser Leu Ala Glu Asn Leu Cys Leu Thr Asp Ser His His Leu Lys Tyr
 435 440 445
 Thr Leu Glu Lys Asn Lys Leu Val Ile His Ser Asn Asp Thr Leu Tyr
 450 455 460
 Leu Ala Lys Glu Met Leu Pro Lys Leu Val Lys Pro Ile Pro Leu Thr
 465 470 475 480
 Ile Glu Phe Ala

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...1073
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GCCAACTACC ATAAAAAGGA TTTTCTATC CAAAATATAG AGCCTAAAAA AATTAAAGA A 60
 Me

 TGC GTT TTA AAC ATC TTA AAG GAA AAA GAA TGA CTT ACA AAG AAC GAC 108
 t Arg Phe Lys His Leu Lys Gly Lys Arg Met Thr Tyr Lys Glu Arg Le
 1 5 10 15

 TCA TAC ACG AAA AAA TAT TGA AAC AAG ACG ACA AGG GTT TTA AAA CAG 156
 u Ile His Glu Lys Ile Leu Lys Gln Asp Asp Lys Gly Phe Lys Thr Gl
 20 25 30

 AAC TGC GCA TTT TGA GTA TTT TTA TCG TGG AAT CTT TAG TGA ATA TTT 204
 u Leu Arg Ile Leu Ser Ile Phe Ile Val Glu Ser Leu Val Asn Ile Le
 35 40 45

 TGG GGT TTA TTT TAG CTA AAA TGC CCC ATT CGT GGT TTT TAA GGT GCA 252
 u Gly Phe Ile Leu Ala Lys Met Pro His Ser Trp Phe Leu Arg Cys Il
 50 55 60 6

 TTA AAG CGG TGG CGT GGC TCA TGA AAA CTT TTG ATA AGT GCC GTT ATT 300

CCC AAG CGA GTT TGT GCG AAG AGG TGA TTA GAA ACC ACC CGG AAA GTT 1020
a Gln Ala Ser Leu Cys Glu Glu Val Ile Arg Asn His Pro Glu Ser Ty
05 310 315 320

ATT TTT GGT TCC ATA GGC GTT TTA AAA GCA CCC ACC CTG AGA TTT ATC 1068
r Phe Trp Phe His Arg Arg Phe Lys Ser Thr His Pro Glu Ile Tyr Gl
325 330 335

AAA GA TAGGGTTTTG TTTTAATCAA AAATTAAAAA CTAAAGCCTT ATTTTAAAGA AAA 1126
n Arg

CTTT 1130

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

Met	Arg	Phe	Lys	His	Leu	Lys	Gly	Lys	Arg	Met	Thr	Tyr	Lys	Glu	Arg
1				5					10					15	
Leu	Ile	His	Glu	Lys	Ile	Leu	Lys	Gln	Asp	Asp	Lys	Gly	Phe	Lys	Thr
			20					25					30		
Glu	Leu	Arg	Ile	Leu	Ser	Ile	Phe	Ile	Val	Glu	Ser	Leu	Val	Asn	Ile
			35					40				45			
Leu	Gly	Phe	Ile	Leu	Ala	Lys	Met	Pro	His	Ser	Trp	Phe	Leu	Arg	Cys
			50				55				60				
Ile	Lys	Ala	Val	Ala	Trp	Leu	Met	Lys	Thr	Phe	Asp	Lys	Cys	Arg	Tyr
					70					75				80	
Phe	Asp	Ala	Lys	Ala	Asn	Leu	Asp	Phe	Val	Phe	Gly	Asp	Ser	Lys	Ser
				85					90					95	
Glu	Glu	Glu	Lys	Lys	Arg	Ile	Ile	Lys	Lys	Gly	Tyr	Glu	Asn	Phe	Ala
				100					105					110	
Phe	Ile	Ile	Leu	Glu	Thr	Ile	Arg	Val	Ile	Phe	Ile	Pro	Lys	Asp	Glu
			115					120					125		
Tyr	Asp	Ala	Arg	Phe	Thr	Leu	Ile	Asn	Glu	Glu	Asn	Val	Trp	Lys	Ser
						135						140			
Leu	Asn	Lys	Glu	Gly	Gln	Ala	Ile	Thr	Leu	Cys	Met	His	Phe	Gly	Tyr
					150					155				160	
Trp	Glu	Ala	Val	Gly	Thr	Thr	Leu	Ala	Gln	Tyr	Tyr	Glu	Asn	Tyr	Gly
				165						170				175	
Arg	Gly	Cys	Leu	Gly	Arg	Leu	Thr	Lys	Phe	Ala	Pro	Ile	Asn	His	Met
			180					185					190		
Ile	Met	Ser	Arg	Arg	Glu	Ala	Phe	Gly	Val	Arg	Phe	Val	Asn	Lys	Ile
			195					200					205		
Gly	Ala	Met	Lys	Glu	Leu	Ile	Lys	Met	Tyr	Asn	Gln	Gly	Asn	Gly	Leu
			210				215					220			
Val	Gly	Ile	Leu	Val	Asp	Gln	Asn	Val	Val	Pro	Lys	Asp	Gly	Val	Val
					230					235				240	
Val	Lys	Phe	Phe	Asp	Arg	Asp	Ala	Thr	His	Thr	Thr	Ile	Ala	Ser	Ile
				245					250					255	

Leu Ser Arg Arg Tyr Asn Ile Asp Ile Gln Pro Val Phe Ile Asp Phe
 260 265 270
 Asn Asp Asp Tyr Ser His Tyr Thr Ala Thr Tyr Tyr Pro Ser Ile Arg
 275 280 285
 Ser Gln Ile Thr Asp Asn Ala Gln Asn Asp Ile Leu Glu Cys Thr Gln
 290 295 300
 Ala Gln Ala Ser Leu Cys Glu Glu Val Ile Arg Asn His Pro Glu Ser
 305 310 315 320
 Tyr Phe Trp Phe His Arg Arg Phe Lys Ser Thr His Pro Glu Ile Tyr
 325 330 335
 Gln Arg

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...8694
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

AGAGGGTAGC ATTTA ATG AAA AAG TTT AAA AAG AAA CCA AAA AGT ATC AAA	51
Met Lys Lys Phe Lys Lys Lys Pro Lys Ser Ile Lys	
1 5 10	
CGA TCG CAT CAA AAT CAA AAA ACA ATC TTA AAG CGT CCT TTA TGG CTT	99
Arg Ser His Gln Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu	
15 20 25	
ATG CCT TTA CTC ATC AGC GGG TTT GCT AGT GGG GTG TAT GCG AAT AAT	147
Met Pro Leu Leu Ile Ser Gly Phe Ala Ser Gly Val Tyr Ala Asn Asn	
30 35 40	
CTG TGG GAT TTG TTA AAC CCA AAA GTG GGG GGT GAG TAT GTG CAT TGG	195
Leu Trp Asp Leu Leu Asn Pro Lys Val Gly Gly Glu Tyr Val His Trp	
45 50 55 60	
GTT AAG GGC AGT CAG TAT TGT GCA TGG TGG GAA TTT GCT GGG TGT TTA	243
Val Lys Gly Ser Gln Tyr Cys Ala Trp Trp Glu Phe Ala Gly Cys Leu	
65 70 75	
AAG AAT GTA TGG GGG GCA AAT CAT AAA GGC TAT GAT GCT GGA AAC GCC	291
Lys Asn Val Trp Gly Ala Asn His Lys Gly Tyr Asp Ala Gly Asn Ala	
80 85 90	
GCT AAC TAT TTG TCT TCT CAA AAC TAT CAA GCT ATT TCG GTG GGT AGT	339
Ala Asn Tyr Leu Ser Ser Gln Asn Tyr Gln Ala Ile Ser Val Gly Ser	
95 100 105	

GGG Gly 110	AAT Asn 110	GAA Glu 110	ACG Thr 110	GGG Gly 115	ACT Thr 115	TAT Tyr 115	AGT Ser 115	TTA Leu 115	AGC Ser 120	GGT Gly 120	TTT Phe 120	ACC Thr 120	AAT Asn 120	TAT Tyr 120	GTT Val 120	387
GGG Gly 125	GGC Gly 125	AAT Asn 125	CTC Leu 125	ACG Thr 130	ATC Ile 130	AAT Asn 130	CTA Leu 130	GGC Gly 135	AAT Asn 135	AGC Ser 135	GTT Val 135	GTT Val 135	TTA Leu 140	GAT Asp 140	TTA Leu 140	435
AGC Ser 145	GGT Gly 145	TCT Ser 145	AAT Asn 145	AGT Ser 145	TTC Phe 145	ACT Thr 145	TCG Ser 145	TAT Tyr 150	CAA Gln 150	GGT Gly 150	TAT Tyr 150	AAT Asn 155	CAA Gln 155	GGC Gly 155	AAA Lys 155	483
GAT Asp 160	GAT Asp 160	GTA Val 160	ACA Thr 160	TTT Phe 160	ACG Thr 165	GTT Val 165	GGC Gly 165	GCA Ala 165	ATC Ile 165	AAT Asn 170	TTA Leu 170	AAC Asn 170	GGC Gly 170	ACT Thr 170	TTA Leu 170	531
GAA Glu 175	GTG Val 175	GGT Gly 175	AAT Asn 175	CGT Arg 175	GTG Val 180	GGA Gly 180	TCG Ser 180	GGA Gly 180	GCT Ala 185	GGC Gly 185	ACG Thr 185	CAC His 185	ACC Thr 185	GGC Gly 185	ACA Thr 185	579
GCC Ala 190	ACT Thr 190	TTA Leu 190	AAC Asn 190	TTG Leu 195	AAC Asn 195	GCT Ala 195	AAT Asn 195	AAG Lys 195	GTC Val 200	AAT Asn 200	ATC Ile 200	AAT Asn 200	TCC Ser 200	AAT Asn 200	ATC Ile 200	627
AAC Asn 205	GCG Ala 205	TAT Tyr 205	AAA Lys 205	ACT Thr 210	TCG Ser 210	CAA Gln 210	GTG Val 210	AAT Asn 215	ATA Ile 215	GGC Gly 215	AAC Asn 215	GCT Ala 215	AAC Asn 215	AGC Ser 215	GTT Val 215	675
ATT Ile 225	ACC Thr 225	ATT Ile 225	GGT Gly 225	TCG Ser 225	GTT Val 230	TCT Ser 230	TTG Leu 230	AGT Ser 230	GGG Gly 230	GAT Asp 230	GTT Val 235	TGC Cys 235	AGT Ser 235	TCT Ser 235	TTA Leu 235	723
GCT Ala 240	AGC Ser 240	GTT Val 240	GGG Gly 240	ATA Ile 245	GGG Gly 245	GCT Ala 245	AAT Asn 245	TGC Cys 245	TCC Ser 245	ACT Thr 250	TCT Ser 250	GGG Gly 250	CCT Pro 250	AGC Ser 250	TAT Tyr 250	771
TCT Ser 255	TTT Phe 255	AAA Lys 255	GGG Gly 255	ACG Thr 260	ACT Thr 260	AAC Asn 260	GCT Ala 260	ACT Thr 265	AAC Asn 265	ACG Thr 265	GCG Ala 265	TTT Phe 265	AGT Ser 265	AAT Asn 265	GCA Ala 265	819
AGC Ser 270	GGC Gly 270	AGT Ser 270	TTC Phe 270	ACT Thr 275	TTT Phe 275	GAA Glu 275	GAG Glu 275	AAC Asn 280	GCC Ala 280	ACT Thr 280	TTT Phe 280	AGC Ser 280	GGG Gly 280	GCG Ala 280	AAA Lys 280	867
TGG Trp 285	AAT Asn 285	GGG Gly 285	GGG Gly 285	ACT Thr 290	TAT Tyr 290	ACC Thr 290	TTT Phe 290	AAT Asn 295	AAA Lys 295	GAG Glu 295	TTT Phe 295	AGC Ser 295	GCT Ala 295	ACC Thr 295	AAT Asn 295	915
AAC Asn 305	ACC Thr 305	GCC Ala 305	TTT Phe 305	AGT Ser 310	AGC Ser 310	GGT Gly 310	AGT Ser 310	TTT Phe 310	AAT Asn 310	TTT Phe 315	AAA Lys 315	GGT Gly 315	GTA Val 315	AGC Ser 315	TCT Ser 315	963
TTT Phe 320	AAT Asn 320	GGT Gly 320	ACT Thr 320	TCG Ser 320	TTT Phe 325	AGT Ser 325	AAC Asn 325	GCT Ala 325	TCT Ser 325	TAT Tyr 325	ACT Thr 325	TTT Phe 330	GAC Asp 330	AAT Asn 330	CAA Gln 330	1011
GCC Ala 1059	ACT Thr 1059	TTC Phe 1059	CAA Gln 1059	AAC Asn 1059	AGC Ser 1059	TCC Ser 1059	TTT Phe 1059	AAT Asn 1059	GGG Gly 1059	GGG Gly 1059	ACT Thr 1059	TTT Phe 1059	ACT Thr 1059	TTT Phe 1059	AAT Asn 1059	1059

	335					340					345					
AAC Asn	CAA Gln	ACT Thr	AAT Asn	CCA Pro	ACT Thr	AAC Asn	AAC Asn	GCT Ala	CAG Gln	CAC His	CCC Pro	CAA Gln	ATT Ile	CAA Gln	AAC Asn	1107
	350					355					360					
AGC Ser	TCT Ser	TTT Phe	AGT Ser	GGT Gly	AAC Asn	GCT Ala	ACC Thr	ACT Thr	CTT Leu	AAG Lys	GGC Gly	TTT Phe	GTG Val	AAT Asn	TTC Phe	1155
365					370					375					380	
CAG Gln	CAA Gln	GCC Ala	TTT Phe	AAC Asn	AAT Asn	TCA Ser	AAC Asn	CAC His	CAA Gln	CTA Leu	ACG Thr	ATC Ile	CAA Gln	AAC Asn	GCT Ala	1203
				385					390					395		
TCC Ser	TTT Phe	AAT Asn	AAC Asn	GCC Ala	ACT Thr	TTT Phe	AAC Asn	AAT Asn	ACC Thr	GGT Gly	AAA Lys	ATC Ile	ACT Thr	ATA Ile	GAA Glu	1251
			400					405					410			
AAA Lys	GAT Asp	GCG Ala	AGT Ser	TTT Phe	AAT Asn	AAC Asn	ACG Thr	ACA Thr	TTC Phe	AAC Asn	ACT Thr	TCT Ser	GTT Val	GAT Asp	ACA Thr	1299
	415						420					425				
AAC Asn	AAC Asn	ATG Met	AGT Ser	GTT Val	ACC Thr	GGT Gly	GGC Gly	GTT Val	ACT Thr	TTA Leu	AGC Ser	GGT Gly	AAA Lys	AAT Asn	GAC Asp	1347
	430					435					440					
TTG Leu	AAA Lys	AAT Asn	GGC Gly	TCA Ser	ACC Thr	CTT Leu	GAT Asp	TTT Phe	GGG Gly	AGT Ser	TCT Ser	AAA Lys	ATC Ile	ACT Thr	CTC Leu	1395
445				450						455					460	
GCT Ala	CAA Gln	GGG Gly	ACG Thr	ACT Thr	TTC Phe	AAC Asn	CTC Leu	ACA Thr	AGT Ser	TTA Leu	GGC Gly	AGT Ser	GAG Glu	AAG Lys	AGC Ser	1443
			465						470					475		
GTA Val	ACG Thr	ATT Ile	TTA Leu	AAT Asn	TCT Ser	AGC Ser	GGT Gly	GGG Gly	ATC Ile	ACT Thr	TAT Tyr	AGT Ser	AAC Asn	CTT Leu	TTA Leu	1491
			480					485					490			
AAC Asn	CAT His	GCA Ala	ATC Ile	AAC Asn	GGC Gly	TTG Leu	ACA Thr	AGT Ser	GCC Ala	TTA Leu	AAA Lys	ACG Thr	AAC Asn	GAA Glu	AGC Ser	1539
	495					500						505				
CTT Leu	TCA Ser	AAT Asn	CCG Pro	CAA Gln	AGT Ser	TTC Phe	GCT Ala	CAA Gln	GGT Gly	TTG Leu	TGG Trp	GAT Asp	ATA Ile	ATC Ile	ACT Thr	1587
	510					515					520					
TAC Tyr	AAT Asn	GGG Gly	GTT Val	ACC Thr	GGG Gly	CAG Gln	CTT Leu	TTG Leu	AAT Asn	GAA Glu	AAC Asn	GCT Ala	GCA Ala	ACA Thr	TCT Ser	1635
525					530					535					540	
AAA Lys	CCC Pro	ACT Thr	GAC Asp	TCT Ser	TCG Ser	CCC Pro	TCT Ser	AAA Lys	TCC Ser	TCT Ser	ACA Thr	AAC Asn	TCT Ser	ACG Thr	CAA Gln	1683
			545					550						555		
GTC Val	TAT Tyr	CAA Gln	GTG Val	GGT Gly	TAC Tyr	AAA Lys	ATA Ile	GGG Gly	GAT Asp	ACT Thr	ATC Ile	TAC Tyr	AAA Lys	CTG Leu	CAA Gln	1731
			560					565					570			

GAA Glu	ACT Thr	TTC Phe 575	AGC Ser	CAC His	AAT Asn	TCC Ser	ATT Ile 580	ATT Ile	ATT Ile	CAG Gln	GCT Ala	TTA Leu 585	GAG Glu	AGC Ser	GGG Gly	1779
ACT Thr	TAC Tyr 590	ACG Thr	CCA Pro	CCC Pro	CCT Pro	GTC Val 595	ATT Ile	AAC Asn	GGC Gly	TCC Ser	AAA Lys 600	TTT Phe	GAC Asp	TTA Leu	TCC Ser	1827
GCT Ala 605	TCA Ser	AAT Asn	TAT Tyr	ATC Ile	AAT Asn 610	GCT Ala	GAC Asp	ATG Met	CCT Pro	TGG Trp 615	TAT Tyr	GAC Asp	CAT His	AAA Lys	TAT Tyr 620	1875
TAC Tyr	ATC Ile	CCT Pro	AAA Lys	TCC Ser 625	CAA Gln	AAT Asn	TTT Phe	ACA Thr	GAG Glu 630	AGC Ser	GGG Gly	ACT Thr	TAT Tyr	TAC Tyr 635	TTG Leu	1923
CCG Pro	AGC Ser	GTC Val	CAA Gln 640	ATA Ile	TGG Trp	GGG Gly	AGC Ser	TAC Tyr 645	ACT Thr	AAC Asn	TCG Ser	TTT Phe 650	AAA Lys	CAA Gln	ACT Thr	1971
TTT Phe	AGC Ser 655	GCA Ala	AAT Asn	GGT Gly	AGT Ser	AAT Asn	CTG Leu 660	GTG Val	ATT Ile	GGG Gly	TAT Tyr 665	AAC Asn	TCA Ser	ACA Thr	TGG Trp	2019
ACT Thr 670	GAT Asp	CAT His	AAT Asn	GTC Val	TCT Ser 675	TCT Ser	AGC Ser	GGC Gly	ACG Thr	GTG Val 680	TCT Ser	TTT Phe	GGG Gly	GAC Asp	ACT Thr	2067
TCA Ser 685	GGG Gly	AGC Ser	GCT Ala	CTT Leu	AAT Asn 690	GGG Gly	CAT His	TGC Cys	GGA Gly	CCT Pro 695	TGG Trp	CCG Pro	TAT Tyr	TAC Tyr	CAA Gln 700	2115
TGC Cys	ACA Thr	GGC Gly	ACG Thr	ACT Thr 705	AAC Asn	GGC Gly	ACT Thr	TAT Tyr	AGC Ser 710	GCC Ala	TAT Tyr	CAT His	GTG Val 715	TAT Tyr	ATC Ile	2163
ACA Thr	GCG Ala	AAT Asn 720	CTG Leu	CGT Arg	TCT Ser	GGC Gly	AAT Asn 725	CGT Arg	ATA Ile	GGC Gly	ACC Thr	GGT Gly 730	GGG Gly	GCA Ala	GCT Ala	2211
AAT Asn	CTA Leu 735	ATC Ile	TTT Phe	AAT Asn	GGG Gly	GTA Val	GAT Asp 740	AGT Ser	ATC Ile	AAT Asn	ATC Ile 745	GCT Ala 745	AAC Asn	GCT Ala	ACC Thr	2259
ATC Ile 750	ACG Thr	CAA Gln	CAT His	AAC Asn	GCC Ala	GGA Gly 755	ATC Ile	TAT Tyr	TCA Ser	AGC Ser 760	TCT Ser	ATG Met	ACT Thr	TTT Phe	TCC Ser	2307
ACG Thr 765	CAA Gln	AGC Ser	ATG Met	GAT Asp	AAT Asn 770	TCG Ser	CAG Gln	AAT Asn	TTG Leu	AAT Asn 775	GGT Gly	CTA Leu	AAT Asn	TCT Ser	AAC Asn 780	2355
GGC Gly	AAA Lys	CTT Leu	TCG Ser	GTG Val 785	TAT Tyr	GGC Gly	ACC Thr	ACT Thr	TTC Phe 790	ACT Thr	AAC Asn	GAA Glu	GCT Ala	AAA Lys 795	GAT Asp	2403
GGG Gly	AAA Lys	TTC Phe	ATT Ile	TTC Phe	AAT Asn	GCA Ala	GGG Gly	CAA Gln	GCG Ala	GTT Val	TTT Phe	GAA Glu	AAC Asn	ACC Thr	AAC Asn	2451

																2499
																2547
																2595
																2643
																2691
																2739
																2787
																2835
																2883
																2931
																2979
																3027
																3075
																3123

AAC Asn	AGC Ser	ATT Ile	TCT Ser	ATC Ile	CGG Arg	CGT Arg	TTG Leu	GGC Gly	GTT Val	AAC Asn	ATG Met	GTG Val	TTT Phe	GAT Asp	TAT Tyr	3171	
1040						1045						1050					
GTG Val	GAT Asp	ATG Met	GAA Glu	AAA Lys	TCG Ser	GAT Asp	CAT His	TTA Leu	TAT Tyr	TAT Tyr	CAA Gln	AAC Asn	GCT Ala	CTC Leu	GGT Gly	3219	
1055						1060						1065					
TTT Phe	ATG Met	ACC Thr	TAC Tyr	ATG Met	CCT Pro	AAT Asn	AGC Ser	TAT Tyr	AAC Asn	AAT Asn	AAT Asn	TTA Leu	GGG Gly	AAT Asn	GCA Ala	3267	
1070						1075						1080					
AAC Asn	AAC Asn	ACC Thr	ATT Ile	TAC Tyr	TAT Tyr	TAC Tyr	GAC Asp	AAG Lys	AGC Ser	ATT Ile	GAT Asp	TTT Phe	TAT Tyr	GCG Ala	AGC Ser	3315	
1085						1090						1095			1100		
GGG Gly	AAA Lys	ACT Thr	CTA Leu	TTC Phe	ACT Thr	AAA Lys	GCG Ala	GAA Glu	TTT Phe	TCT Ser	CAA Gln	ACA Thr	TTC Phe	ACC Thr	GGG Gly	3363	
			1105						1110						1115		
CAA Gln	AAC Asn	AGC Ser	GCG Ala	ATC Ile	GTT Val	TTT Phe	GGG Gly	GCT Ala	AAA Lys	AGC Ser	ATA Ile	TGG Trp	ACG Thr	AGC Ser	TTA Leu	3411	
			1120						1125						1130		
AGC Ser	GAT Asp	GCA Ala	CCG Pro	CAG Gln	TCT Ser	AAC Asn	ACC Thr	ATC Ile	ATT Ile	CGC Arg	TTT Phe	GGG Gly	GAC Asp	AAT Asn	AAG Lys	3459	
1135						1140						1145					
GGA Gly	GCA Ala	GGG Gly	AGT Ser	AAT Asn	GAT Asp	GCG Ala	AGC Ser	GGG Gly	CAT His	TGC Cys	TGG Trp	AAT Asn	TTG Leu	CAA Gln	TGC Cys	3507	
1150						1155						1160					
ATA Ile	GGC Gly	TTT Phe	ATT Ile	ACA Thr	GGG Gly	CAT His	TAT Tyr	GAA Glu	GCG Ala	CAA Gln	AAG Lys	ATT Ile	TAC Tyr	ATC Ile	ACC Thr	3555	
1165						1170						1175			1180		
GGT Gly	AGC Ser	ATT Ile	GAA Glu	AGC Ser	GGG Gly	AAT Asn	CGC Arg	ATT Ile	TCT Ser	AGC Ser	GGT Gly	GGG Gly	GGC Gly	GCG Ala	AGC Ser	3603	
			1185						1190						1195		
CTT Leu	AAT Asn	TTT Phe	AAC Asn	GGG Gly	CTT Leu	CAA Gln	GGC Gly	ATT Ile	CTT Leu	TTA Leu	ACG Thr	AAC Asn	GCG Ala	ACT Thr	TTG Leu	3651	
			1200						1205						1210		
TAT Tyr	AAC Asn	CGC Arg	GCC Ala	GCT Ala	GGC Gly	ACG Thr	CAA Gln	AGC Ser	TCG Ser	TCT Ser	ATG Met	AAT Asn	TTT Phe	ATC Ile	TCT Ser	3699	
1215						1220						1225					
AAC Asn	AGC Ser	GCG Ala	AAC Asn	ATT Ile	CAG Gln	GCT Ala	CAA Gln	AAC Asn	TCC Ser	TAT Tyr	TTT Phe	ATA Ile	GAC Asp	GAT Asp	ACC Thr	3747	
1230						1235						1240					
GCA Ala	CAA Gln	AAT Asn	GGC Gly	GGT Gly	AAC Asn	CCT Pro	AAT Asn	TTC Phe	AGT Ser	TTC Phe	AAC Asn	GCT Ala	TTG Leu	AAT Asn	CTG Leu	3795	
1245						1250						1255			1260		
GAT Asp	TTT Phe	TCT Ser	AAC Asn	AGC Ser	TCT Ser	TTT Phe	AGA Arg	GGC Gly	TAT Tyr	GTG Val	GGG Gly	AAA Lys	ACG Thr	CAA Gln	TCT Ser	3843	

1265					1270					1275						
GTT	TTT	AAA	TTC	AAT	GCC	AAG	AAT	GCG	ATC	AGT	TTC	ACC	AAC	AGC	ACG	3891
Val	Phe	Lys	Phe	Asn	Ala	Lys	Asn	Ala	Ile	Ser	Phe	Thr	Asn	Ser	Thr	
1280					1285					1290						
AAT	TTA	AGC	TCT	GGT	TTG	TAT	CAA	ATG	CAA	GCT	AAA	AGC	GTG	TTG	TTT	3939
Asn	Leu	Ser	Ser	Gly	Leu	Tyr	Gln	Met	Gln	Ala	Lys	Ser	Val	Leu	Phe	
1295					1300					1305						
GAC	AAT	TCC	AAT	TTA	AGC	GTT	TCA	GTG	GGG	ACA	AGC	AGT	ATT	AAA	GCC	3987
Asp	Asn	Ser	Asn	Leu	Ser	Val	Ser	Val	Gly	Thr	Ser	Ser	Ile	Lys	Ala	
1310					1315					1320						
AAT	GCG	ATC	AAT	CTT	TCT	CAA	AAT	GCC	TCT	ATT	AAT	GCG	AGC	AAC	CAT	4035
Asn	Ala	Ile	Asn	Leu	Ser	Gln	Asn	Ala	Ser	Ile	Asn	Ala	Ser	Asn	His	
1325	1330					1335					1340					
TCA	ACC	TTA	GAA	CTT	CAA	GGC	GAT	TTG	AAT	GTG	AAC	GAC	ACC	AGC	TCG	4083
Ser	Thr	Leu	Glu	Leu	Gln	Gly	Asp	Leu	Asn	Val	Asn	Asp	Thr	Ser	Ser	
1345					1350					1355						
CTC	AAC	CTC	AAC	CAA	AGC	ACG	ATT	AAT	GTT	TCC	AAT	AAC	GCC	ACG	ATC	4131
Leu	Asn	Leu	Asn	Gln	Ser	Thr	Ile	Asn	Val	Ser	Asn	Asn	Ala	Thr	Ile	
1360					1365					1370						
AAC	GAT	TAT	GCG	AGC	TTG	ATT	GCG	AGT	AAT	GGC	TCT	CAC	CTT	AAT	TTT	4179
Asn	Asp	Tyr	Ala	Ser	Leu	Ile	Ala	Ser	Asn	Gly	Ser	His	Leu	Asn	Phe	
1375					1380					1385						
AAC	GGG	GCG	GTT	AAT	TTC	AAT	TCA	GCG	AAT	ATT	ACT	ACG	AGT	TTG	AAT	4227
Asn	Gly	Ala	Val	Asn	Phe	Asn	Ser	Ala	Asn	Ile	Thr	Thr	Ser	Leu	Asn	
1390					1395					1400						
AAT	TCC	TCT	ATC	GTG	TTT	AAG	GGG	GCG	GTC	TCT	TTA	GGA	GGG	CAG	TTT	4275
Asn	Ser	Ser	Ile	Val	Phe	Lys	Gly	Ala	Val	Ser	Leu	Gly	Gly	Gln	Phe	
1405	1410					1415					1420					
AAT	TTA	AGC	AAT	AAC	TCT	TCT	TTA	GAT	TTC	CAA	GGC	TCT	AGC	GCT	ATC	4323
Asn	Leu	Ser	Asn	Asn	Ser	Ser	Leu	Asp	Phe	Gln	Gly	Ser	Ser	Ala	Ile	
1425					1430					1435						
ACC	TCT	AAC	ACG	GCG	TTT	AAT	TTC	TAT	GAT	AAC	GCT	TTT	TCT	CAA	AGC	4371
Thr	Ser	Asn	Thr	Ala	Phe	Asn	Phe	Tyr	Asp	Asn	Ala	Phe	Ser	Gln	Ser	
1440					1445					1450						
CCC	ATC	ACT	TTC	CAT	CAA	GCC	CTT	GAC	ATT	AAA	GCG	CCC	TTA	AGT	TTG	4419
Pro	Ile	Thr	Phe	His	Gln	Ala	Leu	Asp	Ile	Lys	Ala	Pro	Leu	Ser	Leu	
1455					1460					1465						
GGA	GGC	AAC	CTT	TTA	AAC	CCT	AAC	AAC	AGC	AGC	GTG	CTG	GAT	TTA	AAA	4467
Gly	Gly	Asn	Leu	Leu	Asn	Pro	Asn	Asn	Ser	Ser	Val	Leu	Asp	Leu	Lys	
1470					1475					1480						
AAC	AGC	CAG	CTT	GTT	TTT	GGC	GAT	CAA	GGG	AGT	TTG	AAT	ATC	GCT	AAC	4515
Asn	Ser	Gln	Leu	Val	Phe	Gly	Asp	Gln	Gly	Ser	Leu	Asn	Ile	Ala	Asn	
1485	1490					1495					1500					

ATT Ile	GAT Asp	TTA Leu	CTA Leu	AGC Ser	GAT Asp	CTA Leu	AAT Asn	GAT Asp	AAT Asn	AAA Lys	AAT Asn	CGT Arg	GTG Val	TAT Tyr	AAC Asn	4563
1505 1510 1515																
ATC Ile	ATT Ile	CAA Gln	GCG Ala	GAC Asp	ATG Met	AAT Asn	AGT Ser	AAT Asn	TGG Trp	TAT Tyr	GAG Glu	CGT Arg	ATC Ile	AGC Ser	TTC Phe	4611
1520 1525 1530																
TTT Phe	GGC Gly	ATG Met	CAC His	ATC Ile	AAT Asn	GAC Asp	GGG Gly	ATT Ile	TAT Tyr	GAT Asp	GCT Ala	AAA Lys	AAC Asn	CAA Gln	ACT Thr	4659
1535 1540 1545																
TAT Tyr	AGT Ser	TTC Phe	ACT Thr	AAC Asn	CCC Pro	CTT Leu	AAT Asn	AAC Asn	GCC Ala	CTA Leu	AAA Lys	ATC Ile	ACC Thr	GAG Glu	AGC Ser	4707
1550 1555 1560																
TTT Phe	AAA Lys	GAC Asp	AAC Asn	CAA Gln	CTA Leu	AGC Ser	GTT Val	ACG Thr	CTC Leu	TCT Ser	CAA Gln	ATC Ile	CCG Pro	GGT Gly	ATT Ile	4755
1565 1570 1575 1580																
AAA Lys	AAC Asn	ACG Thr	CTC Leu	TAT Tyr	AAC Asn	ATT Ile	GGC Gly	TCT Ser	GAA Glu	ATT Ile	TTT Phe	AAC Asn	TAC Tyr	CAA Gln	AAA Lys	4803
1585 1590 1595																
GTT Val	TAT Tyr	AAC Asn	AAC Asn	GCT Ala	AAT Asn	GGC Gly	GTG Val	TAT Tyr	TCT Ser	TAT Tyr	AGC Ser	GAT Asp	GAT Asp	GCA Ala	CAA Gln	4851
1600 1605 1610																
GGC Gly	GTG Val	TTT Phe	TAT Tyr	CTC Leu	ACA Thr	AGC Ser	AAC Asn	GTG Val	AAA Lys	GGC Gly	TAT Tyr	TAC Tyr	AAC Asn	CCT Pro	AAC Asn	4899
1615 1620 1625																
CAA Gln	TCC Ser	TAT Tyr	CAA Gln	GCC Ala	AGC Ser	GGC Gly	AGT Ser	AAC Asn	AAC Asn	ACC Thr	ACG Thr	AAA Lys	AAT Asn	AAT Asn	AAT Asn	4947
1630 1635 1640																
CTA Leu	ACC Thr	TCT Ser	GAA Glu	TCT Ser	TCT Ser	ATC Ile	ATC Ile	TCG Ser	CAA Gln	ACC Thr	TAT Tyr	AAC Asn	GCG Ala	CAA Gln	GGC Gly	4995
1645 1650 1655 1660																
AAC Asn	CCT Pro	ATT Ile	AGC Ser	GCG Ala	TTG Leu	CAC His	ATC Ile	TAT Tyr	AAC Asn	AAG Lys	GGC Gly	TAT Tyr	AAT Asn	TTC Phe	AAC Asn	5043
1665 1670 1675																
AAT Asn	ATC Ile	AAA Lys	GCG Ala	TTA Leu	GGG Gly	CAA Gln	ATG Met	GCT Ala	CTC Leu	AAA Lys	CTC Leu	TAC Tyr	CCT Pro	GAA Glu	ATC Ile	5091
1680 1685 1690																
AAA Lys	AAG Lys	GTA Val	TTA Leu	GGG Gly	AAT Asn	GAT Asp	TTT Phe	TCG Ser	CCC Pro	TCA Ser	AGT Ser	TTG Leu	AAC Asn	GCT Ala	TTA Leu	5139
1695 1700 1705																
AAC Asn	TCT Ser	AAT Asn	GCG Ala	CTA Leu	AAC Asn	CAA Gln	CTT Leu	ACC Thr	AAA Lys	CTC Leu	ATC Ile	ACG Thr	CCT Pro	AAC Asn	GAC Asp	5187
1710 1715 1720																
TGG Trp	AAA Lys	AAC Asn	ATT Ile	AAC Asn	GAG Glu	TTG Leu	ATT Ile	GAT Asp	AAC Asn	GCA Ala	AAC Asn	AAT Asn	TCG Ser	GTG Val	GTG Val	5235

1725	1730						1735						1740						
CAA AAT TTC AAT AAC GGC ACT TTG ATT GTG GGA GCG ACT CAA ATA GGG Gln Asn Phe Asn Asn Gly Thr Leu Ile Val Gly Ala Thr Gln Ile Gly	1745						1750						1755						5283
CAA ACA GAC ACC AAT AGC GCG GTT GTT TTT GGG GGC TTG GGC TAT CAA Gln Thr Asp Thr Asn Ser Ala Val Val Phe Gly Gly Leu Tyr Gln	1760						1765						1770						5331
ACA CCT TGT GAT TAT ACT GAT ATT GTG TGC CAA AAA TTT AGA GGC ACT Thr Pro Cys Asp Tyr Thr Asp Ile Val Cys Gln Lys Phe Arg Gly Thr	1775						1780						1785						5379
TAT TTA GGA CAG CTT TTA GAG TCC AGC TCG GCT GAT TTG GGC TAT ATT Tyr Leu Gly Gln Leu Leu Glu Ser Ser Ser Ala Asp Leu Gly Tyr Ile	1790						1795						1800						5427
GAC ACG ACT TTT AAC GCT AAA GAA ATT TAT CTT ACC GGC ACT TTA GGG Asp Thr Thr Phe Asn Lys Glu Ile Tyr Leu Thr Gly Thr Leu Gly	1805						1810						1815						5475
AGC GGG AAC GCA TGG GGG ACT GGG GGG AGC GCG AGC GTA ACT TTT AAC Ser Gly Asn Ala Trp Gly Thr Gly Gly Ser Ala Ser Val Thr Phe Asn	1825						1830						1835						5523
AGC CAA ACT TCG CTC ATT CTC AAT CAG GCT AAT ATC GTA AGC TCG CAA Ser Gln Thr Ser Leu Ile Leu Asn Gln Ala Asn Ile Val Ser Ser Gln	1840						1845						1850						5571
ACC GAT GGG ATC TTT AGC ATG CTG GGT CAA GAG GGT ATT AAT AAG GTT Thr Asp Gly Ile Phe Ser Met Leu Gly Gln Glu Gly Ile Asn Lys Val	1855						1860						1865						5619
TTC AAT CAA GCC GGG CTC GCT AAT ATT TTG GGC GAA GTG GCG GTG CAA Phe Asn Gln Ala Gly Leu Ala Asn Ile Leu Gly Glu Val Ala Val Gln	1870						1875						1880						5667
TCC ATC AAC AAA GCC GGG GGA TTA GGG AAT TTG ATA GTA AAT ACG CTA Ser Ile Asn Lys Ala Gly Gly Leu Gly Asn Leu Ile Val Asn Thr Leu	1885						1890						1895						5715
GGG AGT AAT AGC GTG ATT GGG GGG TAT TTA ACG CCT GAA CAA AAA AAT Gly Ser Asn Ser Val Ile Gly Gly Tyr Leu Thr Pro Glu Gln Lys Asn	1905						1910						1915						5763
CAA ACC CTA AGC CAG CTT TTA GGG CAG AAT AAC TTT GAT AAT CTC ATG Gln Thr Leu Ser Gln Leu Leu Gly Gln Asn Asn Phe Asp Asn Leu Met	1920						1925						1930						5811
AAC GAT AGC GGT TTG AAT ACG GCG ATT AAG GAT TTG ATC AGA CAA AAA Asn Asp Ser Gly Leu Asn Thr Ala Ile Lys Asp Leu Ile Arg Gln Lys	1935						1940						1945						5859
TTA GGC TTT TGG ACC GGG CTA GTG GGG GGA TTA GCC GGA CTA GGG GGC Leu Gly Phe Trp Thr Gly Leu Val Gly Gly Leu Ala Gly Leu Gly Gly	1950						1955						1960						5907

ATT Ile 1965	GAT Asp	TTG Leu	CAA Gln	AAC Asn	CCT Pro	GAA Glu	AAG Lys	CTT Leu	ATA Ile	GGC Gly	AGC Ser	ATG Met	TCA Ser	ATC Ile	AAT Asn	5955
1970																
1975																
1980																
GAT Asp	TTA Leu	TTG Leu	AGT Ser	AAA Lys	AAA Lys	GGG Gly	TTG Leu	TTC Phe	AAT Asn	CAG Gln	ATC Ile	ACC Thr	GGC Gly	TTT Phe	ATT Ile	6003
1985																
1990																
1995																
TCC Ser	GCT Ala	AAC Asn	GAT Asp	ATA Ile	GGG Gly	CAA Gln	GTC Val	ATA Ile	AGC Ser	GTA Val	ATG Met	TTG Leu	CAA Gln	GAT Asp	ATT Ile	6051
2000																
2005																
2010																
GTC Val	AAA Lys	CCG Pro	AGC Ser	AAC Asn	GCT Ala	TTA Leu	AAA Lys	AAC Asn	GAT Asp	GTA Val	GCG Ala	GCT Ala	TTA Leu	GGC Gly	AAG Lys	6099
2015																
2020																
2025																
CAA Gln	ATG Met	ATT Ile	GGC Gly	GAA Glu	TTT Phe	TTA Leu	GGC Gly	CAA Gln	GAC Asp	ACG Thr	CTC Leu	AAT Asn	TCT Ser	TTA Leu	GAA Glu	6147
2030																
2035																
2040																
AGC Ser	TTG Leu	TTG Leu	CAA Gln	AAC Asn	CAG Gln	CAG Gln	ATT Ile	AAA Lys	AGC Ser	GTT Val	TTA Leu	GAC Asp	AAA Lys	GTC Val	CTA Leu	6195
2045																
2050																
2055																
2060																
GCG Ala	GCT Ala	AAA Lys	GGT Gly	TTA Leu	GGG Gly	CCT Pro	ATT Ile	TAT Tyr	GAA Glu	CAA Gln	GGC Gly	TTG Leu	GGG Gly	GAT Asp	TTG Leu	6243
2065																
2070																
2075																
ATA Ile	CCT Pro	AAT Asn	CTT Leu	GGT Gly	AAA Lys	AAA Lys	GGG Gly	CTT Leu	TTC Phe	GCT Ala	CCT Pro	TAT Tyr	GGC Gly	TTG Leu	AGT Ser	6291
2080																
2085																
2090																
CAA Gln	GTG Val	TGG Trp	CAA Gln	AAA Lys	GGG Gly	GAT Asp	TTT Phe	AGT Ser	TTC Phe	AAC Asn	GCA Ala	CAA Gln	GGC Gly	AAT Asn	GTT Val	6339
2095																
2100																
2105																
TTT Phe	GTG Val	CAA Gln	AAT Asn	TCC Ser	ACT Thr	TTC Phe	TCT Ser	AAC Asn	GCC Ala	AAT Asn	GGA Gly	GGC Gly	ACG Thr	CTC Leu	TCT Ser	6387
2110																
2115																
2120																
TTT Phe	AAC Asn	GCA Ala	GGA Gly	AAT Asn	TCG Ser	CTC Leu	ATT Ile	TTT Phe	GCC Ala	GGA Gly	AAC Asn	AAT Asn	CAT His	ATT Ile	GCA Ala	6435
2125																
2130																
2135																
2140																
TTC Phe	ACT Thr	AAC Asn	CAC His	GCT Ala	GGA Gly	ACT Thr	CTT Leu	CAA Gln	TTA Leu	TTG Leu	TCC Ser	GAT Asp	CAA Gln	GTT Val	TCT Ser	6483
2145																
2150																
2155																
AAC Asn	ATT Ile	AAC Asn	ATC Ile	ACC Thr	ACG Thr	CTT Leu	AAC Asn	GCT Ala	AGC Ser	AAC Asn	GGC Gly	CTT Leu	AAG Lys	ATT Ile	AAC Asn	6531
2160																
2165																
2170																
GCC Ala	GCT Ala	AAT Asn	AAC Asn	AAT Asn	GTT Val	TCT Ser	GTG Val	TCT Ser	CAA Gln	GGC Gly	AAT Asn	CTG Leu	TTT Phe	GTC Val	AGC Ser	6579
2175																
2180																
2185																
GCT Ala	AGC Ser	TGC Cys	GCG Ala	CAA Gln	CAA Gln	AGC Ser	GAT Asp	CCA Pro	ACT Thr	ACA Thr	GCT Ala	AAT Asn	ATT Ile	GCA Ala	AAC Asn	6627

2190					2195					2200							
CCT	TGC	GCG	CTT	AGC	GCC	CAA	AGC	ACG	AAT	GGC	GCT	TCT	TCT	AAT	AAT	6675	
Pro	Cys	Ala	Leu	Ser	Ala	Gln	Ser	Thr	Asn	Gly	Ala	Ser	Ser	Asn	Asn		
2205					2210					2215					2220		
GCG	TCA	AAT	AAC	GCG	CCA	ATC	GCC	TTG	AGT	AAT	AAC	GAT	GAA	AGC	TTG	6723	
Ala	Ser	Asn	Asn	Ala	Pro	Ile	Ala	Leu	Ser	Asn	Asn	Asp	Glu	Ser	Leu		
					2225					2230					2235		
ATG	GTT	GCG	GCG	AAT	GAT	TTC	AAT	TTT	TCA	GGC	AAT	ATT	TAC	GCT	AAT	6771	
Met	Val	Ala	Ala	Asn	Asp	Phe	Asn	Phe	Ser	Gly	Asn	Ile	Tyr	Ala	Asn		
					2240					2245				2250			
GGG	GTG	GTT	GAT	TTT	TCA	AAG	ATT	AAA	GGC	TCT	GCA	AAC	ATT	AAA	AAC	6819	
Gly	Val	Val	Asp	Phe	Ser	Lys	Ile	Lys	Gly	Ser	Ala	Asn	Ile	Lys	Asn		
					2255					2260				2265			
CTG	TAT	CTT	TAC	AAT	AAC	GCT	CAA	TTC	CAA	GCC	AAC	AAT	CTC	ACT	ATT	6867	
Leu	Tyr	Leu	Tyr	Asn	Asn	Ala	Gln	Phe	Gln	Ala	Asn	Asn	Leu	Thr	Ile		
					2270					2275				2280			
TCC	AAT	CAA	GCG	GTG	TTA	GAA	AAA	AAC	GCC	AGC	TTT	GTA	ACG	AAT	AAT	6915	
Ser	Asn	Gln	Ala	Val	Leu	Glu	Lys	Asn	Ala	Ser	Phe	Val	Thr	Asn	Asn		
2285					2290					2295				2300			
TTA	AAC	ATT	CAA	GGA	GCG	TTT	AAC	AAC	AAC	GCC	ACG	CAA	AAA	ATA	GAG	6963	
Leu	Asn	Ile	Gln	Gly	Ala	Phe	Asn	Asn	Asn	Ala	Thr	Gln	Lys	Ile	Glu		
					2305					2310				2315			
GTG	CTT	CAA	AAT	TTA	GTG	ATC	GCT	TCA	AAC	GCT	TCT	TTA	AGC	ACC	GGG	7011	
Val	Leu	Gln	Asn	Leu	Val	Ile	Ala	Ser	Asn	Ala	Ser	Leu	Ser	Thr	Gly		
					2320					2325				2330			
ATT	TAT	GGG	TTA	GAA	GTA	GGG	GGG	GCT	TTG	AAT	AAT	TCT	GGA	GCG	ATC	7059	
Ile	Tyr	Gly	Leu	Glu	Val	Gly	Gly	Ala	Leu	Asn	Asn	Ser	Gly	Ala	Ile		
					2335				2340				2345				
CAT	TTT	AAT	TTA	GAA	AAT	ACC	CAA	ACG	CCA	ACG	CCG	CTC	ATT	CAA	GCA	7107	
His	Phe	Asn	Leu	Glu	Asn	Thr	Gln	Thr	Pro	Thr	Pro	Leu	Ile	Gln	Ala		
					2350				2355				2360				
GAG	GGG	ATC	ATT	AAC	CTC	AAC	ACC	ACC	CAA	ACG	CCT	TTT	ATG	AAT	GTC	7155	
Glu	Gly	Ile	Ile	Asn	Leu	Asn	Thr	Thr	Gln	Thr	Pro	Phe	Met	Asn	Val		
2365					2370				2375				2380				
AAT	AAC	AGC	ATG	GCC	AAT	AAT	ACG	ACT	TAC	ACT	TTA	TTA	AAA	AGC	AGC	7203	
Asn	Asn	Ser	Met	Ala	Asn	Asn	Thr	Thr	Tyr	Thr	Leu	Leu	Lys	Ser	Ser		
					2385				2390				2395				

AAC GGC GCA TTG ACT TAT TTG GGC CAA CGG GTT TTG TTG CAA GAT AAG Asn Gly Ala Leu Thr Tyr Leu Gly Gln Arg Val Leu Leu Gln Asp Lys	7347
2430 2435 2440	
GGG TTA TTG TTA AGC GTA GCG CTG CCC AAC TCA AAC AAC GCT TCT CAA Gly Leu Leu Leu Ser Val Ala Leu Pro Asn Ser Asn Asn Ala Ser Gln	7395
2445 2450 2455 2460	
AAC AAC ATT TTA AGC CTT TCT GTC CTT TAT AAC CAA GTT AAA ATG TCT Asn Asn Ile Leu Ser Leu Ser Val Leu Tyr Asn Asn Gln Val Lys Met Ser	7443
2465 2470 2475	
TGC GGC GAT AAA GCG ATG GAT TTT ACC CCC CCT ACC TTA CAA GAT TAC Cys Gly Asp Lys Ala Met Asp Phe Thr Pro Pro Thr Leu Gln Asp Tyr	7491
2480 2485 2490	
ATT GTG GGC ATT CAA GGG CAA AGC GCG CTC AAT CAA ATT GAA GCT GTT Ile Val Gly Ile Gln Gly Gln Ser Ala Leu Asn Gln Ile Glu Ala Val	7539
2495 2500 2505	
GGG GGG AAC GCT ATC AAG TGG CTT TCA ACA TTG ATG ATG GAG ACT AAA Gly Gly Asn Ala Ile Lys Trp Leu Ser Thr Leu Met Met Glu Thr Lys	7587
2510 2515 2520	
GAA AAC CCG TTT TTT GCG CCG ATT TAT TTA AAA AAC CAC TCT TTG AAT Glu Asn Pro Phe Phe Ala Pro Ile Tyr Leu Lys Asn His Ser Leu Asn	7635
2525 2530 2535 2540	
GAA ATC TTA GGC GTA ACA AAA GAT CTT CAA AAC ACC GCA AGC TTG ATT Glu Ile Leu Gly Val Thr Lys Asp Leu Gln Asn Thr Ala Ser Leu Ile	7683
2545 2550 2555	
TCT AAC CCT AAT TTT AGA GAT AAC GCT ACC AAT CTT TTA GAA TTG GCG Ser Asn Pro Asn Phe Arg Asp Asn Ala Thr Asn Leu Leu Glu Leu Ala	7731
2560 2565 2570	
AGT TAC ACC CAA CAA ACC AGC CGT TTA ACA AAA CTC TCT GAT TTT AGA Ser Tyr Thr Gln Gln Thr Ser Arg Leu Thr Lys Leu Ser Asp Phe Arg	7779
2575 2580 2585	
TCT AGA GAG GGA GAG TCT GAT TTT TCT TTG TTA GAG CTT AAA AAC AAG Ser Arg Glu Gly Glu Ser Asp Phe Ser Leu Leu Glu Leu Lys Asn Lys	7827
2590 2595 2600	
CGT TTT AGC GAT CCT AAT CCA GAG GTT TTT GTC AAA TAC TCT CAA CTT Arg Phe Ser Asp Pro Asn Pro Glu Val Phe Val Lys Tyr Ser Gln Leu	7875
2605 2610 2615 2620	
AGC AAA CAC CCA AAT AAC CTT TGG GTT CAA GGG GTG GGA GGA GCG AGC Ser Lys His Pro Asn Asn Leu Trp Val Gln Gly Val Gly Gly Ala Ser	7923
2625 2630 2635	
TTT ATT TCT GGG GGC AAT GGC ACG CTT TAT GGC TTG AAT GCG GGC TAT Phe Ile Ser Gly Gly Asn Gly Thr Leu Tyr Gly Leu Asn Ala Gly Tyr	7971
2640 2645 2650	
GAC AGG TTG GTT AAA AAT GTG ATC CTT GGG GGT TAT GTG GCT TAT GGC Asp Arg Leu Val Lys Asn Val Ile Leu Gly Gly Tyr Val Ala Tyr Gly	8019

2655					2660					2665						
TAT	AGC	GAC	TTT	AAT	GGG	AAC	ATC	ATG	CAT	TCT	TTG	GGT	AAT	AAT	GTG	8067
Tyr	Ser	Asp	Phe	Asn	Gly	Asn	Ile	Met	His	Ser	Leu	Gly	Asn	Asn	Val	
2670					2675					2680						
GAT	GTG	GGG	ATG	TAT	GCG	AGG	GCT	TTT	TTA	AAA	AGG	AAC	GAA	TTC	ACT	8115
Asp	Val	Gly	Met	Tyr	Ala	Arg	Ala	Phe	Leu	Lys	Arg	Asn	Glu	Phe	Thr	
2685					2690					2695					2700	
TTG	AGC	GCG	AAT	GAA	ACT	TAT	GGA	GGC	AAT	GCA	ACT	AGT	ATC	AAT	TCT	8163
Leu	Ser	Ala	Asn	Glu	Thr	Tyr	Gly	Gly	Asn	Ala	Thr	Ser	Ile	Asn	Ser	
2705					2710					2715						
TCT	AAT	TCT	TTG	CTC	TCT	GTG	TTG	AAC	CAA	CGC	TAC	AAC	TAC	AAC	ACC	8211
Ser	Asn	Ser	Leu	Leu	Ser	Val	Leu	Asn	Gln	Arg	Tyr	Asn	Tyr	Asn	Thr	
2720					2725					2730						
TGG	ACA	ACG	AGC	GTG	AAC	GGG	AAT	TAC	GGC	TAT	GAT	TTC	ATG	TTC	AAA	8259
Trp	Thr	Thr	Ser	Val	Asn	Gly	Asn	Tyr	Gly	Tyr	Asp	Phe	Met	Phe	Lys	
2735					2740					2745						
CAA	AAA	AGC	GTG	GTG	CTA	AAA	CCT	CAA	GTG	GGT	TTG	AGC	TAT	CAT	TTC	8307
Gln	Lys	Ser	Val	Val	Leu	Lys	Pro	Gln	Val	Gly	Leu	Ser	Tyr	His	Phe	
2750					2755					2760						
ATA	GGT	CTA	AGT	GGG	ATG	AAA	GGC	AAT	GAT	GCC	GCT	TAC	AAA	CAA	TTC	8355
Ile	Gly	Leu	Ser	Gly	Met	Lys	Gly	Asn	Asp	Ala	Ala	Tyr	Lys	Gln	Phe	
2765					2770					2775					2780	
CTC	ATG	CAT	TCA	AAC	CCC	TCT	AAC	GAA	TCG	GTT	TTA	ACG	CTC	AAC	ATG	8403
Leu	Met	His	Ser	Asn	Pro	Ser	Asn	Glu	Ser	Val	Leu	Thr	Leu	Asn	Met	
2785					2790					2795						
GGG	TTG	GAG	AGC	CGT	AAA	TAT	TTT	GGT	AAA	AAT	TCC	TAT	TAT	TTT	GTA	8451
Gly	Leu	Glu	Ser	Arg	Lys	Tyr	Phe	Gly	Lys	Asn	Ser	Tyr	Tyr	Phe	Val	
2800					2805					2810						
ACG	GCG	AGA	CTA	GGT	AGG	GAT	CTT	TTG	ATC	AAA	TCT	AAA	GGC	AGC	AAT	8499
Thr	Ala	Arg	Leu	Gly	Arg	Asp	Leu	Leu	Ile	Lys	Ser	Lys	Gly	Ser	Asn	
2815					2820					2825						
ACG	GTG	CGT	TTT	GTG	GGC	GAA	AAC	ACT	TTA	TTG	TAT	CGC	AAG	GGG	GAA	8547
Thr	Val	Arg	Phe	Val	Gly	Glu	Asn	Thr	Leu	Leu	Tyr	Arg	Lys	Gly	Glu	
2830					2835					2840						
GTT	TTT	AAC	ACT	TTT	GCG	AGC	GTG	ATT	ACA	GGG	GGC	GAA	ATG	CAT	TTG	8595
Val	Phe	Asn	Thr	Phe	Ala	Ser	Val	Ile	Thr	Gly	Gly	Glu	Met	His	Leu	
2845					2850					2855					2860	
TGG	CGT	TTG	GTG	TAT	GTG	AAT	GCG	GGG	GTG	GGG	CTT	AAG	ATG	GGC	TTG	8643
Trp	Arg	Leu	Val	Tyr	Val	Asn	Ala	Gly	Val	Gly	Leu	Lys	Met	Gly	Leu	
2865					2870					2875						
CAA	TAC	CAA	GAT	ATT	AAT	ATA	ACC	GGG	AAT	GTG	GGC	ATG	CGA	GTG	GCG	8691
Gln	Tyr	Gln	Asp	Ile	Asn	Ile	Thr	Gly	Asn	Val	Gly	Met	Arg	Val	Ala	

TTT TAGCTTTTTT GCTATAATGC TTCGTTCAAA TTTTATGGTT AGGTTTTTCT ATGT
Phe

8748

(2) INFORMATION FOR SEQ ID NO:522:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2893 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

Met	Lys	Lys	Phe	Lys	Lys	Lys	Pro	Lys	Ser	Ile	Lys	Arg	Ser	His	Gln
1				5					10					15	
Asn	Gln	Lys	Thr	Ile	Leu	Lys	Arg	Pro	Leu	Trp	Leu	Met	Pro	Leu	Leu
			20					25					30		
Ile	Ser	Gly	Phe	Ala	Ser	Gly	Val	Tyr	Ala	Asn	Asn	Leu	Trp	Asp	Leu
		35					40					45			
Leu	Asn	Pro	Lys	Val	Gly	Gly	Glu	Tyr	Val	His	Trp	Val	Lys	Gly	Ser
	50					55					60				
Gln	Tyr	Cys	Ala	Trp	Trp	Glu	Phe	Ala	Gly	Cys	Leu	Lys	Asn	Val	Trp
65					70					75				80	
Gly	Ala	Asn	His	Lys	Gly	Tyr	Asp	Ala	Gly	Asn	Ala	Ala	Asn	Tyr	Leu
				85					90					95	
Ser	Ser	Gln	Asn	Tyr	Gln	Ala	Ile	Ser	Val	Gly	Ser	Gly	Asn	Glu	Thr
			100					105					110		
Gly	Thr	Tyr	Ser	Leu	Ser	Gly	Phe	Thr	Asn	Tyr	Val	Gly	Gly	Asn	Leu
		115					120					125			
Thr	Ile	Asn	Leu	Gly	Asn	Ser	Val	Val	Leu	Asp	Leu	Ser	Gly	Ser	Asn
		130				135						140			
Ser	Phe	Thr	Ser	Tyr	Gln	Gly	Tyr	Asn	Gln	Gly	Lys	Asp	Asp	Val	Thr
145					150					155				160	
Phe	Thr	Val	Gly	Ala	Ile	Asn	Leu	Asn	Gly	Thr	Leu	Glu	Val	Gly	Asn
			165						170					175	
Arg	Val	Gly	Ser	Gly	Ala	Gly	Thr	His	Thr	Gly	Thr	Ala	Thr	Leu	Asn
			180					185					190		
Leu	Asn	Ala	Asn	Lys	Val	Asn	Ile	Asn	Ser	Asn	Ile	Asn	Ala	Tyr	Lys
		195					200					205			
Thr	Ser	Gln	Val	Asn	Ile	Gly	Asn	Ala	Asn	Ser	Val	Ile	Thr	Ile	Gly
	210					215					220				
Ser	Val	Ser	Leu	Ser	Gly	Asp	Val	Cys	Ser	Ser	Leu	Ala	Ser	Val	Gly
225					230					235				240	
Ile	Gly	Ala	Asn	Cys	Ser	Thr	Ser	Gly	Pro	Ser	Tyr	Ser	Phe	Lys	Gly
			245						250					255	
Thr	Thr	Asn	Ala	Thr	Asn	Thr	Ala	Phe	Ser	Asn	Ala	Ser	Gly	Ser	Phe
			260					265					270		
Thr	Phe	Glu	Glu	Asn	Ala	Thr	Phe	Ser	Gly	Ala	Lys	Trp	Asn	Gly	Gly
		275					280					285			
Thr	Tyr	Thr	Phe	Asn	Lys	Glu	Phe	Ser	Ala	Thr	Asn	Asn	Thr	Ala	Phe
	290					295					300				
Ser	Ser	Gly	Ser	Phe	Asn	Phe	Lys	Gly	Val	Ser	Ser	Phe	Asn	Gly	Thr
305					310					315				320	
Ser	Phe	Ser	Asn	Ala	Ser	Tyr	Thr	Phe	Asp	Asn	Gln	Ala	Thr	Phe	Gln

325																330																335																																																																																																																			
Asn	Ser	Ser	Phe	Asn	Gly	Gly	Thr	Phe	Thr	Phe	Asn	Asn	Gln	Thr	Asn	340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	530	535	540	545	550	555	560	565	570	575	580	585	590	595	600	605	610	615	620	625	630	635	640	645	650	655	660	665	670	675	680	685	690	695	700	705	710	715	720	725	730	735	740	745	750	755	760	765	770	775	780	785	790	795	800	805	810	815	820	825	830	835	840	845	850	855	860	865	870	875	880	885	890	895	900	905	910	915	920	925	930	935	940	945	950	955	960	965	970	975	980	985	990	995
Pro	Thr	Asn	Asn	Ala	Gln	His	Pro	Gln	Ile	Gln	Asn	Ser	Ser	Phe	Ser	340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	530	535	540	545	550	555	560	565	570	575	580	585	590	595	600	605	610	615	620	625	630	635	640	645	650	655	660	665	670	675	680	685	690	695	700	705	710	715	720	725	730	735	740	745	750	755	760	765	770	775	780	785	790	795	800	805	810	815	820	825	830	835	840	845	850	855	860	865	870	875	880	885	890	895	900	905	910	915	920	925	930	935	940	945	950	955	960	965	970	975	980	985	990	995
Gly	Asn	Ala	Thr	Thr	Leu	Lys	Gly	Phe	Val	Asn	Phe	Gln	Gln	Ala	Phe	370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	530	535	540	545	550	555	560	565	570	575	580	585	590	595	600	605	610	615	620	625	630	635	640	645	650	655	660	665	670	675	680	685	690	695	700	705	710	715	720	725	730	735	740	745	750	755	760	765	770	775	780	785	790	795	800	805	810	815	820	825	830	835	840	845	850	855	860	865	870	875	880	885	890	895	900	905	910	915	920	925	930	935	940	945	950	955	960	965	970	975	980	985	990	995						
Asn	Asn	Ser	Asn	His	Gln	Leu	Thr	Ile	Gln	Asn	Ala	Ser	Phe	Asn	Asn	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	530	535	540	545	550	555	560	565	570	575	580	585	590	595	600	605	610	615	620	625	630	635	640	645	650	655	660	665	670	675	680	685	690	695	700																																																																				

785					790					795				800
Phe	Asn	Ala	Gly	Gln	Ala	Val	Phe	Glu	Asn	Thr	Asn	Phe	Asn	Gly
				805					810					815
Ser	Tyr	Gln	Phe	Ser	Gly	Asp	Ser	Leu	Asn	Phe	Ser	Asn	Asn	Gln
			820					825					830	
Phe	Asn	Ser	Gly	Ser	Phe	Glu	Ile	Ser	Ala	Lys	Asn	Ala	Ser	Phe
		835					840					845		
Asn	Ala	Asn	Phe	Asn	Asn	Ser	Ala	Ser	Phe	Asn	Phe	Asn	Asn	Ser
	850					855					860			
Ala	Thr	Thr	Ser	Phe	Val	Gly	Asp	Phe	Thr	Asn	Ala	Asn	Ser	Asn
865					870					875				880
Gln	Ile	Ala	Gly	Asn	Ala	Val	Phe	Gly	Asn	Ser	Thr	Asn	Gly	Ser
			885						890					895
Asn	Thr	Ala	Asn	Phe	Asn	Asn	Thr	Gly	Ser	Val	Asn	Ile	Ser	Gly
			900					905					910	
Ala	Thr	Phe	Asp	Asn	Val	Val	Phe	Asn	Gly	Pro	Thr	Asn	Thr	Ser
		915					920					925		
Lys	Gly	Gln	Val	Thr	Leu	Asn	Asn	Ile	Thr	Leu	Lys	Asn	Leu	Asn
	930					935					940			
Pro	Leu	Ser	Phe	Gly	Asp	Gly	Thr	Ile	Thr	Phe	Asn	Ala	His	Ser
945					950					955				960
Ile	Asn	Ile	Ala	Glu	Ser	Ile	Thr	Asn	Gly	Asn	Pro	Ile	Thr	Leu
			965						970					975
Ser	Ser	Ser	Lys	Glu	Ile	Glu	Tyr	Asn	Asn	Ala	Phe	Ser	Lys	Asn
			980					985					990	
Trp	Gln	Leu	Ile	Asn	Tyr	Gln	Gly	His	Gly	Ala	Ser	Ser	Glu	Lys
		995				1000						1005		
Val	Ser	Ser	Ala	Gly	Asn	Gly	Val	Tyr	Asp	Val	Val	Tyr	Ser	Phe
	1010				1015					1020				
Asn	Gln	Thr	Tyr	Asn	Phe	Gln	Glu	Val	Phe	Ser	Gln	Asn	Ser	Ile
025				1030					1035					1040
Ile	Arg	Arg	Leu	Gly	Val	Asn	Met	Val	Phe	Asp	Tyr	Val	Asp	Met
			1045						1050					1055
Lys	Ser	Asp	His	Leu	Tyr	Tyr	Gln	Asn	Ala	Leu	Gly	Phe	Met	Thr
		1060					1065					1070		
Met	Pro	Asn	Ser	Tyr	Asn	Asn	Asn	Leu	Gly	Asn	Ala	Asn	Asn	Thr
		1075				1080					1085			
Tyr	Tyr	Tyr	Asp	Lys	Ser	Ile	Asp	Phe	Tyr	Ala	Ser	Gly	Lys	Thr
	1090				1095						1100			
Phe	Thr	Lys	Ala	Glu	Phe	Ser	Gln	Thr	Phe	Thr	Gly	Gln	Asn	Ser
105				1110					1115					1120
Ile	Val	Phe	Gly	Ala	Lys	Ser	Ile	Trp	Thr	Ser	Leu	Ser	Asp	Ala
			1125					1130						1135
Gln	Ser	Asn	Thr	Ile	Ile	Arg	Phe	Gly	Asp	Asn	Lys	Gly	Ala	Gly
		1140					1145					1150		
Asn	Asp	Ala	Ser	Gly	His	Cys	Trp	Asn	Leu	Gln	Cys	Ile	Gly	Phe
	1155					1160					1165			
Thr	Gly	His	Tyr	Glu	Ala	Gln	Lys	Ile	Tyr	Ile	Thr	Gly	Ser	Ile
	1170				1175					1180				
Ser	Gly	Asn	Arg	Ile	Ser	Ser	Gly	Gly	Gly	Ala	Ser	Leu	Asn	Phe
185				1190					1195					1200
Gly	Leu	Gln	Gly	Ile	Leu	Leu	Thr	Asn	Ala	Thr	Leu	Tyr	Asn	Arg
		1205						1210						1215
Ala	Gly	Thr	Gln	Ser	Ser	Ser	Met	Asn	Phe	Ile	Ser	Asn	Ser	Ala
		1220					1225					1230		
Ile	Gln	Ala	Gln	Asn	Ser	Tyr	Phe	Ile	Asp	Asp	Thr	Ala	Gln	Asn
	1235					1240					1245			
Gly	Asn	Pro	Asn	Phe	Ser	Phe	Asn	Ala	Leu	Asn	Leu	Asp	Phe	Ser

1250					1255					1260					
Ser 265	Ser	Phe	Arg	Gly	Tyr	Val	Gly	Lys	Thr	Gln	Ser	Val	Phe	Lys	Phe
Asn	Ala	Lys	Asn	Ala	Ile	Ser	Phe	Thr	Asn	Ser	Thr	Asn	Leu	Ser	Ser
1285					1290					1295					
Gly	Leu	Tyr	Gln	Met	Gln	Ala	Lys	Ser	Val	Leu	Phe	Asp	Asn	Ser	Asn
1300					1305					1310					
Leu	Ser	Val	Ser	Val	Gly	Thr	Ser	Ser	Ile	Lys	Ala	Asn	Ala	Ile	Asn
1315					1320					1325					
Leu	Ser	Gln	Asn	Ala	Ser	Ile	Asn	Ala	Ser	Asn	His	Ser	Thr	Leu	Glu
1330					1335					1340					
Leu	Gln	Gly	Asp	Leu	Asn	Val	Asn	Asp	Thr	Ser	Ser	Leu	Asn	Leu	Asn
345	1350					1355					1360				
Gln	Ser	Thr	Ile	Asn	Val	Ser	Asn	Asn	Ala	Thr	Ile	Asn	Asp	Tyr	Ala
1365					1370					1375					
Ser	Leu	Ile	Ala	Ser	Asn	Gly	Ser	His	Leu	Asn	Phe	Asn	Gly	Ala	Val
1380					1385					1390					
Asn	Phe	Asn	Ser	Ala	Asn	Ile	Thr	Thr	Ser	Leu	Asn	Asn	Ser	Ser	Ile
1395					1400					1405					
Val	Phe	Lys	Gly	Ala	Val	Ser	Leu	Gly	Gly	Gln	Phe	Asn	Leu	Ser	Asn
1410					1415					1420					
Asn	Ser	Ser	Leu	Asp	Phe	Gln	Gly	Ser	Ser	Ala	Ile	Thr	Ser	Asn	Thr
425	1430					1435					1440				
Ala	Phe	Asn	Phe	Tyr	Asp	Asn	Ala	Phe	Ser	Gln	Ser	Pro	Ile	Thr	Phe
1445					1450					1455					
His	Gln	Ala	Leu	Asp	Ile	Lys	Ala	Pro	Leu	Ser	Leu	Gly	Gly	Asn	Leu
1460					1465					1470					
Leu	Asn	Pro	Asn	Asn	Ser	Ser	Val	Leu	Asp	Leu	Lys	Asn	Ser	Gln	Leu
1475					1480					1485					
Val	Phe	Gly	Asp	Gln	Gly	Ser	Leu	Asn	Ile	Ala	Asn	Ile	Asp	Leu	Leu
1490					1495					1500					
Ser	Asp	Leu	Asn	Asp	Asn	Lys	Asn	Arg	Val	Tyr	Asn	Ile	Ile	Gln	Ala
505	1510					1515					1520				
Asp	Met	Asn	Ser	Asn	Trp	Tyr	Glu	Arg	Ile	Ser	Phe	Phe	Gly	Met	His
1525					1530					1535					
Ile	Asn	Asp	Gly	Ile	Tyr	Asp	Ala	Lys	Asn	Gln	Thr	Tyr	Ser	Phe	Thr
1540					1545					1550					
Asn	Pro	Leu	Asn	Asn	Ala	Leu	Lys	Ile	Thr	Glu	Ser	Phe	Lys	Asp	Asn
1555					1560					1565					
Gln	Leu	Ser	Val	Thr	Leu	Ser	Gln	Ile	Pro	Gly	Ile	Lys	Asn	Thr	Leu
1570					1575					1580					
Tyr	Asn	Ile	Gly	Ser	Glu	Ile	Phe	Asn	Tyr	Gln	Lys	Val	Tyr	Asn	Asn
585	1590					1595					1600				
Ala	Asn	Gly	Val	Tyr	Ser	Tyr	Ser	Asp	Asp	Ala	Gln	Gly	Val	Phe	Tyr
1605					1610					1615					
Leu	Thr	Ser	Asn	Val	Lys	Gly	Tyr	Tyr	Asn	Pro	Asn	Gln	Ser	Tyr	Gln
1620					1625					1630					
Ala	Ser	Gly	Ser	Asn	Asn	Thr	Thr	Lys	Asn	Asn	Asn	Leu	Thr	Ser	Glu
1635					1640					1645					
Ser	Ser	Ile	Ile	Ser	Gln	Thr	Tyr	Asn	Ala	Gln	Gly	Asn	Pro	Ile	Ser
1650					1655					1660					
Ala	Leu	His	Ile	Tyr	Asn	Lys	Gly	Tyr	Asn	Phe	Asn	Asn	Ile	Lys	Ala
665	1670					1675					1680				
Leu	Gly	Gln	Met	Ala	Leu	Lys	Leu	Tyr	Pro	Glu	Ile	Lys	Lys	Val	Leu
1685					1690					1695					
Gly	Asn	Asp	Phe	Ser	Pro	Ser	Ser	Leu	Asn	Ala	Leu	Asn	Ser	Asn	Ala

1715					1720					1725					
Asn	Glu	Leu	Ile	Asp	Asn	Ala	Asn	Asn	Ser	Val	Val	Gln	Asn	Phe	Asn
1730					1735					1740					
Asn	Gly	Thr	Leu	Ile	Val	Gly	Ala	Thr	Gln	Ile	Gly	Gln	Thr	Asp	Thr
745					1750				1755				1760		
Asn	Ser	Ala	Val	Val	Phe	Gly	Gly	Leu	Gly	Tyr	Gln	Thr	Pro	Cys	Asp
1765					1770					1775					
Tyr	Thr	Asp	Ile	Val	Cys	Gln	Lys	Phe	Arg	Gly	Thr	Tyr	Leu	Gly	Gln
1780					1785					1790					
Leu	Leu	Glu	Ser	Ser	Ser	Ala	Asp	Leu	Gly	Tyr	Ile	Asp	Thr	Thr	Phe
1795					1800					1805					
Asn	Ala	Lys	Glu	Ile	Tyr	Leu	Thr	Gly	Thr	Leu	Gly	Ser	Gly	Asn	Ala
1810					1815					1820					
Trp	Gly	Thr	Gly	Gly	Ser	Ala	Ser	Val	Thr	Phe	Asn	Ser	Gln	Thr	Ser
825					1830				1835				1840		
Leu	Ile	Leu	Asn	Gln	Ala	Asn	Ile	Val	Ser	Ser	Gln	Thr	Asp	Gly	Ile
1845					1850					1855					
Phe	Ser	Met	Leu	Gly	Gln	Glu	Gly	Ile	Asn	Lys	Val	Phe	Asn	Gln	Ala
1860					1865					1870					
Gly	Leu	Ala	Asn	Ile	Leu	Gly	Glu	Val	Ala	Val	Gln	Ser	Ile	Asn	Lys
1875					1880					1885					
Ala	Gly	Gly	Leu	Gly	Asn	Leu	Ile	Val	Asn	Thr	Leu	Gly	Ser	Asn	Ser
1890					1895					1900					
Val	Ile	Gly	Gly	Tyr	Leu	Thr	Pro	Glu	Gln	Lys	Asn	Gln	Thr	Leu	Ser
905					1910				1915				1920		
Gln	Leu	Leu	Gly	Gln	Asn	Asn	Phe	Asp	Asn	Leu	Met	Asn	Asp	Ser	Gly
1925					1930					1935					
Leu	Asn	Thr	Ala	Ile	Lys	Asp	Leu	Ile	Arg	Gln	Lys	Leu	Gly	Phe	Trp
1940					1945					1950					
Thr	Gly	Leu	Val	Gly	Gly	Leu	Ala	Gly	Leu	Gly	Gly	Ile	Asp	Leu	Gln
1955					1960					1965					
Asn	Pro	Glu	Lys	Leu	Ile	Gly	Ser	Met	Ser	Ile	Asn	Asp	Leu	Leu	Ser
1970					1975					1980					
Lys	Lys	Gly	Leu	Phe	Asn	Gln	Ile	Thr	Gly	Phe	Ile	Ser	Ala	Asn	Asp
985					1990				1995				2000		
Ile	Gly	Gln	Val	Ile	Ser	Val	Met	Leu	Gln	Asp	Ile	Val	Lys	Pro	Ser
2005					2010					2015					
Asn	Ala	Leu	Lys	Asn	Asp	Val	Ala	Ala	Leu	Gly	Lys	Gln	Met	Ile	Gly
2020					2025					2030					
Glu	Phe	Leu	Gly	Gln	Asp	Thr	Leu	Asn	Ser	Leu	Glu	Ser	Leu	Leu	Gln
2035					2040					2045					
Asn	Gln	Gln	Ile	Lys	Ser	Val	Leu	Asp	Lys	Val	Leu	Ala	Ala	Lys	Gly
2050					2055					2060					
Leu	Gly	Pro	Ile	Tyr	Glu	Gln	Gly	Leu	Gly	Asp	Leu	Ile	Pro	Asn	Leu
065					2070				2075				2080		
Gly	Lys	Lys	Gly	Leu	Phe	Ala	Pro	Tyr	Gly	Leu	Ser	Gln	Val	Trp	Gln
2085					2090					2095					
Lys	Gly	Asp	Phe	Ser	Phe	Asn	Ala	Gln	Gly	Asn	Val	Phe	Val	Gln	Asn
2100					2105					2110					
Ser	Thr	Phe	Ser	Asn	Ala	Asn	Gly	Gly	Thr	Leu	Ser	Phe	Asn	Ala	Gly
2115					2120					2125					
Asn	Ser	Leu	Ile	Phe	Ala	Gly	Asn	Asn	His	Ile	Ala	Phe	Thr	Asn	His
2130					2135					2140					
Ala	Gly	Thr	Leu	Gln	Leu	Leu	Ser	Asp	Gln	Val	Ser	Asn	Ile	Asn	Ile
145					2150				2155				2160		
Thr	Thr	Leu	Asn	Ala</											

2180							2185					2190				
Gln	Gln	Ser	Asp	Pro	Thr	Thr	Ala	Asn	Ile	Ala	Asn	Pro	Cys	Ala	Leu	
2195							2200					2205				
Ser	Ala	Gln	Ser	Thr	Asn	Gly	Ala	Ser	Ser	Asn	Asn	Ala	Ser	Asn	Asn	
2210							2215					2220				
Ala	Pro	Ile	Ala	Leu	Ser	Asn	Asn	Asp	Glu	Ser	Leu	Met	Val	Ala	Ala	
225	2230							2235					2240			
Asn	Asp	Phe	Asn	Phe	Ser	Gly	Asn	Ile	Tyr	Ala	Asn	Gly	Val	Val	Asp	
2245							2250					2255				
Phe	Ser	Lys	Ile	Lys	Gly	Ser	Ala	Asn	Ile	Lys	Asn	Leu	Tyr	Leu	Tyr	
2260							2265					2270				
Asn	Asn	Ala	Gln	Phe	Gln	Ala	Asn	Asn	Leu	Thr	Ile	Ser	Asn	Gln	Ala	
2275							2280					2285				
Val	Leu	Glu	Lys	Asn	Ala	Ser	Phe	Val	Thr	Asn	Asn	Leu	Asn	Ile	Gln	
2290							2295					2300				
Gly	Ala	Phe	Asn	Asn	Asn	Ala	Thr	Gln	Lys	Ile	Glu	Val	Leu	Gln	Asn	
305	2310							2315					2320			
Leu	Val	Ile	Ala	Ser	Asn	Ala	Ser	Leu	Ser	Thr	Gly	Ile	Tyr	Gly	Leu	
2325							2330					2335				
Glu	Val	Gly	Gly	Ala	Leu	Asn	Asn	Ser	Gly	Ala	Ile	His	Phe	Asn	Leu	
2340							2345					2350				
Glu	Asn	Thr	Gln	Thr	Pro	Thr	Pro	Leu	Ile	Gln	Ala	Glu	Gly	Ile	Ile	
2355							2360					2365				
Asn	Leu	Asn	Thr	Thr	Gln	Thr	Pro	Phe	Met	Asn	Val	Asn	Asn	Ser	Met	
2370							2375					2380				
Ala	Asn	Asn	Thr	Thr	Tyr	Thr	Leu	Leu	Lys	Ser	Ser	Arg	Tyr	Ile	Asp	
385	2390							2395					2400			
Tyr	Asn	Ile	Asn	Pro	Asn	Ser	Leu	Gln	Ser	Tyr	Leu	Asn	Leu	Tyr	Thr	
2405							2410					2415				
Leu	Ile	Asn	Ile	Asn	Gly	Asn	His	Ile	Glu	Glu	Lys	Asn	Gly	Ala	Leu	
2420							2425					2430				
Thr	Tyr	Leu	Gly	Gln	Arg	Val	Leu	Gln	Asp	Lys	Gly	Leu	Leu	Leu		
2435							2440					2445				
Ser	Val	Ala	Leu	Pro	Asn	Ser	Asn	Asn	Ala	Ser	Gln	Asn	Asn	Ile	Leu	
2450							2455					2460				
Ser	Leu	Ser	Val	Leu	Tyr	Asn	Gln	Val	Lys	Met	Ser	Cys	Gly	Asp	Lys	
465	2470							2475					2480			
Ala	Met	Asp	Phe	Thr	Pro	Pro	Thr	Leu	Gln	Asp	Tyr	Ile	Val	Gly	Ile	
2485							2490					2495				
Gln	Gly	Gln	Ser	Ala	Leu	Asn	Gln	Ile	Glu	Ala	Val	Gly	Gly	Asn	Ala	
2500							2505					2510				
Ile	Lys	Trp	Leu	Ser	Thr	Leu	Met	Met	Glu	Thr	Lys	Glu	Asn	Pro	Phe	
2515							2520					2525				
Phe	Ala	Pro	Ile	Tyr	Leu	Lys	Asn	His	Ser	Leu	Asn	Glu	Ile	Leu	Gly	
2530							2535					2540				
Val	Thr	Lys	Asp	Leu	Gln	Asn	Thr	Ala	Ser	Leu	Ile	Ser	Asn	Pro	Asn	
545	2550							2555					2560			
Phe	Arg	Asp	Asn	Ala	Thr	Asn	Leu	Leu	Glu	Leu	Ala	Ser	Tyr	Thr	Gln	
2565							2570					2575				
Gln	Thr	Ser	Arg	Leu	Thr	Lys	Leu	Ser	Asp	Phe	Arg	Ser	Arg	Glu	Gly	
2580							2585					2590				
Glu	Ser	Asp	Phe	Ser	Leu	Leu	Glu	Leu	Lys	Asn	Lys	Arg	Phe	Ser	Asp	
2595							2600					2605				
Pro	Asn	Pro	Glu	Val	Phe	Val	Lys	Tyr	Ser	Gln	Leu	Ser	Lys	His	Pro	
2610							2615					2620				
Asn	Asn	Leu	Trp	Val	Gln	Gly	Val	Gly	Gly	Ala						

AGA CTC CAC ACT AAG AAT GAG GTG TTG GAA AAT TGT CGC AAT ATC GCT	148
Arg Leu His Thr Lys Asn Glu Val Leu Glu Asn Cys Arg Asn Ile Ala	
25 30 35	
AAG GTG ATT GGT GGG GTC AAA CAG GGT TTG CCT GGG TTG GAT CTG ATT	196
Lys Val Ile Gly Gly Val Lys Gln Gly Leu Pro Gly Leu Asp Leu Ile	
40 45 50 55	
ATT TTC CCT GAA TAC AGC ACG CAT GGG ATT ATG TAT GAC AGA CAA GAA	244
Ile Phe Pro Glu Tyr Ser Thr His Gly Ile Met Tyr Asp Arg Gln Glu	
60 65 70	
ATG TTT GAT ACA GCC GCA AGC GTT CCT GGA GAA GAA ACC GCG ATC TTT	292
Met Phe Asp Thr Ala Ala Ser Val Pro Gly Glu Glu Thr Ala Ile Phe	
75 80 85	
GCT GAA GCT TGT AAG AAA AAC AAG GTT TGG GGA GTG TTC TCT TTG ACA	340
Ala Glu Ala Cys Lys Lys Asn Lys Val Trp Gly Val Phe Ser Leu Thr	
90 95 100	
GGG GAA AAA CAC GAG CAA GCC AAA AAG AAT CCC TAT AAC ACT TTG ATT	388
Gly Glu Lys His Glu Gln Ala Lys Lys Asn Pro Tyr Asn Thr Leu Ile	
105 110 115	
CTT GTC AAT GAT AAG GGT GAG ATC GTG CAA AAA TAC CGC AAA ATC TTG	436
Leu Val Asn Asp Lys Gly Glu Ile Val Gln Lys Tyr Arg Lys Ile Leu	
120 125 130 135	
CCT TGG TGC CCT ATT GAA TGT TGG TAT CCT GGG GAT AAA ACT TAT GTG	484
Pro Trp Cys Pro Ile Glu Cys Trp Tyr Pro Gly Asp Lys Thr Tyr Val	
140 145 150	
GTT GAT GGG CCT AAG GGC TTG AAA GTT TCT TTG ATT ATT TGC GAT GAT	532
Val Asp Gly Pro Lys Gly Leu Lys Val Ser Leu Ile Ile Cys Asp Asp	
155 160 165	
GGA AAC TAC CCT GAA ATT TGG CGC GAT TGC GCG ATG CGT GGG GCA GAA	580
Gly Asn Tyr Pro Glu Ile Trp Arg Asp Cys Ala Met Arg Gly Ala Glu	
170 175 180	
CTC ATT GTG CGC TGT CAA GGT TAC ATG TAT CCG GCT AAG GAG CAA CAA	628
Leu Ile Val Arg Cys Gln Gly Tyr Met Tyr Pro Ala Lys Glu Gln Gln	
185 190 195	
ATT GCA ATA GTA AAA GCT ATG GCG TGG GCC AAT CAA TGT TAT GTA GCG	676
Ile Ala Ile Val Lys Ala Met Ala Trp Ala Asn Gln Cys Tyr Val Ala	
200 205 210 215	
GTA GCG AAT GCG ACC GGT TTT GAT GGG GTG TAT TCC TAT TTT GGG CAT	724
Val Ala Asn Ala Thr Gly Phe Asp Gly Val Tyr Ser Tyr Phe Gly His	
220 225 230	
TCT AGC ATT ATT GGT TTT GAC GGG CAT ACT TTG GGC GAA TGC GGG GAA	772
Ser Ser Ile Ile Gly Phe Asp Gly His Thr Leu Gly Glu Cys Gly Glu	
235 240 245	
GAA GAA AAT GGT CTT CAA TAC GCT CAA CTT TCT GTG CAA CAA ATC CGT	820
Glu Glu Asn Gly Leu Gln Tyr Ala Gln Leu Ser Val Gln Gln Ile Arg	

250	255	260	
GAT GCG AGA AAA TAC GAC CAA AGC CAA AAC CAA CTC TTC AAA CTC TTG			868
Asp Ala Arg Lys Tyr Asp Gln Ser Gln Asn Gln Leu Phe Lys Leu Leu			
265	270	275	
CAC AGA GGT TAT AGT GGG GTT TTT GCT AGT GGC GAT GGG GAT AAG GGT			916
His Arg Gly Tyr Ser Gly Val Phe Ala Ser Gly Asp Gly Asp Lys Gly			
280	285	290	295
GTG GCG GAA TGC CCT TTT GAG TTC TAT AAA ACT TGG GTG AAT GAC CCC			964
Val Ala Glu Cys Pro Phe Glu Phe Tyr Lys Thr Trp Val Asn Asp Pro			
300	305	310	
AAA AAA GCT CAA GAA AAT GTA GAA AAA ATC ACC CGC CCA AGC GTG GGT			1012
Lys Lys Ala Gln Glu Asn Val Glu Lys Ile Thr Arg Pro Ser Val Gly			
315	320	325	
GTG GCC GCT TGT CCT GTG GGC GAT TTG CCC ACG AAA TAAAGGGCAA AAGGAG			1064
Val Ala Ala Cys Pro Val Gly Asp Leu Pro Thr Lys			
330	335		
GAGGGGGGGG G			1075

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

Met	Arg	His	Gly	Asp	Ile	Ser	Ser	Ser	Pro	Asp	Thr	Val	Gly	Val	Ala
1			5						10					15	
Val	Val	Asn	Tyr	Lys	Met	Pro	Arg	Leu	His	Thr	Lys	Asn	Glu	Val	Leu
		20						25				30			
Glu	Asn	Cys	Arg	Asn	Ile	Ala	Lys	Val	Ile	Gly	Gly	Val	Lys	Gln	Gly
		35					40					45			
Leu	Pro	Gly	Leu	Asp	Leu	Ile	Ile	Phe	Pro	Glu	Tyr	Ser	Thr	His	Gly
	50					55				60					
Ile	Met	Tyr	Asp	Arg	Gln	Glu	Met	Phe	Asp	Thr	Ala	Ala	Ser	Val	Pro
65					70				75					80	
Gly	Glu	Glu	Thr	Ala	Ile	Phe	Ala	Glu	Ala	Cys	Lys	Lys	Asn	Lys	Val
			85						90					95	
Trp	Gly	Val	Phe	Ser	Leu	Thr	Gly	Glu	Lys	His	Glu	Gln	Ala	Lys	Lys
			100				105						110		
Asn	Pro	Tyr	Asn	Thr	Leu	Ile	Leu	Val	Asn	Asp	Lys	Gly	Glu	Ile	Val
		115					120					125			
Gln	Lys	Tyr	Arg	Lys	Ile	Leu	Pro	Trp	Cys	Pro	Ile	Glu	Cys	Trp	Tyr
	130					135					140				
Pro	Gly	Asp	Lys	Thr	Tyr	Val	Val	Asp	Gly	Pro	Lys	Gly	Leu	Lys	Val
145					150					155					160
Ser	Leu	Ile	Ile	Cys	Asp	Asp	Gly	Asn	Tyr	Pro	Glu	Ile	Trp	Arg	Asp
			165						170					175	

Cys Ala Met Arg Gly Ala Glu Leu Ile Val Arg Cys Gln Gly Tyr Met
180 185 190
Tyr Pro Ala Lys Glu Gln Gln Ile Ala Ile Val Lys Ala Met Ala Trp
195 200 205
Ala Asn Gln Cys Tyr Val Ala Val Ala Asn Ala Thr Gly Phe Asp Gly
210 215 220
Val Tyr Ser Tyr Phe Gly His Ser Ser Ile Ile Gly Phe Asp Gly His
225 230 235 240
Thr Leu Gly Glu Cys Gly Glu Glu Glu Asn Gly Leu Gln Tyr Ala Gln
245 250 255
Leu Ser Val Gln Gln Ile Arg Asp Ala Arg Lys Tyr Asp Gln Ser Gln
260 265 270
Asn Gln Leu Phe Lys Leu Leu His Arg Gly Tyr Ser Gly Val Phe Ala
275 280 285
Ser Gly Asp Gly Asp Lys Gly Val Ala Glu Cys Pro Phe Glu Phe Tyr
290 295 300
Lys Thr Trp Val Asn Asp Pro Lys Lys Ala Gln Glu Asn Val Glu Lys
305 310 315 320
Ile Thr Arg Pro Ser Val Gly Val Ala Ala Cys Pro Val Gly Asp Leu
325 330 335
Pro Thr Lys

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...1686
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

ATCTCTATCC TTTATAGAAT TTGTTGTGGA GACTGGCTT ATG AAT AAT GTT TTT	54
Met Asn Asn Val Phe	
1 5	
GTT AAG GGT TTG TTT TTT TTT CTT TTA TTG TTT GGG TTT TTT TTG AAA	102
Val Lys Gly Leu Phe Phe Phe Leu Leu Leu Phe Gly Phe Phe Leu Lys	
10 15 20	
GCT TCA GAA AGC CCA AAC GCT ACT CTT AAT CCA TCT AAA GAA AAT GTT	150
Ala Ser Glu Ser Pro Asn Ala Thr Leu Asn Pro Ser Lys Glu Asn Val	
25 30 35	
TCT GTT GAA GAG CAA AAG CGT TTT GGA GGC GTT TTA GTT TTT GCA AGA	198
Ser Val Glu Glu Gln Lys Arg Phe Gly Gly Val Leu Val Phe Ala Arg	
40 45 50	
GGC GCT GAT GGC TCG AGC ATG GAT CCT GCT TTA GTG ACT GAT GGC GAA	246

Gly	Ala	Asp	Gly	Ser	Ser	Met	Asp	Pro	Ala	Leu	Val	Thr	Asp	Gly	Glu	
55						60					65					
AGC	TAT	GTA	GCA	ACG	GGC	AAT	ATT	TAT	GAC	ACG	CTC	GTG	CAA	TTC	AGA	294
Ser	Tyr	Val	Ala	Thr	Gly	Asn	Ile	Tyr	Asp	Thr	Leu	Val	Gln	Phe	Arg	
70					75					80					85	
TAC	GGC	ACC	ACA	GAA	GTT	GAA	CCC	GCC	TTA	GCG	ACA	AGC	TGG	GAC	ATA	342
Tyr	Gly	Thr	Thr	Glu	Val	Glu	Pro	Ala	Leu	Ala	Thr	Ser	Trp	Asp	Ile	
				90					95					100		
TCC	CCA	GAT	GGT	CTT	GTA	TAT	ACC	TTT	CAT	TTA	CGC	AAA	GGG	GTT	TAT	390
Ser	Pro	Asp	Gly	Leu	Val	Tyr	Thr	Phe	His	Leu	Arg	Lys	Gly	Val	Tyr	
			105					110					115			
TTC	CAC	CAA	ACG	AAG	TAT	TGG	AAT	AAA	AAA	GTA	GAG	TTT	AGC	GCT	AAA	438
Phe	His	Gln	Thr	Lys	Tyr	Trp	Asn	Lys	Lys	Val	Glu	Phe	Ser	Ala	Lys	
		120					125					130				
GAT	GTG	CTG	TTT	TCG	TTT	GAA	CGC	CAG	ATG	GAT	AAA	GCT	AAA	CGA	TAT	486
Asp	Val	Leu	Phe	Ser	Phe	Glu	Arg	Gln	Met	Asp	Lys	Ala	Lys	Arg	Tyr	
	135					140					145					
TAT	AGC	CCG	GGG	GCT	AAA	AGC	TAT	AAG	TAT	TGG	GAA	GGC	ATG	GGC	ATG	534
Tyr	Ser	Pro	Gly	Ala	Lys	Ser	Tyr	Lys	Tyr	Trp	Glu	Gly	Met	Gly	Met	
150					155					160					165	
TCT	CAT	ATT	ATT	AAG	AGC	ATT	GAA	GCT	TTA	GAT	GAC	TAT	ACC	ATT	AGA	582
Ser	His	Ile	Ile	Lys	Ser	Ile	Glu	Ala	Leu	Asp	Asp	Tyr	Thr	Ile	Arg	
				170					175					180		
TTC	ACA	CTT	AAT	GGG	CCA	GAA	GCC	CCG	TTT	TTA	GCG	AAT	TTG	GGC	ATG	630
Phe	Thr	Leu	Asn	Gly	Pro	Glu	Ala	Pro	Phe	Leu	Ala	Asn	Leu	Gly	Met	
			185					190					195			
GAC	TTT	TTG	AGC	ATT	TTG	AGT	AAG	GAT	TAC	GCT	GAT	TAC	CTG	GCT	CAA	678
Asp	Phe	Leu	Ser	Ile	Leu	Ser	Lys	Asp	Tyr	Ala	Asp	Tyr	Leu	Ala	Gln	
		200					205					210				
AAT	AAT	AAA	AAA	GAC	GAG	TTG	GCT	AAA	AAA	CCT	ATT	GGG	ACA	GGG	CCT	726
Asn	Asn	Lys	Lys	Asp	Glu	Leu	Ala	Lys	Lys	Pro	Ile	Gly	Thr	Gly	Pro	
	215					220					225					
TTC	AAA	TTC	TTT	TTG	TGG	AAT	AAA	GAT	GAA	AAA	ATC	ATT	CTT	TTA	AAA	774
Phe	Lys	Phe	Phe	Leu	Trp	Asn	Lys	Asp	Glu	Lys	Ile	Ile	Leu	Leu	Lys	
230					235					240					245	
AAT	CAA	GAT	TAT	TGG	GGG	CCT	AAA	GCG	TAT	TTG	GAT	AAG	GTG	GTG	GTG	822
Asn	Gln	Asp	Tyr	Trp	Gly	Pro	Lys	Ala	Tyr	Leu	Asp	Lys	Val	Val	Val	
				250					255					260		
CGC	ACC	ATT	CCT	AAT	TCT	TCC	ACT	CGC	GCT	TTA	GCG	TTG	CGC	ACC	GGC	870
Arg	Thr	Ile	Pro	Asn	Ser	Ser	Thr	Arg	Ala	Leu	Ala	Leu	Arg	Thr	Gly	
			265					270					275			
GAA	ATC	ATG	CTC	ATG	ACT	GGG	CCT	AAT	CTC	AAT	GAA	GTG	GAG	CAA	TTA	918
Glu	Ile	Met	Leu	Met	Thr	Gly	Pro	Asn	Leu	Asn	Glu	Val	Glu	Gln	Leu	
		280					285					290				

GAA Glu	AAA Lys	GTC Val	CCT Pro	AAT Asn	ATC Ile	GTG Val	GTG Val	GAC Asp	AAA Lys	AGT Ser	GCT Ala	GGG Gly	TTG Leu	TTG Leu	GCG Ala	966
295300305																
AGT Ser	TGG Trp	CTT Leu	TCG Ser	TTG Leu	AAC Asn	ACG Thr	CAA Gln	AAA Lys	AAG Lys	TAT Tyr	TTT Phe	GAC Asp	AAC Asn	CCT Pro	TTG Leu	1014
310315320325																
GTG Val	CGT Arg	TTG Leu	GCT Ala	ATC Ile	AAT Asn	CAT His	GCG Ala	ATC Ile	AAT Asn	GCA Ala	GAT Asp	GAT Asp	TAC Tyr	ATC Ile	AAA Lys	1062
330335340																
GTG Val	CTT Leu	TAT Tyr	GAA Glu	GGC Gly	TTT Phe	GCT Ala	CAA Gln	AAA Lys	ATG Met	GTC Val	AAT Asn	CCT Pro	TTC Phe	CCG Pro	CCC Pro	1110
345350355																
ACC Thr	ATA Ile	TGG Trp	GGT Gly	TAT Tyr	AAC Asn	TAC Tyr	AAT Asn	ATC Ile	AAA Lys	CCC Pro	TAT Tyr	GAA Glu	TAC Tyr	GAT Asp	TTG Leu	1158
360365370																
AAA Lys	AAG Lys	GCT Ala	AAG Lys	GAG Glu	TTG Leu	TTG Leu	AAA Lys	CAA Gln	GCG Ala	GGC Gly	TAT Tyr	CCT Pro	AAC Asn	GGC Gly	TTT Phe	1206
375380385																
AAA Lys	ACC Thr	ACT Thr	ATT Ile	TTT Phe	ACC Thr	ACT Thr	GCC Ala	ACT Thr	CGT Arg	AAC Asn	CCA Pro	AAA Lys	GGA Gly	GCG Ala	GTG Val	1254
390395400405																
TTC Phe	ATA Ile	CAG Gln	GCG Ala	AGC Ser	CTG Leu	GCT Ala	AAA Lys	ATT Ile	GGC Gly	ATT Ile	GAT Asp	GTG Val	AAA Lys	ATT Ile	GAA Glu	1302
410415420																
GTG Val	TAT Tyr	GAG Glu	TGG Trp	GGG Gly	GCT Ala	TAT Tyr	TTG Leu	AAA Lys	AGA Arg	ACG Thr	GGT Gly	CTG Leu	GGC Gly	GAA Glu	CAT His	1350
425430435																
GAA Glu	ATG Met	GCG Ala	TTT Phe	TCA Ser	GGC Gly	TGG Trp	ATG Met	GCA Ala	GAC Asp	ATT Ile	GCG Ala	GAT Asp	CCG Pro	GAT Asp	AAT Asn	1398
440445450																
TTC Phe	TTA Leu	TAC Tyr	ACC Thr	TTA Leu	TGG Trp	AGC Ser	GAG Glu	CAA Gln	GCC Ala	GCC Ala	TCA Ser	GCT Ala	ATA Ile	CCC Pro	ACT Thr	1446
455460465																
CAA Gln	AAC Asn	CAT His	TCC Ser	TTT Phe	TAT Tyr	AAA Lys	AAT Asn	AAG Lys	GAG Glu	TTT Phe	TCC Ser	AAT Asn	CTG Leu	CTC Leu	ATA Ile	1494
470475480485																
AAG Lys	GCT Ala	AAA Lys	CGC Arg	GTT Val	TCG Ser	GAT Asp	CAA Gln	AAA Lys	GAG Glu	AGG Arg	GAA Glu	GCC Ala	CTT Leu	TAT Tyr	TTA Leu	1542
490495500																
AAG Lys	GCA Ala	CAA Gln	GAA Glu	ATT Ile	ATC Ile	CAT His	AAA Lys	GAC Asp	GCG Ala	CCT Pro	TAT Tyr	GTG Val	CCT Pro	TTA Leu	GCC Ala	1590
505510515																
TAT Tyr	CCT Pro	TAT Tyr	TCG Ser	GTG Val	GTG Val	CCG Pro	CAT His	TTG Leu	TCT Ser	AAA Lys	GTT Val	AAG Lys	GGT Gly	TAT Tyr	AAA Lys	1638

Ala Gly Leu Leu Ala Ser Trp Leu Ser Leu Asn Thr Gln Lys Lys Tyr
 305 310 315 320
 Phe Asp Asn Pro Leu Val Arg Leu Ala Ile Asn His Ala Ile Asn Ala
 325 330 335
 Asp Asp Tyr Ile Lys Val Leu Tyr Glu Gly Phe Ala Gln Lys Met Val
 340 345 350
 Asn Pro Phe Pro Pro Thr Ile Trp Gly Tyr Asn Tyr Asn Ile Lys Pro
 355 360 365
 Tyr Glu Tyr Asp Leu Lys Lys Ala Lys Glu Leu Leu Lys Gln Ala Gly
 370 375 380
 Tyr Pro Asn Gly Phe Lys Thr Thr Ile Phe Thr Thr Ala Thr Arg Asn
 385 390 395 400
 Pro Lys Gly Ala Val Phe Ile Gln Ala Ser Leu Ala Lys Ile Gly Ile
 405 410 415
 Asp Val Lys Ile Glu Val Tyr Glu Trp Gly Ala Tyr Leu Lys Arg Thr
 420 425 430
 Gly Leu Gly Glu His Glu Met Ala Phe Ser Gly Trp Met Ala Asp Ile
 435 440 445
 Ala Asp Pro Asp Asn Phe Leu Tyr Thr Leu Trp Ser Glu Gln Ala Ala
 450 455 460
 Ser Ala Ile Pro Thr Gln Asn His Ser Phe Tyr Lys Asn Lys Glu Phe
 465 470 475 480
 Ser Asn Leu Leu Ile Lys Ala Lys Arg Val Ser Asp Gln Lys Glu Arg
 485 490 495
 Glu Ala Leu Tyr Leu Lys Ala Gln Glu Ile Ile His Lys Asp Ala Pro
 500 505 510
 Tyr Val Pro Leu Ala Tyr Pro Tyr Ser Val Val Pro His Leu Ser Lys
 515 520 525
 Val Lys Gly Tyr Lys Thr Thr Gly Val Ser Val Asn Arg Phe Phe Lys
 530 535 540
 Val Tyr Leu Glu Lys
 545

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...1050
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

GCGTGAATCG CTTCTTTAAG GTGTATTTAG AAAAATAAAA GGGGTTGC ATG CTG AGT 57
 Met Leu Ser
 1
 TTT ATC ATT AAG CGT ATT TTG TGG GCG ATC CCC ACG CTG TTT GGA GTG 105
 Phe Ile Ile Lys Arg Ile Leu Trp Ala Ile Pro Thr Leu Phe Gly Val
 5 10 15

AGT Ser 20	ATC Ile	ATT Ile	GTG Val	TTT Phe	ATG Met 25	ATG Met	GTG Val	CAT His	TTA Leu	GTG Val 30	CCA Pro	GGA Gly	GAT Asp	CCG Pro	GCA Ala 35	153
TTA Leu	GTG Val	ATT Ile	TTA Leu	GGT Gly 40	GAA Glu	AAG Lys	GCC Ala	AAT Asn	CAA Gln 45	GCC Ala	GCT Ala	ATT Ile	GAT Asp	GCT Ala 50	TTA Leu	201
AGA Arg	GAG Glu	CAA Gln	TTT Phe 55	GGA Gly	TTG Leu	AAT Asn	AAG Lys	CCC Pro 60	TTG Leu	ATA Ile	GAG Glu	CAG Gln	TAT Tyr 65	TTT Phe	TTC Phe	249
TTT Phe	ATC Ile	AAT Asn 70	AAT Asn	GTG Val	TTG Leu	CAT His	GGC Gly 75	AAT Asn	TTT Phe	GGC Gly	ACT Thr	TCT Ser 80	ATC Ile	ATG Met	ACC Thr	297
GGT Gly	GAG Glu 85	CCT Pro	GTG Val	ATG Met	CAT His 90	GAG Glu	TTT Phe	TGG Trp	CAA Gln	CGC Arg	TTC Phe 95	CCG Pro	GCC Ala	ACG Thr	GTG Val	345
GAA Glu 100	TTA Leu	GCT Ala	TTG Leu	ATC Ile	GCT Ala 105	CTG Leu	TTT Phe	ATG Met	GCT Ala 110	CTT Leu	GTT Val	TTG Leu	GGT Gly	ATT Ile 115	AGC Ser	393
GTT Val	GGC Gly	GTG Val	TTA Leu	GCT Ala 120	GCG Ala	ATC Ile	AAA Lys	CGC Arg	TAT Tyr 125	AGC Ser	GTG Val	TTT Phe	GAT Asp	TAT Tyr 130	TCC Ser	441
AGC Ser	ATG Met	ACT Thr	TTT Phe 135	GCT Ala	TTA Leu	GCC Ala	GGG Gly	ATT Ile 140	TCT Ser	ATG Met	CCG Pro	GTG Val	TTT Phe 145	TGG Trp	CTA Leu	489
GGG Gly	CTC Leu	ATG Met 150	CTG Leu	ATT Ile	TAT Tyr	ATC Ile	TTT Phe 155	AGC Ser	GTG Val	CAA Gln	TTG Leu	GGG Gly 160	TGG Trp	TTG Leu	CCT Pro	537
GTT Val	TTT Phe 165	GGG Gly	CGT Arg	TTG Leu	AGC Ser	GAT Asp 170	GTG Val	TAT Tyr	TAT Tyr	TTA Leu	GAT Asp 175	GGC Gly	CCC Pro	ACA Thr	GGT Gly	585
CTT Leu 180	TAT Tyr	TTG Leu	ATA Ile	GAC Asp	AGC Ser 185	CTG Leu	ATC Ile	GCA Ala	AGG Arg 190	GAT Asp	TAT Tyr	GGG Gly	GCG Ala	TTT Phe	ATG Met 195	633
GAT Asp	ACG Thr	ATC Ile	AAG Lys	CAC His 200	TTG Leu	ATT Ile	TTG Leu	CCT Pro	AGC Ser 205	ATT Ile	GTG Val	TTA Leu	GCC Ala	ACG Thr 210	GTT Val	681
TCT Ser	ACC Thr	GCT Ala	GTT Val 215	ATT Ile	GCC Ala	AGA Arg	ATG Met	ACT Thr 220	CGC Arg	GCG Ala	AGC Ser	ATG Met	GCA Ala 225	GAA Glu	GTG Val	729
TCT Ser	AAA Lys	GAA Glu 230	GAT Asp	TAT Tyr	GTG Val	CGT Arg	ACC Thr 235	GCT Ala	AAA Lys	GCT Ala	AAG Lys	GGG Gly 240	TGT Cys	AGC Ser	TCC Ser	777
TTT Phe	AGG Arg	GTG Val	ATT Ile	TTT Phe	GTG Val	CAC His	ACT Thr	TTG Leu	CGT Arg	AAT Asn	GCT Ala	TTA Leu	ATC Ile	CCT Pro	GTA Val	825

245	250	255	
ACG ACT ATC GCA GGC TTG ATG TTG GCC GGG CTT TTA GGG GGG AGC ATG			873
Thr Thr Ile Ala Gly Leu Met Leu Ala Gly Leu Leu Gly Gly Ser Met			
260	265	270	275
ATA ACT GAA ACG GTT TTC TCA TGG CCT GGG ATT GGT AAG TGG ATT GTT			921
Ile Thr Glu Thr Val Phe Ser Trp Pro Gly Ile Gly Lys Trp Ile Val			
	280	285	290
AAT GCG CTC AAC CAG CGC GAT TTC CCG ATT ATC CAG TCC ATG TCT TTG			969
Asn Ala Leu Asn Gln Arg Asp Phe Pro Ile Ile Gln Ser Met Ser Leu			
	295	300	305
ATT ATT GCC ATG ATG TAT ATT GGG GCT AAT CTC TTA GTG GAT ATT TTA			1017
Ile Ile Ala Met Met Tyr Ile Gly Ala Asn Leu Leu Val Asp Ile Leu			
	310	315	320
TAC GCT TTT ATT GAT CCT AGA ATA AGG TTG TCA TAATGGAGTC TTTTAGAGAG			1070
Tyr Ala Phe Ile Asp Pro Arg Ile Arg Leu Ser			
	325	330	
TTTATCCAAC			1080

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

Met	Leu	Ser	Phe	Ile	Ile	Lys	Arg	Ile	Leu	Trp	Ala	Ile	Pro	Thr	Leu
1				5					10					15	
Phe	Gly	Val	Ser	Ile	Ile	Val	Phe	Met	Met	Val	His	Leu	Val	Pro	Gly
			20					25				30			
Asp	Pro	Ala	Leu	Val	Ile	Leu	Gly	Glu	Lys	Ala	Asn	Gln	Ala	Ala	Ile
		35					40				45				
Asp	Ala	Leu	Arg	Glu	Gln	Phe	Gly	Leu	Asn	Lys	Pro	Leu	Ile	Glu	Gln
	50					55				60					
Tyr	Phe	Phe	Phe	Ile	Asn	Asn	Val	Leu	His	Gly	Asn	Phe	Gly	Thr	Ser
65					70				75					80	
Ile	Met	Thr	Gly	Glu	Pro	Val	Met	His	Glu	Phe	Trp	Gln	Arg	Phe	Pro
				85					90				95		
Ala	Thr	Val	Glu	Leu	Ala	Leu	Ile	Ala	Leu	Phe	Met	Ala	Leu	Val	Leu
			100					105				110			
Gly	Ile	Ser	Val	Gly	Val	Leu	Ala	Ala	Ile	Lys	Arg	Tyr	Ser	Val	Phe
		115					120				125				
Asp	Tyr	Ser	Ser	Met	Thr	Phe	Ala	Leu	Ala	Gly	Ile	Ser	Met	Pro	Val
	130					135				140					
Phe	Trp	Leu	Gly	Leu	Met	Leu	Ile	Tyr	Ile	Phe	Ser	Val	Gln	Leu	Gly
145					150				155					160	
Trp	Leu	Pro	Val	Phe	Gly	Arg	Leu	Ser	Asp	Val	Tyr	Tyr	Leu	Asp	Gly
				165					170					175	

Pro Thr Gly Leu Tyr Leu Ile Asp Ser Leu Ile Ala Arg Asp Tyr Gly
180 185 190
Ala Phe Met Asp Thr Ile Lys His Leu Ile Leu Pro Ser Ile Val Leu
195 200 205
Ala Thr Val Ser Thr Ala Val Ile Ala Arg Met Thr Arg Ala Ser Met
210 215 220
Ala Glu Val Ser Lys Glu Asp Tyr Val Arg Thr Ala Lys Ala Lys Gly
225 230 235 240
Cys Ser Ser Phe Arg Val Ile Phe Val His Thr Leu Arg Asn Ala Leu
245 250 255
Ile Pro Val Thr Thr Ile Ala Gly Leu Met Leu Ala Gly Leu Leu Gly
260 265 270
Gly Ser Met Ile Thr Glu Thr Val Phe Ser Trp Pro Gly Ile Gly Lys
275 280 285
Trp Ile Val Asn Ala Leu Asn Gln Arg Asp Phe Pro Ile Ile Gln Ser
290 295 300
Met Ser Leu Ile Ile Ala Met Met Tyr Ile Gly Ala Asn Leu Leu Val
305 310 315 320
Asp Ile Leu Tyr Ala Phe Ile Asp Pro Arg Ile Arg Leu Ser
325 330

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 955 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 32...892
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

ATCCTAAACG CACCTCTTAA AAGGAGCTTG C ATG ATT TTA GAA GTT AAA GAT	52
Met Ile Leu Glu Val Lys Asp	
1 5	
TTA AAA ACT TAT TTT TTC ACC GAT AAG GGC GTG AAT AAA GCA GTG GAT	100
Leu Lys Thr Tyr Phe Phe Thr Asp Lys Gly Val Asn Lys Ala Val Asp	
10 15 20	
GGT GTG AGT TTT GGT TTG AAA AAG TCT CAA ACG CTC TGC ATT GTA GGG	148
Gly Val Ser Phe Gly Leu Lys Lys Ser Gln Thr Leu Cys Ile Val Gly	
25 30 35	
GAG AGC GGG AGC GGG AAA AGC ATC ACT TCG CTC TCT ATT TTA GGG TTG	196
Glu Ser Gly Ser Gly Lys Ser Ile Thr Ser Leu Ser Ile Leu Gly Leu	
40 45 50 55	
ATT GAA AAA CCG GGT CAA ATT GTG GGA GGG AGC ATT CAA TTT TTA GGG	244
Ile Glu Lys Pro Gly Gln Ile Val Gly Gly Ser Ile Gln Phe Leu Gly	
60 65 70	

CAG GAT TTG TTG CAA CTC AAA GAA AAG CAG ATG CAA AAA GAA ATT AGG Gln Asp Leu Leu Gln Leu Lys Glu Lys Gln Met Gln Lys Glu Ile Arg 75 80 85	292
GGT AAA AAA ATT GGC ATG ATC TTT CAA GAG CCT ATG ACA AGC CTA AAC Gly Lys Lys Ile Gly Met Ile Phe Gln Glu Pro Met Thr Ser Leu Asn 90 95 100	340
CCT TCC TAC ACG GTG GGG TTT CAA ATC AAT GAA GTG TTG AAA ATC CAC Pro Ser Tyr Thr Val Gly Phe Gln Ile Asn Glu Val Leu Lys Ile His 105 110 115	388
CAC CCT AAC CTC AAT AAA AAA GAA CGC TTA GAA AGG GTG GTT TAT GAA His Pro Asn Leu Asn Lys Lys Glu Arg Leu Glu Arg Val Val Tyr Glu 120 125 130 135	436
TTA GAG CGT GTG GGC ATT CCC CAT GCA GGG GAT AAA TAC CAC GAA TAC Leu Glu Arg Val Gly Ile Pro His Ala Gly Asp Lys Tyr His Glu Tyr 140 145 150	484
CCT TTC AAT CTC AGC GGG GGG CAG CGC CAA AGG GTG ATG ATC GCT ATG Pro Phe Asn Leu Ser Gly Gly Gln Arg Gln Arg Val Met Ile Ala Met 155 160 165	532
GCT ATG GTG TGT GAG CCT GAA ATC TTG ATC GCT GAT GAG CCT ACG ACA Ala Met Val Cys Glu Pro Glu Ile Leu Ile Ala Asp Glu Pro Thr Thr 170 175 180	580
GCC TTA GAT GTA ACC ATT CAA GCG CAA ATT TTA GAA TTG ATG AAA GAA Ala Leu Asp Val Thr Ile Gln Ala Gln Ile Leu Glu Leu Met Lys Glu 185 190 195	628
TTG CAA CAA AAA AAA GGC ACT TCT ATT TTG TTT ATC ACC CAT GAT TTA Leu Gln Gln Lys Lys Gly Thr Ser Ile Leu Phe Ile Thr His Asp Leu 200 205 210 215	676
GGC GTG GTG GCG CAA ATC GCT GAT GAA GTG GTG GTG ATG TAT AAA GGG Gly Val Val Ala Gln Ile Ala Asp Glu Val Val Val Met Tyr Lys Gly 220 225 230	724
CAT GTG GTG GAG CAA GCG AGT GCG AAA GAG CTT TTT GCT GAT CCA AGA His Val Val Glu Gln Ala Ser Ala Lys Glu Leu Phe Ala Asp Pro Arg 235 240 245	772
CAC CCT TAT ACG AAA GCT CTT TTA AGC GCG ATC CCT AAA CCG GGC AAA His Pro Tyr Thr Lys Ala Leu Leu Ser Ala Ile Pro Lys Pro Gly Lys 250 255 260	820
GAA TAC CGC AAA AAA CGC TTA GAG ACC GTG GAT GAA AAT GTG GAT TAT Glu Tyr Arg Lys Lys Arg Leu Glu Thr Val Asp Glu Asn Val Asp Tyr 265 270 275	868
TTG AGT TTT CAA AAG GAG TTG CGA TGAAGCTCTT AGAAATTAAA GAATTGAAAA Leu Ser Phe Gln Lys Glu Leu Arg 280 285	922
AATCCTATGC GATAGACAGG GGGTTATTCA AGC	955

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

Met	Ile	Leu	Glu	Val	Lys	Asp	Leu	Lys	Thr	Tyr	Phe	Phe	Thr	Asp	Lys	1	5	10	15
Gly	Val	Asn	Lys	Ala	Val	Asp	Gly	Val	Ser	Phe	Gly	Leu	Lys	Lys	Ser	20	25	30	
Gln	Thr	Leu	Cys	Ile	Val	Gly	Glu	Ser	Gly	Ser	Gly	Lys	Ser	Ile	Thr	35	40	45	
Ser	Leu	Ser	Ile	Leu	Gly	Leu	Ile	Glu	Lys	Pro	Gly	Gln	Ile	Val	Gly	50	55	60	
Gly	Ser	Ile	Gln	Phe	Leu	Gly	Gln	Asp	Leu	Leu	Gln	Leu	Lys	Glu	Lys	65	70	75	80
Gln	Met	Gln	Lys	Glu	Ile	Arg	Gly	Lys	Lys	Ile	Gly	Met	Ile	Phe	Gln	85	90	95	
Glu	Pro	Met	Thr	Ser	Leu	Asn	Pro	Ser	Tyr	Thr	Val	Gly	Phe	Gln	Ile	100	105	110	
Asn	Glu	Val	Leu	Lys	Ile	His	His	Pro	Asn	Leu	Asn	Lys	Lys	Glu	Arg	115	120	125	
Leu	Glu	Arg	Val	Val	Tyr	Glu	Leu	Glu	Arg	Val	Gly	Ile	Pro	His	Ala	130	135	140	
Gly	Asp	Lys	Tyr	His	Glu	Tyr	Pro	Phe	Asn	Leu	Ser	Gly	Gly	Gln	Arg	145	150	155	160
Gln	Arg	Val	Met	Ile	Ala	Met	Ala	Met	Val	Cys	Glu	Pro	Glu	Ile	Leu	165	170	175	
Ile	Ala	Asp	Glu	Pro	Thr	Thr	Ala	Leu	Asp	Val	Thr	Ile	Gln	Ala	Gln	180	185	190	
Ile	Leu	Glu	Leu	Met	Lys	Glu	Leu	Gln	Gln	Lys	Lys	Gly	Thr	Ser	Ile	195	200	205	
Leu	Phe	Ile	Thr	His	Asp	Leu	Gly	Val	Val	Ala	Gln	Ile	Ala	Asp	Glu	210	215	220	
Val	Val	Val	Met	Tyr	Lys	Gly	His	Val	Val	Glu	Gln	Ala	Ser	Ala	Lys	225	230	235	240
Glu	Leu	Phe	Ala	Asp	Pro	Arg	His	Pro	Tyr	Thr	Lys	Ala	Leu	Leu	Ser	245	250	255	
Ala	Ile	Pro	Lys	Pro	Gly	Lys	Glu	Tyr	Arg	Lys	Lys	Arg	Leu	Glu	Thr	260	265	270	
Val	Asp	Glu	Asn	Val	Asp	Tyr	Leu	Ser	Phe	Gln	Lys	Glu	Leu	Arg		275	280	285	

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...840
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

AAATGTGGAT TATTTGAGTT TTCAAAAGGA GTTGCG	ATG AAG CTC TTA GAA ATT	54
	Met Lys Leu Leu Glu Ile	
	1 5	
AAA GAA TTG AAA AAA TCC TAT GCG ATA GAC AGG GGG TTA TTC AAG CCT	102	
Lys Glu Leu Lys Lys Ser Tyr Ala Ile Asp Arg Gly Leu Phe Lys Pro		
	10 15 20	
AAA AGA GTG ATC CAT GCG CTC AAT GGG ATC AGT TTT GAA GTG GAA CAA	150	
Lys Arg Val Ile His Ala Leu Asn Gly Ile Ser Phe Glu Val Glu Gln		
	25 30 35	
AAT GAA GTT TTG AGC ATT GTG GGG GAG AGC GGT TGC GGG AAA AGC ACG	198	
Asn Glu Val Leu Ser Ile Val Gly Glu Ser Gly Cys Gly Lys Ser Thr		
	40 45 50	
ACA GCC AAA ATT TTA GCC GGG ATT GAA AGG CAA GAT AGC GGG GCG ATT	246	
Thr Ala Lys Ile Leu Ala Gly Ile Glu Arg Gln Asp Ser Gly Ala Ile		
	55 60 65 70	
TAT TTC AAT GGT AAG CGC CAT TTG CAT TTT AGC AAA CAG GAT TGG TTT	294	
Tyr Phe Asn Gly Lys Arg His Leu His Phe Ser Lys Gln Asp Trp Phe		
	75 80 85	
GAT TAC CGC AAA AAG GTG CAA ATG ATT TTT CAA GAC CCT TAT TCT AGC	342	
Asp Tyr Arg Lys Lys Val Gln Met Ile Phe Gln Asp Pro Tyr Ser Ser		
	90 95 100	
CTA AAC CCT CGG TGG AAA GTG GGC GAG ATC ATC GCT GAA CCC TTG CTT	390	
Leu Asn Pro Arg Trp Lys Val Gly Glu Ile Ile Ala Glu Pro Leu Leu		
	105 110 115	
TTA AAT TCT CAT TTT TCA AAA AAA GAA ATC AAA ACA AAA GTG CTA GAG	438	
Leu Asn Ser His Phe Ser Lys Lys Glu Ile Lys Thr Lys Val Leu Glu		
	120 125 130	
ATC ATG CAA AAA GTG GGC TTG AAA TTA GAA TGG ATC GAT CGT TAC CCC	486	
Ile Met Gln Lys Val Gly Leu Lys Leu Glu Trp Ile Asp Arg Tyr Pro		
	135 140 145 150	
CAC CAA TTT TCA GGC GGT CAA AGG CAA CGA ATC GGC ATT GCT AGG GCG	534	
His Gln Phe Ser Gly Gly Gln Arg Gln Arg Ile Gly Ile Ala Arg Ala		
	155 160 165	
CTC ATT TTG CAT CCT AGC GTG GTG ATT TGC GAT GAG CCT GTG TCT GCG	582	
Leu Ile Leu His Pro Ser Val Val Ile Cys Asp Glu Pro Val Ser Ala		
	170 175 180	
CTA GAC GTG TCC ATT CAA GCG CAA GTG TTG AAT TTG CTC TTG GAT TTG	630	

Leu Asp Val Ser Ile Gln Ala Gln Val Leu Asn Leu Leu Leu Asp Leu
 185 190 195
 CAA AAA GAA ATG GGG CTG ACT TAT ATT TTT ATC AGC CAT GAT TTA GGG 678
 Gln Lys Glu Met Gly Leu Thr Tyr Ile Phe Ile Ser His Asp Leu Gly
 200 205 210
 GTG GTG GAG CAT ATA AGC GAT AAA ATC ATC GTA ATG AAT CAG GGG CAA 726
 Val Val Glu His Ile Ser Asp Lys Ile Ile Val Met Asn Gln Gly Gln
 215 220 225 230
 ATC GTA GAA ACG GGG GAT GTG GAT AGC GTG ATA AGC GCT CCA AAG CAC 774
 Ile Val Glu Thr Gly Asp Val Asp Ser Val Ile Ser Ala Pro Lys His
 235 240 245
 CCT TAT ACG CAG AAA TTA CTC AAT GCG GTG CCG CAT TTG GAA AAA TCC 822
 Pro Tyr Thr Gln Lys Leu Leu Asn Ala Val Pro His Leu Glu Lys Ser
 250 255 260
 ATG CAA AGA TTT GCC AAA TAAAAGAAAG GATTTTAAAG CTGTGTTTGT AGATAGCG 878
 Met Gln Arg Phe Ala Lys
 265
 TGGAAATTAT CATCGC 894

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

Met Lys Leu Leu Glu Ile Lys Glu Leu Lys Lys Ser Tyr Ala Ile Asp
 1 5 10 15
 Arg Gly Leu Phe Lys Pro Lys Arg Val Ile His Ala Leu Asn Gly Ile
 20 25 30
 Ser Phe Glu Val Glu Gln Asn Glu Val Leu Ser Ile Val Gly Glu Ser
 35 40 45
 Gly Cys Gly Lys Ser Thr Thr Ala Lys Ile Leu Ala Gly Ile Glu Arg
 50 55 60
 Gln Asp Ser Gly Ala Ile Tyr Phe Asn Gly Lys Arg His Leu His Phe
 65 70 75 80
 Ser Lys Gln Asp Trp Phe Asp Tyr Arg Lys Lys Val Gln Met Ile Phe
 85 90 95
 Gln Asp Pro Tyr Ser Ser Leu Asn Pro Arg Trp Lys Val Gly Glu Ile
 100 105 110
 Ile Ala Glu Pro Leu Leu Leu Asn Ser His Phe Ser Lys Lys Glu Ile
 115 120 125
 Lys Thr Lys Val Leu Glu Ile Met Gln Lys Val Gly Leu Lys Leu Glu
 130 135 140
 Trp Ile Asp Arg Tyr Pro His Gln Phe Ser Gly Gly Gln Arg Gln Arg
 145 150 155 160
 Ile Gly Ile Ala Arg Ala Leu Ile Leu His Pro Ser Val Val Ile Cys

				165						170					175				
Asp	Glu	Pro	Val	Ser	Ala	Leu	Asp	Val	Ser	Ile	Gln	Ala	Gln	Val	Leu				
			180					185					190						
Asn	Leu	Leu	Leu	Asp	Leu	Gln	Lys	Glu	Met	Gly	Leu	Thr	Tyr	Ile	Phe				
		195					200					205							
Ile	Ser	His	Asp	Leu	Gly	Val	Val	Glu	His	Ile	Ser	Asp	Lys	Ile	Ile				
	210					215					220								
Val	Met	Asn	Gln	Gly	Gln	Ile	Val	Glu	Thr	Gly	Asp	Val	Asp	Ser	Val				
225					230					235					240				
Ile	Ser	Ala	Pro	Lys	His	Pro	Tyr	Thr	Gln	Lys	Leu	Leu	Asn	Ala	Val				
			245						250					255					
Pro	His	Leu	Glu	Lys	Ser	Met	Gln	Arg	Phe	Ala	Lys								
			260				265												

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 62...1087
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

TTAAGCTGTG TTTGTAGATA GCGTGGAAAT TATCATCGCT TCGGGTAAGG GGGGGCCTGG	60
A ATG GTG AGT TTT AGG CGA GAA AAA TTT GTC ATC AAA GGA GGC CCT GAT	109
Met Val Ser Phe Arg Arg Glu Lys Phe Val Ile Lys Gly Gly Pro Asp	
1 5 10 15	
GGG GGC GAT GGA GGC GAT GGA GGC GAT GTG TAT TTT GAA GTG GAT AAC	157
Gly Gly Asp Gly Gly Asp Gly Gly Asp Val Tyr Phe Glu Val Asp Asn	
20 25 30	
AAT ACC GAC ACT CTA GCG AGT TTT AGA GGC ACC AAA CAC CAT AAG GCT	205
Asn Thr Asp Thr Leu Ala Ser Phe Arg Gly Thr Lys His His Lys Ala	
35 40 45	
AAA AAT GGG GCT CCA GGA GGT ACA CGA AAT TGC GCG GGC AAA AAG GGC	253
Lys Asn Gly Ala Pro Gly Gly Thr Arg Asn Cys Ala Gly Lys Lys Gly	
50 55 60	
GAA GAC AAG ATC ATT GTC GTG CCA CCA GGA ACG CAG GTT TTT GTA GGT	301
Glu Asp Lys Ile Ile Val Val Pro Pro Gly Thr Gln Val Phe Val Gly	
65 70 75 80	
GAT GAG TTG TGG CTT GAT TTA GTG GAA CCT AAA GAA AGG GTG TTA GCC	349
Asp Glu Leu Trp Leu Asp Leu Val Glu Pro Lys Glu Arg Val Leu Ala	
85 90 95	
TTA AAA GGG GGC AAG GGG GGG TTA GGG AAT GCA CAT TTT AAA AGC GCG	397

Leu	Lys	Gly	Gly	Lys	Gly	Gly	Leu	Gly	Asn	Ala	His	Phe	Lys	Ser	Ala		
			100					105					110				
ACT	AAA	CAA	CAA	CCC	ACT	TAC	GCG	CAA	AAA	GGC	TTA	GAG	GGG	GTT	GAA	445	
Thr	Lys	Gln	Gln	Pro	Thr	Tyr	Ala	Gln	Lys	Gly	Leu	Glu	Gly	Val	Glu		
		115					120					125					
AAA	TGC	GTG	CGT	TTG	GAA	TTA	AAA	CTC	ATC	GCT	GAT	ATA	GGG	TTA	GTG	493	
Lys	Cys	Val	Arg	Leu	Glu	Leu	Lys	Leu	Ile	Ala	Asp	Ile	Gly	Leu	Val		
	130					135					140						
GGC	TTC	CCT	AAT	GCG	GGT	AAA	TCC	ACG	CTC	ATT	TCC	ACC	ATC	TCT	AAC	541	
Gly	Phe	Pro	Asn	Ala	Gly	Lys	Ser	Thr	Leu	Ile	Ser	Thr	Ile	Ser	Asn		
145					150					155					160		
GCT	AAG	CCT	AAA	ATC	GCT	AAC	TAT	GAA	TTT	ACG	ACT	CTA	GTG	CCT	AAT	589	
Ala	Lys	Pro	Lys	Ile	Ala	Asn	Tyr	Glu	Phe	Thr	Thr	Leu	Val	Pro	Asn		
				165					170					175			
TTA	GGG	GTT	GTG	AGC	GTG	GAT	GAA	AAA	AGC	GGA	TTT	CTA	ATG	GCG	GAT	637	
Leu	Gly	Val	Val	Ser	Val	Asp	Glu	Lys	Ser	Gly	Phe	Leu	Met	Ala	Asp		
			180					185					190				
ATT	CCT	GGC	ATT	ATT	GAA	GGG	GCT	AGC	GAG	GGA	AAG	GGC	TTA	GGG	ATT	685	
Ile	Pro	Gly	Ile	Ile	Glu	Gly	Ala	Ser	Glu	Gly	Lys	Gly	Leu	Gly	Ile		
		195					200					205					
AGC	TTT	TTA	AAG	CAT	ATT	GAA	CGC	ACC	AAA	GTT	CTA	GCT	TTT	GTT	TTA	733	
Ser	Phe	Leu	Lys	His	Ile	Glu	Arg	Thr	Lys	Val	Leu	Ala	Phe	Val	Leu		
	210					215					220						
GAC	GCT	TCC	AGG	CTG	GAT	TTA	GGC	ATT	AAA	GAG	CAA	TAC	CAA	CGC	TTG	781	
Asp	Ala	Ser	Arg	Leu	Asp	Leu	Gly	Ile	Lys	Glu	Gln	Tyr	Gln	Arg	Leu		
225					230					235					240		
AGG	TTG	GAG	TTG	GAA	AAA	TTT	TCA	TCC	GCT	TTG	GCC	AAT	AAG	CCT	TTT	829	
Arg	Leu	Glu	Leu	Glu	Lys	Phe	Ser	Ser	Ala	Leu	Ala	Asn	Lys	Pro	Phe		
				245				250						255			
GGG	GTG	TTG	CTC	AAT	AAA	TGC	GAT	GTT	GTA	GAA	AAC	ATT	GAT	GAG	ATG	877	
Gly	Val	Leu	Leu	Asn	Lys	Cys	Asp	Val	Val	Glu	Asn	Ile	Asp	Glu	Met		
			260					265					270				
ACT	AAG	GAT	TTT	TGT	GCC	TTT	TTA	AAT	TTG	GGA	GCG	CAG	AAA	TTA	AAC	925	
Thr	Lys	Asp	Phe	Cys	Ala	Phe	Leu	Asn	Leu	Gly	Ala	Gln	Lys	Leu	Asn		
		275					280					285					
GAG	TTT	GGT	TTA	GAG	CCG	TAT	TTA	GGG	TTT	TTG	CAC	CCC	CAT	TTA	ACC	973	
Glu	Phe	Gly	Leu	Glu	Pro	Tyr	Leu	Gly	Phe	Leu	His	Pro	His	Leu	Thr		
	290					295					300						
AAT	GAT	TTT	GAA	AAT	AAC	CCT	AAT	GAG	CAA	TCA	GCG	CTC	TTT	GTC	TTG	1021	
Asn	Asp	Phe	Glu	Asn	Asn	Pro	Asn	Glu	Gln	Ser	Ala	Leu	Phe	Val	Leu		
305					310					315					320		
CCC	CTT	TCA	GCG	GTT	AGC	GCT	CTT	AAT	GTG	CAT	GCA	CTC	AAA	TTT	GTG	1069	
Pro	Leu	Ser	Ala	Val	Ser	Ala	Leu	Asn	Val	His	Ala	Leu	Lys	Phe	Val		
				325					330					335			

TTG TTG GAA GCG TTA CCC TAAAACGCTA TTTTAAAAT AATCCATTAA AATAAAGG 1125
Leu Leu Glu Ala Leu Pro
340

CGAGGAATGA AAAGAT 1141

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

Met	Val	Ser	Phe	Arg	Arg	Glu	Lys	Phe	Val	Ile	Lys	Gly	Gly	Pro	Asp	1	5	10	15
Gly	Gly	Asp	Gly	Gly	Asp	Gly	Gly	Asp	Val	Tyr	Phe	Glu	Val	Asp	Asn	20	25	30	
Asn	Thr	Asp	Thr	Leu	Ala	Ser	Phe	Arg	Gly	Thr	Lys	His	His	Lys	Ala	35	40	45	
Lys	Asn	Gly	Ala	Pro	Gly	Gly	Thr	Arg	Asn	Cys	Ala	Gly	Lys	Lys	Gly	50	55	60	
Glu	Asp	Lys	Ile	Ile	Val	Val	Pro	Pro	Gly	Thr	Gln	Val	Phe	Val	Gly	65	70	75	80
Asp	Glu	Leu	Trp	Leu	Asp	Leu	Val	Glu	Pro	Lys	Glu	Arg	Val	Leu	Ala	85	90	95	
Leu	Lys	Gly	Gly	Lys	Gly	Gly	Leu	Gly	Asn	Ala	His	Phe	Lys	Ser	Ala	100	105	110	
Thr	Lys	Gln	Gln	Pro	Thr	Tyr	Ala	Gln	Lys	Gly	Leu	Glu	Gly	Val	Glu	115	120	125	
Lys	Cys	Val	Arg	Leu	Glu	Leu	Lys	Leu	Ile	Ala	Asp	Ile	Gly	Leu	Val	130	135	140	
Gly	Phe	Pro	Asn	Ala	Gly	Lys	Ser	Thr	Leu	Ile	Ser	Thr	Ile	Ser	Asn	145	150	155	160
Ala	Lys	Pro	Lys	Ile	Ala	Asn	Tyr	Glu	Phe	Thr	Thr	Leu	Val	Pro	Asn	165	170	175	
Leu	Gly	Val	Val	Ser	Val	Asp	Glu	Lys	Ser	Gly	Phe	Leu	Met	Ala	Asp	180	185	190	
Ile	Pro	Gly	Ile	Ile	Glu	Gly	Ala	Ser	Glu	Gly	Lys	Gly	Leu	Gly	Ile	195	200	205	
Ser	Phe	Leu	Lys	His	Ile	Glu	Arg	Thr	Lys	Val	Leu	Ala	Phe	Val	Leu	210	215	220	
Asp	Ala	Ser	Arg	Leu	Asp	Leu	Gly	Ile	Lys	Glu	Gln	Tyr	Gln	Arg	Leu	225	230	235	240
Arg	Leu	Glu	Leu	Glu	Lys	Phe	Ser	Ser	Ala	Leu	Ala	Asn	Lys	Pro	Phe	245	250	255	
Gly	Val	Leu	Leu	Asn	Lys	Cys	Asp	Val	Val	Glu	Asn	Ile	Asp	Glu	Met	260	265	270	
Thr	Lys	Asp	Phe	Cys	Ala	Phe	Leu	Asn	Leu	Gly	Ala	Gln	Lys	Leu	Asn	275	280	285	
Glu	Phe	Gly	Leu	Glu	Pro	Tyr	Leu	Gly	Phe	Leu	His	Pro	His	Leu	Thr	290	295	300	
Asn	Asp	Phe	Glu	Asn	Asn	Pro	Asn	Glu	Gln	Ser	Ala	Leu	Phe	Val	Leu	305	310	315	320
Pro	Leu	Ser	Ala	Val	Ser	Ala	Leu	Asn	Val	His	Ala	Leu	Lys	Phe	Val	325	330	335	
Leu	Leu	Glu	Ala	Leu	Pro											340			

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...567
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

ATTAAAGGAT AATGA ATG AAA AAA ATG GTT TTG GTA TCG GTT TTA CTA GCA	51
Met Lys Lys Met Val Leu Val Ser Val Leu Leu Ala	
1 5 10	
GGG TTT TTG CAA GCG GTG AAT TTG GAT TTA TCT TCG GCT AAG CTA ACA	99
Gly Phe Leu Gln Ala Val Asn Leu Asp Leu Ser Ser Ala Lys Leu Thr	
15 20 25	
TGG ACA GCC TTT AAA ACT AAG GCT AAA ACA CCA GTA AAT GGG AGT TTT	147
Trp Thr Ala Phe Lys Thr Lys Ala Lys Thr Pro Val Asn Gly Ser Phe	
30 35 40	
GAA AGC ATC ACC TAT AAA TTG GGT AAA TCT CAA GAT AGT TTA AAA ACC	195
Glu Ser Ile Thr Tyr Lys Leu Gly Lys Ser Gln Asp Ser Leu Lys Thr	
45 50 55 60	
CTT TTA GAG GGA GCG AGC GCG AGC ATG GAT AGC TTG AAA GTC AAT TTA	243
Leu Leu Glu Gly Ala Ser Ala Ser Met Asp Ser Leu Lys Val Asn Leu	
65 70 75	
GGC GAT GAA TTG AAA AAC AAA AAT GTG AAA GAA GCT TTT TTC GCT CTT	291
Gly Asp Glu Leu Lys Asn Lys Asn Val Lys Glu Ala Phe Phe Ala Leu	
80 85 90	
TTT AAA AAC ACT AAC ATC AAA GTA ACT TTC AGG AAT GTG ATA GAA GGC	339
Phe Lys Asn Thr Asn Ile Lys Val Thr Phe Arg Asn Val Ile Glu Gly	
95 100 105	
GAT CAT GCA GGT TCT CTT ACG GCT TAT GTG AGA ATG AAT GAA AAG CTG	387
Asp His Ala Gly Ser Leu Thr Ala Tyr Val Arg Met Asn Glu Lys Leu	
110 115 120	
GTG AAA GTG CCT ATG CAA TAC ACG ATT GCT GAG GAT AAG ATC GTG GTT	435
Val Lys Val Pro Met Gln Tyr Thr Ile Ala Glu Asp Lys Ile Val Val	
125 130 135 140	
AAA GGG GTT TTG GAT TTA TTG AAT TTT GGC TTG AAA AAC GAA TTA GCG	483
Lys Gly Val Leu Asp Leu Leu Asn Phe Gly Leu Lys Asn Glu Leu Ala	
145 150 155	
AGC TTG GCC AAA CGA TGC GAA AGC TTT CAT GAG GGC TTG ACT TGG TCG	531
Ser Leu Ala Lys Arg Cys Glu Ser Phe His Glu Gly Leu Thr Trp Ser	

160 165 170

CAA GTG GAA ATC CAA TTT GAA AGC ATG ATC AAG GGA TAATGTAAAA TCATGG 583
 Gln Val Glu Ile Gln Phe Glu Ser Met Ile Lys Gly
 175 180

AGTTGTTGCA CAGCATTAAT GATTTCATG AAGCTAAG 621

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

Met Lys Lys Met Val Leu Val Ser Val Leu Leu Ala Gly Phe Leu Gln
 1 5 10 15
 Ala Val Asn Leu Asp Leu Ser Ser Ala Lys Leu Thr Trp Thr Ala Phe
 20 25 30
 Lys Thr Lys Ala Lys Thr Pro Val Asn Gly Ser Phe Glu Ser Ile Thr
 35 40 45
 Tyr Lys Leu Gly Lys Ser Gln Asp Ser Leu Lys Thr Leu Leu Glu Gly
 50 55 60
 Ala Ser Ala Ser Met Asp Ser Leu Lys Val Asn Leu Gly Asp Glu Leu
 65 70 75 80
 Lys Asn Lys Asn Val Lys Glu Ala Phe Phe Ala Leu Phe Lys Asn Thr
 85 90 95
 Asn Ile Lys Val Thr Phe Arg Asn Val Ile Glu Gly Asp His Ala Gly
 100 105 110
 Ser Leu Thr Ala Tyr Val Arg Met Asn Glu Lys Leu Val Lys Val Pro
 115 120 125
 Met Gln Tyr Thr Ile Ala Glu Asp Lys Ile Val Val Lys Gly Val Leu
 130 135 140
 Asp Leu Leu Asn Phe Gly Leu Lys Asn Glu Leu Ala Ser Leu Ala Lys
 145 150 155 160
 Arg Cys Glu Ser Phe His Glu Gly Leu Thr Trp Ser Gln Val Glu Ile
 165 170 175
 Gln Phe Glu Ser Met Ile Lys Gly
 180

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...1338

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

CAAGTGGAAA	TCCAATTTGA	AAGCATGATC	AAGGGATAAT	GTAAAATC	ATG	GAG	TTG	57
					Met	Glu	Leu	
					1			
TTG	CAC	AGC	ATT	AAT	GAT	TTC	AAT	105
Leu	His	Ser	Ile	Asn	Asp	Phe	Asn	
5						10		
GGG	GTC	AAT	TCA	CCT	GTT	AGG	GCG	153
Gly	Val	Asn	Ser	Pro	Val	Arg	Ala	
20					25			
CCC	TTT	ATT	TTA	AAA	GGC	AAG	GGG	201
Pro	Phe	Ile	Leu	Lys	Gly	Lys	Gly	
			40				45	
AAC	CAT	TAT	ATA	GAT	TTT	GTG	CAA	249
Asn	His	Tyr	Ile	Asp	Phe	Val	Gln	
			55				60	
CAT	GCT	GAT	GAA	GAG	ATT	GAA	GAA	297
His	Ala	Asp	Glu	Glu	Ile	Glu	Glu	
		70				75		
GGC	ACT	TCT	TTT	GGC	GCT	CCC	ACA	345
Gly	Thr	Ser	Phe	Gly	Ala	Pro	Thr	
85						90		
GAA	ATC	ATT	TCT	TGT	TAT	GAA	GGC	393
Glu	Ile	Ile	Ser	Cys	Tyr	Glu	Gly	
100					105			
AGC	GGC	ACA	GAA	GCG	ACC	ATG	AGC	441
Ser	Gly	Thr	Glu	Ala	Thr	Met	Ser	
				120				
AGC	CAA	AAA	GAT	GAT	TTG	ATC	AAG	489
Ser	Gln	Lys	Asp	Asp	Leu	Ile	Lys	
			135				140	
AGC	GAC	TCC	TTA	TTG	GTG	AAA	GCG	537
Ser	Asp	Ser	Leu	Leu	Val	Lys	Ala	
			150				155	
TCG	CCT	TCT	TCT	TTA	GGC	GTG	CCG	585
Ser	Pro	Ser	Ser	Leu	Gly	Val	Pro	
	165					170		
GTG	GCT	CGT	TAT	AAC	GAT	TTA	AAC	633
Val	Ala	Arg	Tyr	Asn	Asp	Leu	Asn	
180					185			
GGC	AAT	GTG	GGT	TGC	GTC	ATC	ATT	681

Gly	Asn	Val	Gly	Cys	Val	Ile	Ile	Glu	Pro	Ile	Ala	Gly	Asn	Met	Gly	
				200					205					210		
TTA	GTG	CCG	GCT	CAA	AAA	GAG	TTT	TTA	TTG	GGC	TTA	AAG	GCC	TTG	TGT	729
Leu	Val	Pro	Ala	Gln	Lys	Glu	Phe	Leu	Leu	Gly	Leu	Lys	Ala	Leu	Cys	
			215					220					225			
GAA	AAA	TAC	CAA	GCG	GTG	CTG	ATT	TTA	GAT	GAA	GTG	ATG	AGC	GGT	TTT	777
Glu	Lys	Tyr	Gln	Ala	Val	Leu	Ile	Leu	Asp	Glu	Val	Met	Ser	Gly	Phe	
		230					235					240				
AGA	GCG	AGC	TTG	AGC	GGT	TCG	CAA	GAA	TTT	TAT	GGC	GTG	GTG	CCG	GAT	825
Arg	Ala	Ser	Leu	Ser	Gly	Ser	Gln	Glu	Phe	Tyr	Gly	Val	Val	Pro	Asp	
	245					250					255					
TTG	GTA	ACC	TTT	GGT	AAG	GTG	ATA	GGT	GCT	GGG	CTT	CCT	TTG	GCG	TGT	873
Leu	Val	Thr	Phe	Gly	Lys	Val	Ile	Gly	Ala	Gly	Leu	Pro	Leu	Ala	Cys	
260					265					270					275	
TTT	GGA	GGG	CGT	GCA	GAA	ATT	ATG	GAC	TTG	CTT	TCG	CCC	ATT	GGA	AGC	921
Phe	Gly	Gly	Arg	Ala	Glu	Ile	Met	Asp	Leu	Leu	Ser	Pro	Ile	Gly	Ser	
				280					285					290		
GTG	TAT	CAA	GCA	GGC	ACT	TTG	AGC	GGT	AAC	CCC	CTA	GCG	GTG	TGC	GCG	969
Val	Tyr	Gln	Ala	Gly	Thr	Leu	Ser	Gly	Asn	Pro	Leu	Ala	Val	Cys	Ala	
			295					300					305			
GGG	TTG	AGT	GCG	CTT	TAT	AAA	ATC	AAA	AGA	GAC	AAA	ACC	CTT	TAT	ACT	1017
Gly	Leu	Ser	Ala	Leu	Tyr	Lys	Ile	Lys	Arg	Asp	Lys	Thr	Leu	Tyr	Thr	
		310					315					320				
CGC	TTA	GAC	GCT	TTA	GCT	ATT	CGT	TTG	ACT	CAA	GGC	TTA	CAA	AAG	AGC	1065
Arg	Leu	Asp	Ala	Leu	Ala	Ile	Arg	Leu	Thr	Gln	Gly	Leu	Gln	Lys	Ser	
	325					330					335					
GCT	CAA	AAC	TAT	AAC	ATC	GCT	TTA	GAG	ACG	CTT	AAC	ATG	GGG	AGC	ATG	1113
Ala	Gln	Asn	Tyr	Asn	Ile	Ala	Leu	Glu	Thr	Leu	Asn	Met	Gly	Ser	Met	
340					345					350					355	
TTT	GGC	TTT	TTC	TTT	AAC	GAA	AAT	GCG	GTG	CAC	GAT	TTT	GAT	GAC	GCT	1161
Phe	Gly	Phe	Phe	Phe	Asn	Glu	Asn	Ala	Val	His	Asp	Phe	Asp	Asp	Ala	
				360					365					370		
TTA	AAA	AGC	GAT	ACG	GAG	ATG	TTT	GCA	AAA	TTC	CAC	CAA	AAA	ATG	CTC	1209
Leu	Lys	Ser	Asp	Thr	Glu	Met	Phe	Ala	Lys	Phe	His	Gln	Lys	Met	Leu	
			375					380					385			
TTT	AAG	GGC	GTG	TAT	TTG	GCG	TGC	TCA	AGC	TTT	GAA	ACC	GGC	TTT	ATT	1257
Phe	Lys	Gly	Val	Tyr	Leu	Ala	Cys	Ser	Ser	Phe	Glu	Thr	Gly	Phe	Ile	
		390					395					400				
TGT	GAG	CCT	ATG	ACT	GAA	GAG	ATG	ATT	GAT	TTA	ACG	ATC	GCA	AAA	GCC	1305
Cys	Glu	Pro	Met	Thr	Glu	Glu	Met	Ile	Asp	Leu	Thr	Ile	Ala	Lys	Ala	
	405					410						415				
GAT	GAA	AGT	TTT	GAT	GAA	ATC	ATA	AAA	GGT	GTG	TGAATTTTTT	GAAAAAGCCA				1358
Asp	Glu	Ser	Phe	Asp	Glu	Ile	Ile	Lys	Gly	Val						
420					425					430						

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

Met	Glu	Leu	Leu	His	Ser	Ile	Asn	Asp	Phe	Asn	Glu	Ala	Lys	Gln	Val	1	5	10	15
Ile	Ala	Gly	Gly	Val	Asn	Ser	Pro	Val	Arg	Ala	Phe	Lys	Ser	Val	Lys	20	25	30	
Gly	Thr	Pro	Pro	Phe	Ile	Leu	Lys	Gly	Lys	Gly	Ala	Tyr	Leu	Tyr	Asp	35	40	45	
Val	Asp	Asn	Asn	His	Tyr	Ile	Asp	Phe	Val	Gln	Ser	Trp	Gly	Pro	Leu	50	55	60	
Ile	Phe	Gly	His	Ala	Asp	Glu	Glu	Ile	Glu	Glu	Asn	Ile	Ile	Asn	Ala	65	70	75	80
Leu	Lys	Lys	Gly	Thr	Ser	Phe	Gly	Ala	Pro	Thr	Glu	Leu	Glu	Thr	Thr	85	90	95	
Leu	Ala	Lys	Glu	Ile	Ile	Ser	Cys	Tyr	Glu	Gly	Leu	Asp	Lys	Val	Arg	100	105	110	
Leu	Val	Ser	Ser	Gly	Thr	Glu	Ala	Thr	Met	Ser	Ala	Ile	Arg	Leu	Ala	115	120	125	
Arg	Ala	Tyr	Ser	Gln	Lys	Asp	Leu	Ile	Lys	Phe	Glu	Gly	Cys	Tyr		130	135	140	
His	Gly	His	Ser	Asp	Ser	Leu	Leu	Val	Lys	Ala	Gly	Ser	Gly	Cys	Ala	145	150	155	160
Thr	Phe	Gly	Ser	Pro	Ser	Ser	Leu	Gly	Val	Pro	Asn	Asp	Phe	Ser	Lys	165	170	175	
His	Thr	Leu	Val	Ala	Arg	Tyr	Asn	Asp	Leu	Asn	Ser	Thr	Glu	Glu	Cys	180	185	190	
Phe	Lys	Lys	Gly	Asn	Val	Gly	Cys	Val	Ile	Ile	Glu	Pro	Ile	Ala	Gly	195	200	205	
Asn	Met	Gly	Leu	Val	Pro	Ala	Gln	Lys	Glu	Phe	Leu	Leu	Gly	Leu	Lys	210	215	220	
Ala	Leu	Cys	Glu	Lys	Tyr	Gln	Ala	Val	Leu	Ile	Leu	Asp	Glu	Val	Met	225	230	235	240
Ser	Gly	Phe	Arg	Ala	Ser	Leu	Ser	Gly	Ser	Gln	Glu	Phe	Tyr	Gly	Val	245	250	255	
Val	Pro	Asp	Leu	Val	Thr	Phe	Gly	Lys	Val	Ile	Gly	Ala	Gly	Leu	Pro	260	265	270	
Leu	Ala	Cys	Phe	Gly	Gly	Arg	Ala	Glu	Ile	Met	Asp	Leu	Leu	Ser	Pro	275	280	285	
Ile	Gly	Ser	Val	Tyr	Gln	Ala	Gly	Thr	Leu	Ser	Gly	Asn	Pro	Leu	Ala	290	295	300	
Val	Cys	Ala	Gly	Leu	Ser	Ala	Leu	Tyr	Lys	Ile	Lys	Arg	Asp	Lys	Thr	305	310	315	320
Leu	Tyr	Thr	Arg	Leu	Asp	Ala	Leu	Ala	Ile	Arg	Leu	Thr	Gln	Gly	Leu	325	330	335	
Gln	Lys	Ser	Ala	Gln	Asn	Tyr	Asn	Ile	Ala	Leu	Glu	Thr	Leu	Asn	Met	340	345	350	

Gly Ser Met Phe Gly Phe Phe Phe Asn Glu Asn Ala Val His Asp Phe
 355 360 365
 Asp Asp Ala Leu Lys Ser Asp Thr Glu Met Phe Ala Lys Phe His Gln
 370 375 380
 Lys Met Leu Phe Lys Gly Val Tyr Leu Ala Cys Ser Ser Phe Glu Thr
 385 390 395 400
 Gly Phe Ile Cys Glu Pro Met Thr Glu Glu Met Ile Asp Leu Thr Ile
 405 410 415
 Ala Lys Ala Asp Glu Ser Phe Asp Glu Ile Ile Lys Gly Val
 420 425 430

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 90...1052
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

AAGGCGCAAA	ACTTAGCCAA	AAAAGAGATG	GACGCACTAG	ATTCTCATCT	GTTAGCGTTT	60
TTAAATCAAA	ATGCAAATGC	CATTCAGTG	ATG CCC AAA	ATC CCT ATC	ACG CTC	113
		Met Pro Lys	Ile Pro	Ile Thr	Leu	
		1		5		
ATC ACC GGT	TTT TTA GGC	AGC GGT AAA	ACG AGT TTT	TTG AGC GAA	TAT	161
Ile Thr Gly	Phe Leu Gly	Ser Gly Lys	Thr Ser Phe	Leu Ser Glu	Tyr	
10		15		20		
TTA AAC CAA	ACA GAT CAC	CAA GGC GTC	GCT CTT ATC	ATC AAT GAA	ATC	209
Leu Asn Gln	Thr Asp His	Gln Gly Val	Ala Leu Ile	Ile Asn Glu	Ile	
25		30		35	40	
GGT CAA GCC	GCT TTG GAT	CAG CGC ATC	TTA AGC GTT	CAA TAT TGC	GGT	257
Gly Gln Ala	Ala Leu Asp	Gln Arg Ile	Leu Ser Val	Gln Tyr Cys	Gly	
	45		50		55	
GAA AAA ATG	CTC TAT CTT	AAC GCA GGG	TGC GTG TGT	TGC AAC AAA	CGC	305
Glu Lys Met	Leu Tyr Leu	Asn Ala Gly	Cys Val Cys	Cys Asn Lys	Arg	
	60		65		70	
TTG GAT TTA	GTG GAG TCT	CTA AAA GCC	ACG CTC AAC	AAC TAT GAA	TGG	353
Leu Asp Leu	Val Glu Ser	Leu Lys Ala	Thr Leu Asn	Asn Tyr Glu	Trp	
	75		80		85	
CAC GGC GAA	ATT CTA AGG	CGC ATC ATC	ATT GAA ACT	ACC GGT TTA	GCC	401
His Gly Glu	Ile Leu Arg	Arg Ile Ile	Ile Glu Thr	Thr Gly Leu	Ala	
	90		95		100	

AAC CCG GCA CCG ATT TTA TGG ACG ATT TTG AGC GAC ACT TTT TTA GGA Asn Pro Ala Pro Ile Leu Trp Thr Ile Leu Ser Asp Thr Phe Leu Gly 105 110 115 120	449
GTG CAT TTT GAG ATT CAA AGC GTG GTG GCT TGC GTG GAT GCA TTG AAT Val His Phe Glu Ile Gln Ser Val Val Ala Cys Val Asp Ala Leu Asn 125 130 135	497
GCT AGA GAG CAT TTA ACC AAC AAT GAA GCT AAA GAG CAA ATC GTT TTT Ala Arg Glu His Leu Thr Asn Asn Glu Ala Lys Glu Gln Ile Val Phe 140 145 150	545
GCT GAT AGC GTT TTA TTG ACC AAA ACG GAT TTA CAA AAC GAT AGC GCG Ala Asp Ser Val Leu Leu Thr Lys Thr Asp Leu Gln Asn Asp Ser Ala 155 160 165	593
GCT TTA ACA AAA CTA AAA GAG AGG ATA CAA GCC CTT AAC CCT AGT GCA Ala Leu Thr Lys Leu Lys Glu Arg Ile Gln Ala Leu Asn Pro Ser Ala 170 175 180	641
GAA ATT TTT GAC AAG AGG GCG ATA GAC TAT GAG AGC CTC TTT TCA CGC Glu Ile Phe Asp Lys Arg Ala Ile Asp Tyr Glu Ser Leu Phe Ser Arg 185 190 195 200	689
AAA AAT AGG GCG CGA AAT TTT ATG CCA AGA ATG CCA AAA GAT TCG CAC Lys Asn Arg Ala Arg Asn Phe Met Pro Arg Met Pro Lys Asp Ser His 205 210 215	737
TCG CAA GGC TTT GAG ACT TTA AGC ATT AAT TTT GAA GGC ACG ATG GAG Ser Gln Gly Phe Glu Thr Leu Ser Ile Asn Phe Glu Gly Thr Met Glu 220 225 230	785
TGG AGC GCG TTT GGG ATT TGG CTG AGT TTG TTA TTG CAT CAA TAC GGC Trp Ser Ala Phe Gly Ile Trp Leu Ser Leu Leu Leu His Gln Tyr Gly 235 240 245	833
ACA CAG ATT TTA CGC ATC AAG GGG ATT ATT GAC ATT GGA AGC GGC TTT Thr Gln Ile Leu Arg Ile Lys Gly Ile Ile Asp Ile Gly Ser Gly Phe 250 255 260	881
TTG GTG AGT ATT AAC GGC GTG ATG CAT GTC ATT TAC CCG CCT AAG CAT Leu Val Ser Ile Asn Gly Val Met His Val Ile Tyr Pro Pro Lys His 265 270 275 280	929
ATT TTA AAG GAT CAA AAC GGC TCT AAC CTC GTT TTT ATC ATG CGC CAT Ile Leu Lys Asp Gln Asn Gly Ser Asn Leu Val Phe Ile Met Arg His 285 290 295	977
TTA GAG CGT GAA AAA ATC TTA AAT TCC TTA AAG GGT TTT AAG GAT TTT Leu Glu Arg Glu Lys Ile Leu Asn Ser Leu Lys Gly Phe Lys Asp Phe 300 305 310	1025
CTC GGC ATC AAG GGT TTT GAA ACC CAA TAATTTTCT ATTTATGGAT AGCTGTT Leu Gly Ile Lys Gly Phe Glu Thr Gln 315 320	1079
TGCATTTTGA TGGGGAAAAG A	1100

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

Met	Pro	Lys	Ile	Pro	Ile	Thr	Leu	Ile	Thr	Gly	Phe	Leu	Gly	Ser	Gly	1	5	10	15
Lys	Thr	Ser	Phe	Leu	Ser	Glu	Tyr	Leu	Asn	Gln	Thr	Asp	His	Gln	Gly	20	25	30	
Val	Ala	Leu	Ile	Ile	Asn	Glu	Ile	Gly	Gln	Ala	Ala	Leu	Asp	Gln	Arg	35	40	45	
Ile	Leu	Ser	Val	Gln	Tyr	Cys	Gly	Glu	Lys	Met	Leu	Tyr	Leu	Asn	Ala	50	55	60	
Gly	Cys	Val	Cys	Cys	Asn	Lys	Arg	Leu	Asp	Leu	Val	Glu	Ser	Leu	Lys	65	70	75	80
Ala	Thr	Leu	Asn	Asn	Tyr	Glu	Trp	His	Gly	Glu	Ile	Leu	Arg	Arg	Ile	85	90	95	
Ile	Ile	Glu	Thr	Thr	Gly	Leu	Ala	Asn	Pro	Ala	Pro	Ile	Leu	Trp	Thr	100	105	110	
Ile	Leu	Ser	Asp	Thr	Phe	Leu	Gly	Val	His	Phe	Glu	Ile	Gln	Ser	Val	115	120	125	
Val	Ala	Cys	Val	Asp	Ala	Leu	Asn	Ala	Arg	Glu	His	Leu	Thr	Asn	Asn	130	135	140	
Glu	Ala	Lys	Glu	Gln	Ile	Val	Phe	Ala	Asp	Ser	Val	Leu	Leu	Thr	Lys	145	150	155	160
Thr	Asp	Leu	Gln	Asn	Asp	Ser	Ala	Ala	Leu	Thr	Lys	Leu	Lys	Glu	Arg	165	170	175	
Ile	Gln	Ala	Leu	Asn	Pro	Ser	Ala	Glu	Ile	Phe	Asp	Lys	Arg	Ala	Ile	180	185	190	
Asp	Tyr	Glu	Ser	Leu	Phe	Ser	Arg	Lys	Asn	Arg	Ala	Arg	Asn	Phe	Met	195	200	205	
Pro	Arg	Met	Pro	Lys	Asp	Ser	His	Ser	Gln	Gly	Phe	Glu	Thr	Leu	Ser	210	215	220	
Ile	Asn	Phe	Glu	Gly	Thr	Met	Glu	Trp	Ser	Ala	Phe	Gly	Ile	Trp	Leu	225	230	235	240
Ser	Leu	Leu	Leu	His	Gln	Tyr	Gly	Thr	Gln	Ile	Leu	Arg	Ile	Lys	Gly	245	250	255	
Ile	Ile	Asp	Ile	Gly	Ser	Gly	Phe	Leu	Val	Ser	Ile	Asn	Gly	Val	Met	260	265	270	
His	Val	Ile	Tyr	Pro	Pro	Lys	His	Ile	Leu	Lys	Asp	Gln	Asn	Gly	Ser	275	280	285	
Asn	Leu	Val	Phe	Ile	Met	Arg	His	Leu	Glu	Arg	Glu	Lys	Ile	Leu	Asn	290	295	300	
Ser	Leu	Lys	Gly	Phe	Lys	Asp	Phe	Leu	Gly	Ile	Lys	Gly	Phe	Glu	Thr	305	310	315	320
Gln																			

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1713 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 26...1648
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

TTAAAAGCAA	ACAAGAAAGT	TAAGC	ATG	CAC	ACT	CTC	ATT	AAG	GGC	ATT	TTA	52
			Met	His	Thr	Leu	Ile	Lys	Gly	Ile	Leu	
			1				5					
GAA GAG ATT TTA	GAA GAA GAA GTC	ATT GTT	GAA TAC	CCT AAA	GAC AGA	100						
Glu Glu Ile Leu	Glu Glu Glu Val	Ile Val	Glu Tyr	Pro Lys	Asp Arg							
10	15		20		25							
GAG CAT GGG CAT	TAC GCT ACG CCC	ATT GCT TTC	AAT CTC	GCC AAA	GTT	148						
Glu His Gly His	Tyr Ala Thr Pro	Ile Ala Phe	Asn Leu	Ala Lys	Val							
	30		35		40							
TTT AAA AAA TCG	CCC TTA GCC ATC	GCT GAA GAG	TTA GCC	CTT AAA	ATC	196						
Phe Lys Lys Ser	Pro Leu Ala Ile	Ala Glu Glu	Leu Ala	Leu Lys	Ile							
	45		50		55							
AGC ACG CAT GAA	AAA ACT CAA GGG	CTT TTT GAC	AGC GTA	GTG GCT	TGT	244						
Ser Thr His Glu	Lys Thr Gln Gly	Leu Phe Asp	Ser Val	Val Ala	Cys							
	60		65		70							
AAG GGC TAT ATC	AAT TTC ACG CTT	TCT TTA GAT	TTT TTG	GAG CGT	TTC	292						
Lys Gly Tyr Ile	Asn Phe Thr Leu	Ser Leu Asp	Phe Leu	Glu Arg	Phe							
	75		80		85							
ACC CAA AAA GCT	TTG GAA TTG AAA	GAA AAA TTT	GGC TCT	CAA GTT	AAA	340						
Thr Gln Lys Ala	Leu Glu Leu Lys	Glu Lys Phe	Gly Ser	Gln Val	Lys							
	90		95		100							
AGC GAA CGT TCT	CAA AAA ATC TTT	TTA GAA TTT	GTG AGC	GCT AAC	CCC	388						
Ser Glu Arg Ser	Gln Lys Ile Phe	Leu Glu Phe	Val Ser	Ala Asn	Pro							
	110		115		120							
ACA GGG CCT TTA	CAC ATA GGG CAT	GCT AGA GGG	GCG GTG	TTT GGC	GAT	436						
Thr Gly Pro Leu	His Ile Gly His	Ala Arg Gly	Ala Val	Phe Gly	Asp							
	125		130		135							
AGT TTG GCT AAA	ATC GCT CGC TTT	TTA GGG CAT	GAA GTT	TTA TGC	GAG	484						
Ser Leu Ala Lys	Ile Ala Arg Phe	Leu Gly His	Glu Val	Leu Cys	Glu							
	140		145		150							
TAT TAT GTC AAT	GAC ATG GGA TCT	CAA ATC CGC	TTG TTA	GGG CTT	TCT	532						
Tyr Tyr Val Asn	Asp Met Gly Ser	Gln Ile Arg	Leu Leu	Gly Leu	Ser							
	155		160		165							

GTA Val 170	TGG Trp	CTC Leu	GCT Ala	TAC Tyr	AGA Arg 175	GAA Glu	CAT His	GTT Val	TTA Leu	AAA Lys 180	GAA Glu	AGC Ser	GTA Val	ACT Thr	TAC Tyr 185	580
CCA Pro	GAA Glu	GTC Val	TTT Phe	TAC Tyr 190	AAA Lys	GGC Gly	GAA Glu	TAC Tyr	ATC Ile 195	ATT Ile	GAA Glu	ATC Ile	GCT Ala	AAA Lys 200	AAG Lys	628
GCG Ala	AAC Asn	AAC Asn	GAT Asp 205	TTA Leu	GAA Glu	CCA Pro	AGC Ser	CTT Leu 210	TTA Leu	AAA Lys	GAA Glu	AAC Asn	GAA Glu 215	GAA Glu	ACG Thr	676
ATT Ile	ATT Ile	GAA Glu 220	GTT Val	TTA Leu	AGC Ser	GGC Gly	TAT Tyr 225	GCT Ala	AGG Arg	GAT Asp	CTA Leu	ATG Met 230	CTT Leu	TTA Leu	GAA Glu	724
ATT Ile	AAA Lys 235	GAT Asp	AAT Asn	TTA Leu	GAC Asp 240	GCT Ala	TTA Leu	GGC Gly	ATT Ile	CAT His	TTT Phe 245	GAT Asp	TCC Ser	TAT Tyr	GCG Ala	772
AGC Ser 250	GAA Glu	AAA Lys	GAA Glu	GTT Val	TTT Phe 255	AAA Lys	CAT His	AAA Lys	GAT Asp	GCG Ala 260	GTG Val	TTT Phe	GAA Glu	CAA Gln	TTA Leu 265	820
GAA Glu	AAA Lys	GCG Ala	AAC Asn	GCC Ala 270	CTT Leu	TAT Tyr	GAA Glu	AAG Lys	GAT Asp 275	TCT Ser	AAA Lys	ATC Ile	TGG Trp	CTC Leu	AAA Lys	868
TCT Ser	TCA Ser	CTC Leu	TAC Tyr 285	CAG Gln	GAT Asp	GAA Glu	AGC Ser	GAT Asp 290	CGG Arg	GTG Val	CTC Leu	ATT Ile	AAA Lys 295	GAA Glu	GAT Asp	916
AAA Lys	AGC Ser	TAC Tyr 300	ACT Thr	TAT Tyr	TTA Leu	GCG Ala	GGC Gly 305	GAT Asp	ATT Ile	GTC Val	TAT Tyr	CAT His 310	GAT Asp	GAA Glu	AAA Lys	964
TTC Phe	AAG Lys 315	CAA Gln	GAT Asp	TAT Tyr	ACC Thr	AAA Lys 320	TAC Tyr	ATC Ile	AAC Asn	ATT Ile	TGG Trp 325	GGG Gly	GCA Ala	GAC Asp	CAC His	1012
CAC His 330	GGC Gly	TAT Tyr	ATC Ile	GCT Ala	AGA Arg 335	GTG Val	AAA Lys	GCC Ala	AGC Ser	CTT Leu 340	GAG Glu	TTT Phe	TTG Leu	GGC Gly	TAT Tyr 345	1060
GAT Asp	TCC Ser	AAC Asn	AAG Lys	CTT Leu 350	GAA Glu	GTC Val	TTG Leu	CTC Leu	GCT Ala 355	CAA Gln	ATG Met	GTG Val	CGC Arg	TTG Leu 360	CTC Leu	1108
AAA Lys	GAT Asp	AAC Asn	GAG Glu 365	CCT Pro	TAC Tyr	AAG Lys	ATG Met	AGT Ser 370	AAA Lys	AGA Arg	GCG Ala	GGT Gly	AAT Asn 375	TTT Phe	ATT Ile	1156
TTG Leu	ATT Ile	AAA Lys 380	GAT Asp	GTG Val	GTT Val	GAT Asp	GAT Asp 385	GTG Val	GGT Gly	AAG Lys	GAC Asp	GCT Ala 390	TTG Leu	AGG Arg	TTT Phe	1204
ATT Ile	TTT Phe	TTG Leu	AGC Ser	AAA Lys	CGG Arg	CTT Leu	GAC Asp	ACT Thr	CAT His	TTA Leu	GAA Glu	TTT Phe	GAT Asp	GTC Val	AAT Asn	1252

395	400	405	
ACT TTA AAA AAG CAA GAC AGC TCA AAC CCC ATT TAC TAT ATC CAT TAC Thr Leu Lys Lys Gln Asp Ser Ser Asn Pro Ile Tyr Tyr Ile His Tyr 410 415 420 425			1300
GCT AAT TCG CGC ATC CAC ACC ATG CTA GAA AAA TCG CCC TTT TCT AAA Ala Asn Ser Arg Ile His Thr Met Leu Glu Lys Ser Pro Phe Ser Lys 430 435 440			1348
GAA GAG GTT TTG CAA ACC CCT TTA ACC AAT TTA AAC GCT GAA GAA AAA Glu Glu Val Leu Gln Thr Pro Leu Thr Asn Leu Asn Ala Glu Glu Lys 445 450 455			1396
TAC TTG CTT TTT AGC GCT TTA AGC TTG CCT AAA GCA ATT GAA TCC TCT Tyr Leu Leu Phe Ser Ala Leu Ser Leu Pro Lys Ala Ile Glu Ser Ser 460 465 470			1444
TTT GAA GAA TAC GGC TTG CAA AAA ATG TGC GAA TAC GCA AAA ACC CTC Phe Glu Glu Tyr Gly Leu Gln Lys Met Cys Glu Tyr Ala Lys Thr Leu 475 480 485			1492
GCA TCA GAA TTC CAC CGC TTC TAT AAC GCT GGC AAA ATC TTA GAC ACC Ala Ser Glu Phe His Arg Phe Tyr Asn Ala Gly Lys Ile Leu Asp Thr 490 495 500 505			1540
CCT AAA GCT AAA GAG CTT TTA AAA ATT TGT TTA ATA GTA AGC TTG AGC Pro Lys Ala Lys Glu Leu Leu Lys Ile Cys Leu Ile Val Ser Leu Ser 510 515 520			1588
TTA AGC AAC GCT TTT AAA CTT TTA GGC ATA GAG ATA AAG ACC AAA ATT Leu Ser Asn Ala Phe Lys Leu Leu Gly Ile Glu Ile Lys Thr Lys Ile 525 530 535			1636
TCC GCT AGA GAT TAAGCCAATA TTTAATTTTT TGTATAACA TTCCCCTTAT TTTTT Ser Ala Arg Asp 540			1693
GAAACTAAGG AGAATATTAT			1713

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

Met	His	Thr	Leu	Ile	Lys	Gly	Ile	Leu	Glu	Glu	Ile	Leu	Glu	Glu	Glu
1				5				10					15		
Val	Ile	Val	Glu	Tyr	Pro	Lys	Asp	Arg	Glu	His	Gly	His	Tyr	Ala	Thr
			20				25					30			
Pro	Ile	Ala	Phe	Asn	Leu	Ala	Lys	Val	Phe	Lys	Lys	Ser	Pro	Leu	Ala
		35				40					45				

Ile 50	Ala	Glu	Glu	Leu	Ala	Leu	Lys	Ile	Ser	Thr	His	Glu	Lys	Thr	Gln
Gly 65	Leu	Phe	Asp	Ser	Val	Val	Ala	Cys	Lys	Gly	Tyr	Ile	Asn	Phe	Thr
Leu	Ser	Leu	Asp	Phe	Leu	Glu	Arg	Phe	Thr	Gln	Lys	Ala	Leu	Glu	Leu
Lys	Glu	Lys	Phe	Gly	Ser	Gln	Val	Lys	Ser	Glu	Arg	Ser	Gln	Lys	Ile
Phe	Leu	Glu	Phe	Val	Ser	Ala	Asn	Pro	Thr	Gly	Pro	Leu	His	Ile	Gly
His	Ala	Arg	Gly	Ala	Val	Phe	Gly	Asp	Ser	Leu	Ala	Lys	Ile	Ala	Arg
Phe 145	Leu	Gly	His	Glu	Val	Leu	Cys	Glu	Tyr	Tyr	Val	Asn	Asp	Met	Gly
Ser	Gln	Ile	Arg	Leu	Leu	Gly	Leu	Ser	Val	Trp	Leu	Ala	Tyr	Arg	Glu
His	Val	Leu	Lys	Glu	Ser	Val	Thr	Tyr	Pro	Glu	Val	Phe	Tyr	Lys	Gly
Glu	Tyr	Ile	Ile	Glu	Ile	Ala	Lys	Lys	Ala	Asn	Asn	Asp	Leu	Glu	Pro
Ser	Leu	Leu	Lys	Glu	Asn	Glu	Glu	Thr	Ile	Ile	Glu	Val	Leu	Ser	Gly
Tyr 225	Ala	Arg	Asp	Leu	Met	Leu	Leu	Glu	Ile	Lys	Asp	Asn	Leu	Asp	Ala
Leu	Gly	Ile	His	Phe	Asp	Ser	Tyr	Ala	Ser	Glu	Lys	Glu	Val	Phe	Lys
His	Lys	Asp	Ala	Val	Phe	Glu	Gln	Leu	Glu	Lys	Ala	Asn	Ala	Leu	Tyr
Glu	Lys	Asp	Ser	Lys	Ile	Trp	Leu	Lys	Ser	Ser	Leu	Tyr	Gln	Asp	Glu
Ser	Asp	Arg	Val	Leu	Ile	Lys	Glu	Asp	Lys	Ser	Tyr	Thr	Tyr	Leu	Ala
Gly 305	Asp	Ile	Val	Tyr	His	Asp	Glu	Lys	Phe	Lys	Gln	Asp	Tyr	Thr	Lys
Tyr	Ile	Asn	Ile	Trp	Gly	Ala	Asp	His	His	Gly	Tyr	Ile	Ala	Arg	Val
Lys	Ala	Ser	Leu	Glu	Phe	Leu	Gly	Tyr	Asp	Ser	Asn	Lys	Leu	Glu	Val
Leu	Leu	Ala	Gln	Met	Val	Arg	Leu	Lys	Asp	Asn	Glu	Pro	Tyr	Lys	
Met	Ser	Lys	Arg	Ala	Gly	Asn	Phe	Ile	Leu	Ile	Lys	Asp	Val	Val	Asp
Asp 385	Val	Gly	Lys	Asp	Ala	Leu	Arg	Phe	Ile	Phe	Leu	Ser	Lys	Arg	Leu
Asp	Thr	His	Leu	Glu	Phe	Asp	Val	Asn	Thr	Leu	Lys	Lys	Gln	Asp	Ser
Ser	Asn	Pro	Ile	Tyr	Tyr	Ile	His	Tyr	Ala	Asn	Ser	Arg	Ile	His	Thr
Met	Leu	Glu	Lys	Ser	Pro	Phe	Ser	Lys	Glu	Glu	Val	Leu	Gln	Thr	Pro
Leu	Thr	Asn	Leu	Asn	Ala	Glu	Glu	Lys	Tyr	Leu	Leu	Phe	Ser	Ala	Leu
Ser 465	Leu	Pro	Lys	Ala	Ile	Glu	Ser	Ser	Phe	Glu	Glu	Tyr	Gly	Leu	Gln
Lys	Met	Cys	Glu	Tyr	Ala	Lys	Thr	Leu	Ala	Ser	Glu	Phe	His	Arg	Phe
Tyr	Asn	Ala	Gly	Lys	Ile	Leu	Asp	Thr	Pro	Lys	Ala	Lys	Glu	Leu	Leu

Lys	Ile	Cys	Leu	Ile	Val	Ser	Leu	Ser	Leu	Ser	Asn	Ala	Phe	Lys	Leu
		515					520					525			
Leu	Gly	Ile	Glu	Ile	Lys	Thr	Lys	Ile	Ser	Ala	Arg	Asp			
	530					535					540				

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 38...835
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

AAGTAGAGAT TATATTACCT AGATAGTGAA TCAACGA ATG AAA AGC CAC TTC CAA	55
Met Lys Ser His Phe Gln	
1 5	
TAC AGC ACG CTA GAA AAT ATC CCT AAA GCC TTT GAC ATT CTC AAA GAC	103
Tyr Ser Thr Leu Glu Asn Ile Pro Lys Ala Phe Asp Ile Leu Lys Asp	
10 15 20	
CCC CCT AAA AAA CTC TAT TGT GTG GGC GAT ACC AAG CTT TTG GAC ACG	151
Pro Pro Lys Lys Leu Tyr Cys Val Gly Asp Thr Lys Leu Leu Asp Thr	
25 30 35	
CCT TTA AAA GTG GCG ATC ATA GGC ACA AGA AGA CCC ACC CCT TAC AGC	199
Pro Leu Lys Val Ala Ile Ile Gly Thr Arg Arg Pro Thr Pro Tyr Ser	
40 45 50	
AAG CAA CAC ACG ATC ACT CTA GCT AGA GAG CTT GCT AAA AAT GGC GCG	247
Lys Gln His Thr Ile Thr Leu Ala Arg Glu Leu Ala Lys Asn Gly Ala	
55 60 65 70	
GTT ATT GTG AGT GGG GGA GCG TTA GGC GTG GAT ATT ATC GCT CAA GAA	295
Val Ile Val Ser Gly Gly Ala Leu Gly Val Asp Ile Ile Ala Gln Glu	
75 80 85	
AAC GCC TTG CCA AAA ACG ATC ATG CTT TCG CCT TGC AGT TTG GAT TTC	343
Asn Ala Leu Pro Lys Thr Ile Met Leu Ser Pro Cys Ser Leu Asp Phe	
90 95 100	
ATC TAT CCT ACG AAC AAT CAT AAA GTG ATC CAA GAA ATC GCG CAA AAC	391
Ile Tyr Pro Thr Asn Asn His Lys Val Ile Gln Glu Ile Ala Gln Asn	
105 110 115	
GGC TTG ATT TTA AGC GAA TAT GAA AAG GAT TTC ATG CCC ATT AAA GGC	439
Gly Leu Ile Leu Ser Glu Tyr Glu Lys Asp Phe Met Pro Ile Lys Gly	
120 125 130	

TCT TTT TTG GCG AGA AAC CGC CTG GTG ATC GCT TTA AGC GAT GTG GTG	487
Ser Phe Leu Ala Arg Asn Arg Leu Val Ile Ala Leu Ser Asp Val Val	
135 140 145 150	
ATT ATC CCC CAA GCG GAT TTA AAA AGC GGC TCT ATG AGC AGC GCG AGA	535
Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly Ser Met Ser Ser Ala Arg	
155 160 165	
TTA GCC CAG AAA TAC CAA AAG CCT TTA TTT GTT TTA CCC CAA CGC CTG	583
Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe Val Leu Pro Gln Arg Leu	
170 175 180	
AAT GAG AGC GAT GGC ACT AAT GAG CTT TTA GAA AAA GGG CAG GCT CAA	631
Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu Glu Lys Gly Gln Ala Gln	
185 190 195	
GGG ATA TTT AAT ATT CAA AAT TTT ATA AAC ACC CTT TTA AAA GAC TAC	679
Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn Thr Leu Leu Lys Asp Tyr	
200 205 210	
CAT TTA AAA GAA ATG CCT GAA ATG GAA GAT GAA TTT TTA GAA TAT TGT	727
His Leu Lys Glu Met Pro Glu Met Glu Asp Glu Phe Leu Glu Tyr Cys	
215 220 225 230	
GCC AAA AAC CCG AGC TAT GAA GAA GCG TAT CTC AAA TTT GGG GAT AAG	775
Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr Leu Lys Phe Gly Asp Lys	
235 240 245	
CTT TTA GAA TAC GAG CTG TTG GGT AAG ATC AAG CGC ATC AAT CAC ATT	823
Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile Lys Arg Ile Asn His Ile	
250 255 260	
GTG GTG TTA GCG TGATTTTGGC ATGCGATGTG GGGTTAAAAC GCATTGGCAT CGCTG	880
Val Val Leu Ala	
265	
CGCTTTTAAA TGCGGT	896

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

Met Lys Ser His Phe Gln Tyr Ser Thr Leu Glu Asn Ile Pro Lys Ala	
1 5 10 15	
Phe Asp Ile Leu Lys Asp Pro Pro Lys Lys Leu Tyr Cys Val Gly Asp	
20 25 30	
Thr Lys Leu Leu Asp Thr Pro Leu Lys Val Ala Ile Ile Gly Thr Arg	
35 40 45	
Arg Pro Thr Pro Tyr Ser Lys Gln His Thr Ile Thr Leu Ala Arg Glu	
50 55 60	

ATC TTA AAG CCT GAG TTT AAA TAC GGC GTT TCG CTC ATT TAC TTG ATA	255
Ile Leu Lys Pro Glu Phe Lys Tyr Gly Val Ser Leu Ile Tyr Leu Ile	
45 50 55	
GAG AGC ACA ATC CTT TAC TTT GTC AGC AAA GAT CTT TCT TGG ATA GTA	303
Glu Ser Thr Ile Leu Tyr Phe Val Ser Lys Asp Leu Ser Trp Ile Val	
60 65 70	
GCG CTA ACG ATA TTC TCA CTA TCT TTG ATA CTG GTA GCG TTT AAG ATC	351
Ala Leu Thr Ile Phe Ser Leu Ser Leu Ile Leu Val Ala Phe Lys Ile	
75 80 85 90	
TTC CTC CTT AAA GAC AAC CCT AAC AAA CGC TTC AAA AAC AAC AAG AGG	399
Phe Leu Leu Lys Asp Asn Pro Asn Lys Arg Phe Lys Asn Asn Lys Arg	
95 100 105	
GAT AAA AAA TAATGTCTTA TTTTTTTTAAA ATCATTCTGG GCACAAGCGT GATCGTGGG	457
Asp Lys Lys	
GG	459

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

Met	Leu	Val	Asp	Lys	Asn	Ser	Ala	Asp	Gln	Lys	Met	Trp	Arg	Ile	Pro
1				5					10					15	
Glu	Lys	Ala	Leu	Trp	Val	Leu	Ser	Leu	Leu	Gly	Gly	Ser	Val	Gly	Phe
			20					25					30		
Leu	Val	Ala	Met	Val	Val	Ser	His	His	Lys	Ile	Leu	Lys	Pro	Glu	Phe
			35				40					45			
Lys	Tyr	Gly	Val	Ser	Leu	Ile	Tyr	Leu	Ile	Glu	Ser	Thr	Ile	Leu	Tyr
			50			55					60				
Phe	Val	Ser	Lys	Asp	Leu	Ser	Trp	Ile	Val	Ala	Leu	Thr	Ile	Phe	Ser
65				70					75					80	
Leu	Ser	Leu	Ile	Leu	Val	Ala	Phe	Lys	Ile	Phe	Leu	Leu	Lys	Asp	Asn
				85				90						95	
Pro	Asn	Lys	Arg	Phe	Lys	Asn	Asn	Lys	Arg	Asp	Lys	Lys			
			100					105							

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 47...379
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

AGCGCTCAAA TCATTTATTG GTTATCAAAA TATTTTAGGA GTGAGT ATG GAA AAT	55
Met Glu Asn	
1	
GAT GTT AAA GAA GAT CTA GAG CAA GCA AGA CCA AAG TTA GAG CCA GAA	103
Asp Val Lys Glu Asp Leu Glu Gln Ala Arg Pro Lys Leu Glu Pro Glu	
5 10 15	
AAG CAA AAG CAA GAG CCA GAG GAA CAG AAA CAA GAA AAA CAA GAC AAA	151
Lys Gln Lys Gln Glu Pro Glu Glu Gln Lys Gln Glu Lys Gln Asp Lys	
20 25 30 35	
CAA GAG CAG AAG CCA AAG CAA GAA AAA GAA GAG TCA AAG AGC AAG GAA	199
Gln Glu Gln Lys Pro Lys Gln Glu Lys Glu Glu Ser Lys Ser Lys Glu	
40 45 50	
CAA GAA GAA AAC AAA AAA CAA AAG AGA TCT AGC TAT ATT TTT TGG GGA	247
Gln Glu Glu Asn Lys Lys Gln Lys Arg Ser Ser Tyr Ile Phe Trp Gly	
55 60 65	
TGT ATT ATT GGT TTG TGT ATA GTT GTT ATT ATT GCC AAA ATT ATT GCG	295
Cys Ile Ile Gly Leu Cys Ile Val Val Ile Ile Ala Lys Ile Ile Ala	
70 75 80	
TTT GGC GGA TCT AGT GAG GAG GCA AAA GCA GAC AAA CCA AAA AAC TCT	343
Phe Gly Gly Ser Ser Glu Glu Ala Lys Ala Asp Lys Pro Lys Asn Ser	
85 90 95	
TTA AGT ATG CTG AAA AAC TTT TAC CTA CCG ATA TTA TAAAAGATAA TCTTAA	395
Leu Ser Met Leu Lys Asn Phe Tyr Leu Pro Ile Leu	
100 105 110	
TAAC	399

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

Met Glu Asn Asp Val Lys Glu Asp Leu Glu Gln Ala Arg Pro Lys Leu	
1 5 10 15	
Glu Pro Glu Lys Gln Lys Gln Glu Pro Glu Glu Gln Lys Gln Glu Lys	

ACG Thr	GTG Val	GAT Asp	AAC Asn 110	GGG Gly	ATT Ile	AAC Asn	GCC Ala	TTT Phe 115	GAA Glu	GCC Ala	GCG Ala	CGA Arg	TTT Phe 120	TGT Cys	AAA Lys	386
GAA Glu	AAA Lys	AAT Asn 125	TAC Tyr	ACC Thr	CTT Leu	ATC Ile	ATC Ile 130	ACA Thr	GAT Asp	CAC His	CAT His	TGC Cys 135	TTA Leu	CAC His	CAT His	434
GAT Asp	GAA Glu	GTC Val	CCA Pro	GAC Asp	GCT Ala	TAT Tyr 145	GCG Ala	GTG Val	ATC Ile	AAC Asn	CCC Pro 150	AAG Lys	CAA Gln	CCG Pro	GAT Asp	482
TGT Cys 155	GAT Asp	TTT Phe	ATC Ile	CAA Gln	AAG Lys 160	GAA Glu	GTG Val	TGC Cys	GGG Gly 165	GCG Ala	TTG Leu	GTA Val	GCG Ala	TTT Phe	TAT Tyr 170	530
TTG Leu	TGC Cys	TAT Tyr	GGG Gly	ATC Ile 175	CAT His	CAG Gln	CTT Leu	TTA Leu	GGA Gly 180	AAA Lys	GAA Glu	AAA Lys	AGC Ser	CAT His 185	TCT Ser	578
AGT Ser	GAG Glu	TTA Leu	TTA Leu 190	TGT Cys	TTA Leu	GCG Ala	GGC Gly	GTG Val 195	GCG Ala	ACT Thr	ATT Ile	GCT Ala	GAC Asp 200	ATG Met	ATG Met	626
CCT Pro	TTG Leu	ACT Thr 205	TTT Phe	TTT Phe	AAC Asn	CGC Arg	TTT Phe 210	TTA Leu	GTT Val	TCT Ser	AAA Lys	GCC Ala 215	TTG Leu	TAT Tyr	TTT Phe	674
TTG Leu	CAA Gln 220	AAA Lys	GAA Glu	TCC Ser	TTA Leu	GGG Gly 225	GCG Ala	ATG Met	GGT Gly	TTT Phe	TTG Leu 230	CGC Arg	CAA Gln	AGA Arg	GAA Glu	722
GTT Val 235	TTT Phe	AGA Arg	AAA Lys	CGC Arg	TCT Ser 240	TTA Leu	AAA Lys	GCG Ala	AGT Ser	GAT Asp 245	ATT Ile	TCT Ser	TTT Phe	AAT Asn	ATC Ile 250	770
GCC Ala	CCC Pro	TTA Leu	ATC Ile	AAC Asn 255	TCC Ser	GCA Ala	GGG Gly	CGC Arg	ATG Met 260	CAA Gln	GAT Asp	GCG Ala	AAA Lys	ATG Met 265	GCT Ala	818
TTA Leu	GAT Asp	TTT Phe	TTA Leu 270	AGC Ser	GCG Ala	AAT Asn	AAT Asn	TCT Ser 275	CAA Gln	GAT Asp	GGC Gly	TAT Tyr	TCT Ser 280	TTG Leu	TAT Tyr	866
GAA Glu	CGC Arg	TTG Leu 285	AAA Lys	GCA Ala	TGC Cys	AAT Asn	TTG Leu 290	AAG Lys	CGT Arg	AAA Lys	ATG Met	ATC Ile 295	CAA Gln	CAG Gln	CAG Gln	914
GTT Val	TTT Phe 300	GAA Glu	GAA Glu	GCT Ala	TTT Phe	AAG Lys 305	CAT His	GCG Ala	ATG Met	GTT Val	GGA Gly 310	GAA Glu	AAA Lys	ATT Ile	ATC Ile	962
GTC Val 315	GCT Ala	TTT Phe	AAG Lys	GAC Asp	AAT Asn 320	TGG Trp	CAT His	GAG Glu	GGA Gly 325	GTG Val	CTG Leu	GGG Gly	ATT Ile	GTG Val	GCT Ala 330	1010
TCA Ser	AAA Lys	TTA Leu	GTG Val	GAA Glu	GCC Ala	ACT Thr	CAA Gln	AAG Lys	CCA Pro	AGC Ser	CTG Leu	GTT Val	TTT Phe	ACC Thr	TTT Phe	1058

				335				340				345							
AAA Lys	GAA Glu	GGG Gly	GTG Val	TAT Tyr	AAA Lys	GGG Gly	AGC Ser	GCT Ala	CGT Arg	AGC Ser	TCT Ser	TCA Ser	AAC Asn	ATT Ile	GAC Asp	1106			
350				355				360											
TTG Leu	ATT Ile	GAC Asp	GCT Ala	TTG Leu	AAT Asn	GGG Gly	GTT Val	TCT Ser	TCT Ser	TTA Leu	TTG Leu	CTC Leu	GGC Gly	TAT Tyr	GGA Gly	1154			
365				370				375											
GGG Gly	CAT His	AGG Arg	CAA Gln	GCT Ala	TGC Cys	GGG Gly	TTG Leu	AGC Ser	GTT Val	GAA Glu	AAA Lys	AAC Asn	AAT Asn	ATC Ile	ATC Ile	1202			
380				385				390											
TCG Ser	CTC Leu	TTT Phe	GAA Glu	ACT Thr	TTA Leu	GAA Glu	AAT Asn	TTT Phe	GAT Asp	TTT Phe	AAA Lys	GTT Val	TTA Leu	CCT Pro	TTT Phe	1250			
395				400				405											
TGT Cys	AAA Lys	ACA Thr	GAG Glu	CCC Pro	CCT Pro	TTA Leu	ACG Thr	CTC Leu	AAA Lys	TTA Leu	AAA Lys	GAC Asp	ATT Ile	GAC Asp	AGA Arg	1298			
415				420				425											
GAG Glu	CTT Leu	TTA Leu	GAG Glu	ATT Ile	ATA Ile	GAA Glu	ATG Met	GGC Gly	GAA Glu	CCT Pro	TAT Tyr	GGG Gly	CAA Gln	GAA Glu	AAC Asn	1346			
430				435				440											
CCT Pro	GAA Glu	CCC Pro	CTA Leu	TTC Phe	CAA Gln	GCA Ala	AAA Lys	AAT Asn	TTA Leu	GAA Glu	GTC Val	ATA Ile	GAA Glu	GAA Glu	AAA Lys	1394			
445				450				455											
ATC Ile	ATT Ile	AAA Lys	GAA Glu	AGC Ser	CAC His	CAG Gln	GTT Val	TTG Leu	CGT Arg	TTT Phe	AAG Lys	GAT Asp	AAA Lys	GAA Glu	TGC Cys	1442			
460				465				470											
GTC Val	AAA Lys	GAG Glu	GCT Ala	ATT Ile	TAT Tyr	TTT Phe	AGC Ser	GCT Ala	GAG Glu	CGG Arg	TTT Phe	TTG Leu	AAA Lys	GCG Ala	GGC Gly	1490			
475				480				485											
GAA Glu	AAG Lys	GTG Val	AGC Ser	GTG Val	CTT Leu	TTT Phe	AGC Ser	GTG Val	GAA Glu	TTA Leu	GAT Asp	GAG Glu	TGT Cys	TCT Ser	AAT Asn	1538			
495				500				505											
GAG Glu	CCT Pro	AAA Lys	ATG Met	TTT Phe	GTT Val	AAA Lys	AGT Ser	TTG Leu	TTG Leu	TAGTGCCTTT		TGTTGAAGAA		GAA	1591				
510				515															
TTTGAAATTT TAAAACCCAC CAAAGCCTTG TTTTTT																1627			

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

```

Met Lys Gln Lys Leu Lys Ala Gln Ile Lys Glu Arg Met Ala Ser Ile
 1      5      10      15
Ala Tyr Asn Glu Lys Gly Phe Pro Ser Pro Phe Leu Phe Lys Asp Leu
 20      25      30
Lys Lys Ala Ala Leu Lys Ile Ile Glu Ala Met Arg Thr Asn Thr Glu
 35      40      45
Ile Leu Val Val Gly Asp Tyr Asp Ala Asp Gly Val Ile Ser Ser Ala
 50      55      60
Ile Met Ala Lys Phe Phe Glu Ser Leu Asn Tyr Lys His Val Arg Ile
 65      70      75      80
Ala Ile Pro Asn Arg Phe Met Asp Gly Tyr Gly Ile Ser Lys Lys Phe
 85      90      95
Leu Glu Lys His His Ala Pro Leu Ile Ile Thr Val Asp Asn Gly Ile
100      105      110
Asn Ala Phe Glu Ala Ala Arg Phe Cys Lys Glu Lys Asn Tyr Thr Leu
115      120      125
Ile Ile Thr Asp His His Cys Leu His His Asp Glu Val Pro Asp Ala
130      135      140
Tyr Ala Val Ile Asn Pro Lys Gln Pro Asp Cys Asp Phe Ile Gln Lys
145      150      155      160
Glu Val Cys Gly Ala Leu Val Ala Phe Tyr Leu Cys Tyr Gly Ile His
165      170      175
Gln Leu Leu Gly Lys Glu Lys Ser His Ser Ser Glu Leu Leu Cys Leu
180      185      190
Ala Gly Val Ala Thr Ile Ala Asp Met Met Pro Leu Thr Phe Phe Asn
195      200      205
Arg Phe Leu Val Ser Lys Ala Leu Tyr Phe Leu Gln Lys Glu Ser Leu
210      215      220
Gly Ala Met Gly Phe Leu Arg Gln Arg Glu Val Phe Arg Lys Arg Ser
225      230      235      240
Leu Lys Ala Ser Asp Ile Ser Phe Asn Ile Ala Pro Leu Ile Asn Ser
245      250      255
Ala Gly Arg Met Gln Asp Ala Lys Met Ala Leu Asp Phe Leu Ser Ala
260      265      270
Asn Asn Ser Gln Asp Gly Tyr Ser Leu Tyr Glu Arg Leu Lys Ala Cys
275      280      285
Asn Leu Lys Arg Lys Met Ile Gln Gln Gln Val Phe Glu Glu Ala Phe
290      295      300
Lys His Ala Met Val Gly Glu Lys Ile Ile Val Ala Phe Lys Asp Asn
305      310      315      320
Trp His Glu Gly Val Leu Gly Ile Val Ala Ser Lys Leu Val Glu Ala
325      330      335
Thr Gln Lys Pro Ser Leu Val Phe Thr Phe Lys Glu Gly Val Tyr Lys
340      345      350
Gly Ser Ala Arg Ser Ser Ser Asn Ile Asp Leu Ile Asp Ala Leu Asn
355      360      365
Gly Val Ser Ser Leu Leu Leu Gly Tyr Gly Gly His Arg Gln Ala Cys
370      375      380
Gly Leu Ser Val Glu Lys Asn Asn Ile Ile Ser Leu Phe Glu Thr Leu
385      390      395      400
Glu Asn Phe Asp Phe Lys Val Leu Pro Phe Cys Lys Thr Glu Pro Pro
405      410      415
Leu Thr Leu Lys Leu Lys Asp Ile Asp Arg Glu Leu Leu Glu Ile Ile
420      425      430
Glu Met Gly Glu Pro Tyr Gly Gln Glu Asn Pro Glu Pro Leu Phe Gln
435      440      445

```

Ala	Lys	Asn	Leu	Glu	Val	Ile	Glu	Glu	Lys	Ile	Ile	Lys	Glu	Ser	His
450						455					460				
Gln	Val	Leu	Arg	Phe	Lys	Asp	Lys	Glu	Cys	Val	Lys	Glu	Ala	Ile	Tyr
465					470				475						480
Phe	Ser	Ala	Glu	Arg	Phe	Leu	Lys	Ala	Gly	Glu	Lys	Val	Ser	Val	Leu
				485					490						495
Phe	Ser	Val	Glu	Leu	Asp	Glu	Cys	Ser	Asn	Glu	Pro	Lys	Met	Phe	Val
			500					505					510		
Lys	Ser	Leu	Leu												
			515												

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...908
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

ATCGTAATGA AATAATCACC ACCCCTATAA GCTTTGTAGC GACGGCTAAC	ATG CTT	56
	Met Leu	
	1	
TTA GAA AGC GGT TAT ACA CCC GTA TTT GCT GGA ATT AAA AAC GAT GGC		104
Leu Glu Ser Gly Tyr Thr Pro Val Phe Ala Gly Ile Lys Asn Asp Gly		
5	10	15
AAT ATA GAT GAA TTA GCC CTA GAA AAG CTC ATT AAC GAA AGA ACC AAA		152
Asn Ile Asp Glu Leu Ala Leu Glu Lys Leu Ile Asn Glu Arg Thr Lys		
20	25	30
GCC ATA GTG AGC GTG GAT TAT GCC GGT AAA AGC GTG GAA GTA GAA AGC		200
Ala Ile Val Ser Val Asp Tyr Ala Gly Lys Ser Val Glu Val Glu Ser		
35	40	45
GTT CAA AAG CTT TGC AAA AAG CAT TCT TTG AGC TTT CTT TCT GAC AGC		248
Val Gln Lys Leu Cys Lys Lys His Ser Leu Ser Phe Leu Ser Asp Ser		
	55	60
TCG CAT GCT CTA GGA AGC GAG TAT CAA AAC AAA AAA GTA GGA GGC TTT		296
Ser His Ala Leu Gly Ser Glu Tyr Gln Asn Lys Lys Val Gly Gly Phe		
70	75	80
GCG TTA GCG AGC GTG TTT AGT TTC CAT GCC ATT AAG CCC ATC ACT ACG		344
Ala Leu Ala Ser Val Phe Ser Phe His Ala Ile Lys Pro Ile Thr Thr		
85	90	95
GCT GAA GGG GGA GCG GTC GTT ACT AAC GAT AGC GAA TTG CAT GAA AAA		392

[illegible]

(2) INFORMATION FOR SEQ ID NO:552:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

Met	Leu	Leu	Glu	Ser	Gly	Tyr	Thr	Pro	Val	Phe	Ala	Gly	Ile	Lys	Asn	1	5	10	15
Asp	Gly	Asn	Ile	Asp	Glu	Leu	Ala	Leu	Glu	Lys	Leu	Ile	Asn	Glu	Arg	20	25	30	
Thr	Lys	Ala	Ile	Val	Ser	Val	Asp	Tyr	Ala	Gly	Lys	Ser	Val	Glu	Val	35	40	45	
Glu	Ser	Val	Gln	Lys	Leu	Cys	Lys	Lys	His	Ser	Leu	Ser	Phe	Leu	Ser	50	55	60	
Asp	Ser	Ser	His	Ala	Leu	Gly	Ser	Glu	Tyr	Gln	Asn	Lys	Lys	Val	Gly	65	70	75	80
Gly	Phe	Ala	Leu	Ala	Ser	Val	Phe	Ser	Phe	His	Ala	Ile	Lys	Pro	Ile	85	90	95	
Thr	Thr	Ala	Glu	Gly	Gly	Ala	Val	Val	Thr	Asn	Asp	Ser	Glu	Leu	His	100	105	110	
Glu	Lys	Met	Lys	Leu	Phe	Arg	Ser	His	Gly	Met	Leu	Lys	Lys	Asp	Phe	115	120	125	
Phe	Glu	Gly	Glu	Val	Lys	Ser	Ile	Gly	His	Asn	Phe	Arg	Leu	Asn	Glu	130	135	140	
Ile	Gln	Ser	Ala	Leu	Gly	Leu	Ser	Gln	Leu	Lys	Lys	Ala	Pro	Phe	Leu	145	150	155	160
Met	Gln	Lys	Arg	Glu	Glu	Ala	Ala	Leu	Thr	Tyr	Asp	Arg	Ile	Phe	Lys	165	170	175	
Asp	Asn	Pro	Tyr	Phe	Thr	Pro	Leu	His	Pro	Leu	Leu	Lys	Asp	Lys	Ser	180	185	190	
Ser	Asn	His	Leu	Tyr	Pro	Ile	Leu	Met	His	Gln	Lys	Phe	Phe	Thr	Cys	195	200	205	
Lys	Lys	Leu	Ile	Leu	Glu	Ser	Leu	His	Lys	Arg	Gly	Ile	Leu	Ala	Gln	210	215	220	
Val	His	Tyr	Lys	Pro	Ile	Tyr	Gln	Tyr	Gln	Leu	Tyr	Gln	Gln	Leu	Phe	225	230	235	240
Asn	Thr	Ala	Pro	Leu	Lys	Ser	Ala	Glu	Asp	Phe	Tyr	His	Ala	Glu	Ile	245	250	255	
Ser	Leu	Pro	Cys	His	Ala	Asn	Leu	Asn	Leu	Glu	Ser	Val	Gln	Asn	Ile	260	265	270	
Ala	His	Ser	Val	Leu	Lys	Thr	Phe	Glu	Ser	Phe	Lys	Ile	Glu			275	280	285	

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 15...692
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

TAATGGGCCT	TTGA	ATG	CGT	TTT	GTC	TAT	CAC	CCT	TTA	GCC	AAA	GAG	CCT			50		
		Met	Arg	Phe	Val	Tyr	His	Pro	Leu	Ala	Lys	Glu	Pro					
		1				5					10							
GTT	TTA	AAA	ATA	GAA	GGC	GAG	AGT	TAT	ACG	CAT	TTA	TAC	CGA	TCA	AGG	98		
Val	Leu	Lys	Ile	Glu	Gly	Glu	Ser	Tyr	Thr	His	Leu	Tyr	Arg	Ser	Arg			
		15				20						25						
CGT	GTC	AAA	AGT	GCG	AGT	CGT	TTG	GAT	TTG	AGA	AAT	TTA	AAA	GAC	GGC	146		
Arg	Val	Lys	Ser	Ala	Ser	Arg	Leu	Asp	Leu	Arg	Asn	Leu	Lys	Asp	Gly			
	30					35					40							
TTT	TTA	TAC	ACC	TAT	GAG	CAT	GCA	GAA	ATC	ACT	AAA	AAA	CAC	GCC	CTT	194		
Phe	Leu	Tyr	Thr	Tyr	Glu	His	Ala	Glu	Ile	Thr	Lys	Lys	His	Ala	Leu			
45				50					55						60			
TTA	AAG	CTA	GTG	GGC	GCG	CGA	TTA	TTA	GAG	GTT	ATG	GCC	AGT	AAA	AAA	242		
Leu	Lys	Leu	Val	Gly	Ala	Arg	Leu	Leu	Glu	Val	Met	Ala	Ser	Lys	Lys			
			65					70					75					
ACG	CAT	TTG	ATT	TTA	AGC	GTG	ATT	GAA	ATC	AAA	AAC	ATT	GAA	AAA	ATC	290		
Thr	His	Leu	Ile	Leu	Ser	Val	Ile	Glu	Ile	Lys	Asn	Ile	Glu	Lys	Ile			
		80				85						90						
CTA	CCC	TTT	TTA	AAT	CAG	TTA	GGC	GTG	AGC	AAG	TTG	AGT	TTA	TTC	TAT	338		
Leu	Pro	Phe	Leu	Asn	Gln	Leu	Gly	Val	Ser	Lys	Leu	Ser	Leu	Phe	Tyr			
		95				100						105						
GCG	GAT	TTT	AGC	CAA	CGC	AAT	GAA	AAA	ATA	GAC	ATC	GCT	AAA	TTA	GAG	386		
Ala	Asp	Phe	Ser	Gln	Arg	Asn	Glu	Lys	Ile	Asp	Ile	Ala	Lys	Leu	Glu			
	110					115					120							
CGC	TTT	CAA	AAG	ATT	TTG	ATC	CAT	TCT	TGC	GAG	CAG	TGT	GGT	AGG	AGT	434		
Arg	Phe	Gln	Lys	Ile	Leu	Ile	His	Ser	Cys	Glu	Gln	Cys	Gly	Arg	Ser			
125				130					135						140			
GCT	TTA	ATG	GAA	TTG	GAA	GTG	TTT	TCA	AAC	ACT	AAA	GAG	GCG	CTA	AAA	482		
Ala	Leu	Met	Glu	Leu	Glu	Val	Phe	Ser	Asn	Thr	Lys	Glu	Ala	Leu	Lys			
			145					150						155				
GCC	TAT	CCT	AAG	GCG	AGC	GTT	TTG	GAT	TTT	AAG	GGC	GAA	ACC	TTA	NCC	530		
Ala	Tyr	Pro	Lys	Ala	Ser	Val	Leu	Asp	Phe	Lys	Gly	Glu	Thr	Leu	Xaa			
		160				165						170						
GCA	AGC	GCG	GAT	TTT	GAA	AAG	GGC	GTT	ATC	ATA	GGG	CCT	GAG	GGG	GGC	578		
Ala	Ser	Ala	Asp	Phe	Glu	Lys	Gly	Val	Ile	Ile	Gly	Pro	Glu	Gly	Gly			
		175				180						185						
TTT	AGC	GAA	CCA	GAA	AGA	GGG	TAT	TTT	AAA	GAG	CGT	GAA	ATT	TAT	CGC	626		
Phe	Ser	Glu	Pro	Glu	Arg	Gly	Tyr	Phe	Lys	Glu	Arg	Glu	Ile	Tyr	Arg			
	190					195					200							
ATC	CCG	TTA	GAT	ATG	GTG	CTA	AAG	TCT	GAG	AGT	GCA	TGC	GTG	TTT	GTA	674		
Ile	Pro	Leu	Asp	Met	Val	Leu	Lys	Ser	Glu	Ser	Ala	Cys	Val	Phe	Val			
205				210					215						220			
GCG	AGT	ATC	GCA	CAA	GTT	TAGGGGGTTA				TTGGGGATTT				TAAATCCTAA		AAAATC	728	
Ala	Ser	Ile	Ala	Gln	Val													

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

```

Met Arg Phe Val Tyr His Pro Leu Ala Lys Glu Pro Val Leu Lys Ile
 1           5           10           15
Glu Gly Glu Ser Tyr Thr His Leu Tyr Arg Ser Arg Arg Val Lys Ser
          20           25           30
Ala Ser Arg Leu Asp Leu Arg Asn Leu Lys Asp Gly Phe Leu Tyr Thr
          35           40           45
Tyr Glu His Ala Glu Ile Thr Lys Lys His Ala Leu Lys Leu Val
          50           55           60
Gly Ala Arg Leu Leu Glu Val Met Ala Ser Lys Lys Thr His Leu Ile
65           70           75           80
Leu Ser Val Ile Glu Ile Lys Asn Ile Glu Lys Ile Leu Pro Phe Leu
          85           90           95
Asn Gln Leu Gly Val Ser Lys Leu Ser Leu Phe Tyr Ala Asp Phe Ser
          100          105          110
Gln Arg Asn Glu Lys Ile Asp Ile Ala Lys Leu Glu Arg Phe Gln Lys
          115          120          125
Ile Leu Ile His Ser Cys Glu Gln Cys Gly Arg Ser Ala Leu Met Glu
          130          135          140
Leu Glu Val Phe Ser Asn Thr Lys Glu Ala Leu Lys Ala Tyr Pro Lys
145          150          155          160
Ala Ser Val Leu Asp Phe Lys Gly Glu Thr Leu Xaa Ala Ser Ala Asp
          165          170          175
Phe Glu Lys Gly Val Ile Ile Gly Pro Glu Gly Gly Phe Ser Glu Pro
          180          185          190
Glu Arg Gly Tyr Phe Lys Glu Arg Glu Ile Tyr Arg Ile Pro Leu Asp
          195          200          205
Met Val Leu Lys Ser Glu Ser Ala Cys Val Phe Val Ala Ser Ile Ala
210          215          220
Gln Val
225

```

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

(B) LOCATION: 13...840
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

TTATGAAATT GA ATG ACC CTT TCG CAA GCC CTA AAC AAA GCC AAA AAA GGA	51
Met Thr Leu Ser Gln Ala Leu Asn Lys Ala Lys Lys Gly	
1 5 10	
TTA TCG CAA AAA GGT TTT AGG GGG GGC TTA GAA TCT GAA ATT TTA TTA	99
Leu Ser Gln Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu	
15 20 25	
GGC TTT GTC TTG CAA AAA GAA AGG GTT TTT TTG CAC ACG CAT GCC TAT	147
Gly Phe Val Leu Gln Lys Glu Arg Val Phe Leu His Thr His Ala Tyr	
30 35 40 45	
TTA GAG TTA AAC CAC GAA GAA GAG GTG CGT TTT TTT GAA TTG GTA GAA	195
Leu Glu Leu Asn His Glu Glu Glu Val Arg Phe Phe Glu Leu Val Glu	
50 55 60	
AAG CGC TTG AAT AAC TGC CCC ATA GAG TAT TTA TTA GAA AGC TGT GAT	243
Lys Arg Leu Asn Asn Cys Pro Ile Glu Tyr Leu Leu Glu Ser Cys Asp	
65 70 75	
TTT TAT GGG CGC TCT TTT TTT GTG AAT GAG CAT GTT TTA ATC CCA CGA	291
Phe Tyr Gly Arg Ser Phe Phe Val Asn Glu His Val Leu Ile Pro Arg	
80 85 90	
CCT GAA ACC GAG ATT TTG GTC CAA AAA GCC CTT GAT ATT ATT TCT CAA	339
Pro Glu Thr Glu Ile Leu Val Gln Lys Ala Leu Asp Ile Ile Ser Gln	
95 100 105	
TAC CAT TTA AAA GAG ATA GGC GAA ATC GGC ATA GGG AGC GGA TGC GTG	387
Tyr His Leu Lys Glu Ile Gly Glu Ile Gly Ile Gly Ser Gly Cys Val	
110 115 120 125	
TCT GTG AGT TTG GCT TTA GAA AAC CCT AAT CTC TCT ATT TAT GCG AGC	435
Ser Val Ser Leu Ala Leu Glu Asn Pro Asn Leu Ser Ile Tyr Ala Ser	
130 135 140	
GAT ATT TCA CCA AAC GCT TTA GAA GTG GCG TCC AAA AAT ATT GAG CAC	483
Asp Ile Ser Pro Asn Ala Leu Glu Val Ala Ser Lys Asn Ile Glu His	
145 150 155	
TTT TGT CTA AAA GAG CGT GTT TTT TTA AAA CAA ACA CGC CTT TGG GAT	531
Phe Cys Leu Lys Glu Arg Val Phe Leu Lys Gln Thr Arg Leu Trp Asp	
160 165 170	
CAT ATG CCC ATG ATA GAA ATG CTT GTC TCT AAC CCG CCC TAT ATC GCT	579
His Met Pro Met Ile Glu Met Leu Val Ser Asn Pro Pro Tyr Ile Ala	
175 180 185	
AGA AAT TAT CCT TTG GAA AAA TCC GTC CTC AAA GAA CCG CAT GAA GCC	627
Arg Asn Tyr Pro Leu Glu Lys Ser Val Leu Lys Glu Pro His Glu Ala	
190 195 200 205	

Pro	Leu	Glu	Lys	Ser	Val	Leu	Lys	Glu	Pro	His	Glu	Ala	Leu	Phe	Gly
	195						200					205			
Gly	Val	Lys	Gly	Asp	Glu	Ile	Leu	Lys	Glu	Ile	Val	Phe	Leu	Ala	Ala
	210					215					220				
Lys	Leu	Lys	Ile	Pro	Phe	Leu	Val	Cys	Glu	Met	Gly	Tyr	Asp	Gln	Leu
225				230					235						240
Lys	Ser	Leu	Lys	Glu	Cys	Leu	Glu	Phe	Cys	Gly	Tyr	Asp	Ala	Glu	Phe
			245						250					255	
Tyr	Lys	Asp	Leu	Ser	Gly	Phe	Asp	Arg	Gly	Phe	Val	Gly	Val	Leu	Lys
		260					265						270		
Ser	Phe	Leu	Arg												
		275													

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...960
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

CCATCTCAAA ATAAGGACGC CTAAATC ATG GCA GAA AAA ACA GCT AAC GAT TTA	54
Met Ala Glu Lys Thr Ala Asn Asp Leu	
1 5	
AAA CTA AGT GAG ATA GAA CTC GTG GAT TTT CGT ATT TAT GGC ATG CAA	102
Lys Leu Ser Glu Ile Glu Leu Val Asp Phe Arg Ile Tyr Gly Met Gln	
10 15 20 25	
GAG GGC GTC CCT TAT GAG GGG ATT TAT GGT ATC AAT GTG GCT AAA GTC	150
Glu Gly Val Pro Tyr Glu Gly Ile Tyr Gly Ile Asn Val Ala Lys Val	
30 35 40	
CAA GAA ATC ATC CCC ATG CCC ACC CTT TTT GAA TAC CCC ACG AAT TTG	198
Gln Glu Ile Ile Pro Met Pro Thr Leu Phe Glu Tyr Pro Thr Asn Leu	
45 50 55	
GAT TAC ATT ATC GGC GTG TTT GAT TTG CGC TCC ATA ATC ATT CCG CTT	246
Asp Tyr Ile Ile Gly Val Phe Asp Leu Arg Ser Ile Ile Ile Pro Leu	
60 65 70	
ATA GAC TTG GCT AAA TGG ATA GGG ATT ATC CCA GAT AAA AGC AAG GAA	294
Ile Asp Leu Ala Lys Trp Ile Gly Ile Ile Pro Asp Lys Ser Lys Glu	
75 80 85	
AAC GAA AAA ATC GTC ATT ATC ACT GAA TTT AAC AAC GTT AAA ATG GGT	342
Asn Glu Lys Ile Val Ile Ile Thr Glu Phe Asn Asn Val Lys Met Gly	
90 95 100 105	

TTT TTA GTC CAT TCG GCT AGG CGT ATC AGG CGC ATT AGC TGG AAA GAT	390
Phe Leu Val His Ser Ala Arg Arg Ile Arg Arg Ile Ser Trp Lys Asp	
110 115 120	
GTG GAG CCT GCA TCC TTT AGC GCC TCT AAT AGC ATC AAT AAA GAA AAT	438
Val Glu Pro Ala Ser Phe Ser Ala Ser Asn Ser Ile Asn Lys Glu Asn	
125 130 135	
ATT ACC GGC ACG ACA CGC ATT GAA AAC GAC AAA ACC CTG CTC ATT TTG	486
Ile Thr Gly Thr Thr Arg Ile Glu Asn Asp Lys Thr Leu Leu Ile Leu	
140 145 150	
GAT TTA GAA AGC ATT TTA GAC GAT TTA AAG CTT AAT GAA GAC GCT AAA	534
Asp Leu Glu Ser Ile Leu Asp Asp Leu Lys Leu Asn Glu Asp Ala Lys	
155 160 165	
AAC GCT AAA GAT ACC CAT AAA GAG CGT TTT GAA GGC GAA GTG TTG TTT	582
Asn Ala Lys Asp Thr His Lys Glu Arg Phe Glu Gly Glu Val Leu Phe	
170 175 180 185	
TTA GAC GAT AGC AAG ACC GCA AGA AAA ACC TTA AAA AAC CAT TTG AGC	630
Leu Asp Asp Ser Lys Thr Ala Arg Lys Thr Leu Lys Asn His Leu Ser	
190 195 200	
AAA TTA GGT TTT AGC ATC ACT GAA GCT GTG GAT GGG GAA GAC GGG TTG	678
Lys Leu Gly Phe Ser Ile Thr Glu Ala Val Asp Gly Glu Asp Gly Leu	
205 210 215	
AAC AAA TTA GAA ATG TTA TTC AAA AAA TAC GGG GAC GAT TTG AGA AAG	726
Asn Lys Leu Glu Met Leu Phe Lys Lys Tyr Gly Asp Asp Leu Arg Lys	
220 225 230	
CAT TTG AAA TTC ATT ATT TCA GAT GTT GAA ATG CCT AAA ATG GAT GGC	774
His Leu Lys Phe Ile Ile Ser Asp Val Glu Met Pro Lys Met Asp Gly	
235 240 245	
TAT CAT TTC TTA TTC AAG CTC CAA AAA GAC CCT AGG TTT GCT TAT ATT	822
Tyr His Phe Leu Phe Lys Leu Gln Lys Asp Pro Arg Phe Ala Tyr Ile	
250 255 260 265	
CCT GTG ATT TTT AAT TCT TCT ATT TGC GAT AAT TAC AGC GCT GAA AGG	870
Pro Val Ile Phe Asn Ser Ser Ile Cys Asp Asn Tyr Ser Ala Glu Arg	
270 275 280	
GCT AAA GAA ATG GGG GCT GTA GCG TAT TTA GTC AAG TTT GAC GCA GAA	918
Ala Lys Glu Met Gly Ala Val Ala Tyr Leu Val Lys Phe Asp Ala Glu	
285 290 295	
AAA TTC ACC GAA GAA ATT TCT AAG ATT TTA GAC AAG AAT GCG TAATTCTTT	969
Lys Phe Thr Glu Glu Ile Ser Lys Ile Leu Asp Lys Asn Ala	
300 305 310	
TTATAAAATT GTAAAATACT CTTATCTCAA ACGCTAAAAA GGGGTTTTAA ATGGATG	1026

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

```

Met Ala Glu Lys Thr Ala Asn Asp Leu Lys Leu Ser Glu Ile Glu Leu
 1      5      10      15
Val Asp Phe Arg Ile Tyr Gly Met Gln Glu Gly Val Pro Tyr Glu Gly
      20      25      30
Ile Tyr Gly Ile Asn Val Ala Lys Val Gln Glu Ile Ile Pro Met Pro
      35      40      45
Thr Leu Phe Glu Tyr Pro Thr Asn Leu Asp Tyr Ile Ile Gly Val Phe
      50      55      60
Asp Leu Arg Ser Ile Ile Ile Pro Leu Ile Asp Leu Ala Lys Trp Ile
      65      70      75      80
Gly Ile Ile Pro Asp Lys Ser Lys Glu Asn Glu Lys Ile Val Ile Ile
      85      90      95
Thr Glu Phe Asn Asn Val Lys Met Gly Phe Leu Val His Ser Ala Arg
      100     105     110
Arg Ile Arg Arg Ile Ser Trp Lys Asp Val Glu Pro Ala Ser Phe Ser
      115     120     125
Ala Ser Asn Ser Ile Asn Lys Glu Asn Ile Thr Gly Thr Thr Arg Ile
      130     135     140
Glu Asn Asp Lys Thr Leu Leu Ile Leu Asp Leu Glu Ser Ile Leu Asp
      145     150     155     160
Asp Leu Lys Leu Asn Glu Asp Ala Lys Asn Ala Lys Asp Thr His Lys
      165     170     175
Glu Arg Phe Glu Gly Glu Val Leu Phe Leu Asp Asp Ser Lys Thr Ala
      180     185     190
Arg Lys Thr Leu Lys Asn His Leu Ser Lys Leu Gly Phe Ser Ile Thr
      195     200     205
Glu Ala Val Asp Gly Glu Asp Gly Leu Asn Lys Leu Glu Met Leu Phe
      210     215     220
Lys Lys Tyr Gly Asp Asp Leu Arg Lys His Leu Lys Phe Ile Ile Ser
      225     230     235     240
Asp Val Glu Met Pro Lys Met Asp Gly Tyr His Phe Leu Phe Lys Leu
      245     250     255
Gln Lys Asp Pro Arg Phe Ala Tyr Ile Pro Val Ile Phe Asn Ser Ser
      260     265     270
Ile Cys Asp Asn Tyr Ser Ala Glu Arg Ala Lys Glu Met Gly Ala Val
      275     280     285
Ala Tyr Leu Val Lys Phe Asp Ala Glu Lys Phe Thr Glu Glu Ile Ser
      290     295     300
Lys Ile Leu Asp Lys Asn Ala
      305     310

```

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 32...697
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GATCTATAAA GAATAGCCAT AAAGAAGAAT T ATG TTA GAT TAT CGC CAA AAA	52
Met Leu Asp Tyr Arg Gln Lys	
1 5	
ATT GAT GCT CTC ATC ACC AAA ATA GAA AAG GCT CGC ACC GCC TAT TCA	100
Ile Asp Ala Leu Ile Thr Lys Ile Glu Lys Ala Arg Thr Ala Tyr Ser	
10 15 20	
AGG CAC CAC ATT GTC AAA ATC GTG GCT GTT TCA AAA AAC GCT TCC CCA	148
Arg His His Ile Val Lys Ile Val Ala Val Ser Lys Asn Ala Ser Pro	
25 30 35	
GAA GCT ATC CAA CAT TAT TAT AAC TGC TCT CAA AGG GCT TTT GGA GAA	196
Glu Ala Ile Gln His Tyr Tyr Asn Cys Ser Gln Arg Ala Phe Gly Glu	
40 45 50 55	
AAT AAA GTT CAA GAT TTA AAA ACT AAA ATG CAT TCT TTA GAG CAT TTG	244
Asn Lys Val Gln Asp Leu Lys Thr Lys Met His Ser Leu Glu His Leu	
60 65 70	
CCC CTT GAA TGG CAC ATG ATA GGC TCT TTA CAA GAA AAT AAA ATC AAT	292
Pro Leu Glu Trp His Met Ile Gly Ser Leu Gln Glu Asn Lys Ile Asn	
75 80 85	
GCG CTT TTG AGT TTA AAG CCC GCT CTT TTG CAT TCT TTA GAC TCT TTA	340
Ala Leu Leu Ser Leu Lys Pro Ala Leu Leu His Ser Leu Asp Ser Leu	
90 95 100	
AAA CTC GCT TTG AAA ATA GAA AAG CGT TGC GAA ATA TTG GGC GTC AAT	388
Lys Leu Ala Leu Lys Ile Glu Lys Arg Cys Glu Ile Leu Gly Val Asn	
105 110 115	
TTA AAC GCT CTT TTA CAG GTT AAT AGC GCG TAT GAG GAA AGT AAA AGC	436
Leu Asn Ala Leu Leu Gln Val Asn Ser Ala Tyr Glu Glu Ser Lys Ser	
120 125 130 135	
GGG GTG GTG CCT GAA GAA GCG CTA GAA ATT TAT TCT CAA ATC AGT GAA	484
Gly Val Val Pro Glu Glu Ala Leu Glu Ile Tyr Ser Gln Ile Ser Glu	
140 145 150	
ACT TGC AAG CAC CTC AAG CTT AAG GGG CTT ATG TGT ATA GGG GCA CAC	532
Thr Cys Lys His Leu Lys Leu Lys Gly Leu Met Cys Ile Gly Ala His	
155 160 165	
ACA GAT GAT GAA AAG GAA ATT GAA AAA TCC TTT ATC ACC ACC AAA AAG	580
Thr Asp Asp Glu Lys Glu Ile Glu Lys Ser Phe Ile Thr Thr Lys Lys	
170 175 180	
CTT TTT GAC CAA ATA AAG AAT GCG AGC GTT CTT TCA ATG GGC ATG AGT	628

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 22...1593
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

TTTTAAATTC AAAGGATAAA A ATG TAT CAA GTA GCC ATT TGC GAC CCC ATC	51
Met Tyr Gln Val Ala Ile Cys Asp Pro Ile	
1 5 10	
CAT GCT AAA GGC ATT CAA ATT TTA GAA GCT CAA AAA GAC ATT GTC TTG	99
His Ala Lys Gly Ile Gln Ile Leu Glu Ala Gln Lys Asp Ile Val Leu	
15 20 25	
CAT GAT TAT TCC AAA TGC CCT AAA AAG GAG CTT TTA GAA AAA CTC ACT	147
His Asp Tyr Ser Lys Cys Pro Lys Lys Glu Leu Leu Glu Lys Leu Thr	
30 35 40	
CCC ATG GAT GCG CTC ATC ACT CGC AGC ATG ACC CCT ATC ACA AGC GAT	195
Pro Met Asp Ala Leu Ile Thr Arg Ser Met Thr Pro Ile Thr Ser Asp	
45 50 55	
TTT TTA AAG CCC TTA ACC CAC TTA AAA TCC ATC GTG AGA GCG GGC GTG	243
Phe Leu Lys Pro Leu Thr His Leu Lys Ser Ile Val Arg Ala Gly Val	
60 65 70	
GGA GTG GAT AAT ATT GAT TTA GAA AGC TGC TCT CAA AAA GGG ATT GTA	291
Gly Val Asp Asn Ile Asp Leu Glu Ser Cys Ser Gln Lys Gly Ile Val	
75 80 85 90	
GTG ATG AAT ATC CCT ACC GCT AAC ACG ATT GCC GCT GTG GAA TTG ACC	339
Val Met Asn Ile Pro Thr Ala Asn Thr Ile Ala Ala Val Glu Leu Thr	
95 100 105	
ATG GCG CAT TTG ATC AAT GCA GTG CGT TCG TTC CCT TGT GCA AAC GAT	387
Met Ala His Leu Ile Asn Ala Val Arg Ser Phe Pro Cys Ala Asn Asp	
110 115 120	
CAA ATC AAA CAC CAA AGG TTA TGG AAA AGA GAA GAT TGG TAT GGC ACG	435
Gln Ile Lys His Gln Arg Leu Trp Lys Arg Glu Asp Trp Tyr Gly Thr	
125 130 135	
GAA TTG AAA AAT AAA AAG CTG GGC ATC ATT GGT TTT GGG AAT ATT GGC	483
Glu Leu Lys Asn Lys Lys Leu Gly Ile Ile Gly Phe Gly Asn Ile Gly	
140 145 150	
TCT AGG GTG GGC ATT AGA GCA AAA GCC TTT GAA ATG GAA GTT CTA GCC	531
Ser Arg Val Gly Ile Arg Ala Lys Ala Phe Glu Met Glu Val Leu Ala	
155 160 165 170	

TAT Tyr	GAT Asp	CCT Pro	TAT Tyr	ATC Ile 175	CCT Pro	TCT Ser	TCA Ser	AAA Lys	GCC Ala 180	ACT Thr	GAT Asp	TTA Leu	GGA Gly	GTC Val 185	ATT Ile	579
TAC Tyr	ACG Thr	AAA Lys	AAT Asn 190	TTT Phe	GAA Glu	GAC Asp	ATT Ile	TTG Leu 195	CAA Gln	TGC Cys	GAT Asp	ATG Met	ATC Ile 200	ACT Thr	ATC Ile	627
CAC His	ACC Thr	CCT Pro 205	AAA Lys	AAT Asn	AAA Lys	GAA Glu	ACG Thr 210	ATT Ile	AAC Asn	ATG Met	ATA Ile	GGT Gly 215	GCT Ala	AAA Lys	GAG Glu	675
ATT Ile	GAG Glu 220	CGC Arg	ATG Met	AAA Lys	AAA Lys	GGG Gly 225	GTT Val	ATT Ile	TTG Leu	CTC Leu	AAT Asn 230	TGC Cys	GCT Ala	AGG Arg	GGT Gly	723
GGG Gly 235	CTT Leu	TAT Tyr	AAT Asn	GAA Glu	GAC Asp 240	GCT Ala	CTT Leu	TAT Tyr	GAG Glu	GCT Ala 245	TTA Leu	GAA Glu	ACC Thr	AAA Lys	AAA Lys 250	771
GTG Val	CGT Arg	TGG Trp	CTT Leu	GGC Gly 255	ATT Ile	GAT Asp	GTC Val	TTT Phe	TCT Ser 260	AAA Lys	GAG Glu	CCT Pro	GGC Gly	ATT Ile 265	CAC His	819
AAC Asn	AAG Lys	CTT Leu 270	TTA Leu	GAC Asp	TTG Leu	CCC Pro	AAT Asn	GTT Val 275	TAT Tyr	GCG Ala	ACC Thr	CCC Pro	CAT His 280	ATT Ile	GGC Gly	867
GCA Ala	AAC Asn	ACT Thr 285	TTA Leu	GAA Glu	TCC Ser	CAA Gln	GAA Glu 290	GAA Glu	ATT Ile	TCC Ser	AAA Lys	CAA Gln 295	GCC Ala	GCT Ala	CAA Gln	915
GGG Gly 300	GTT Val	ATG Met	GAA Glu	TCT Ser	TTA Leu	AGG Arg 305	GGT Gly	TCA Ser	AGC Ser	CAC His	CCG Pro 310	CAT His	GCT Ala	TTG Leu	AAT Asn	963
TTA Leu 315	CCC Pro	ATG Met	CAA Gln	GCT Ala 320	TTT Phe	GAC Asp	GCG Ala	AGC Ser	GCA Ala	AAA Lys 325	GCC Ala	TAC Tyr	TTG Leu	AAT Asn	TTA Leu 330	1011
GCG Ala	CAA Gln	AAA Lys	TTG Leu	GGT Gly 335	TAT Tyr	TTT Phe	TCC Ser	AGT Ser	CAA Gln 340	ATC Ile	CAT His	AAG Lys	GGC Gly	GTG Val 345	TGC Cys	1059
CAA Gln	AAA Lys	ATT Ile 350	GAG Glu	CTC Leu	AGT Ser	CTT Leu	TGT Cys	GGG Gly 355	GAG Glu	ATC Ile	AAC Asn	CAA Gln 360	TTT Phe	AAA Lys	GAC Asp	1107
GCT Ala	CTT Leu	GTA Val 365	GCC Ala	TTT Phe	ATG Met	TTA Leu	GTG Val 370	GGG Gly	GTG Val	TTA Leu	AAA Lys	CCT Pro 375	GTT Val	GTA Val	GGG Gly	1155
GAT Asp	AAA Lys 380	ATC Ile	AAT Asn	TAC Tyr	ATT Ile	AAC Asn 385	GCC Ala	CCC Pro	TTT Phe	GTG Val	GCC Ala 390	AAA Lys	GAA Glu	AGA Arg	GGT Gly	1203
ATT Ile	GAG Glu	ATT Ile	AAG Lys	GTT Val	AGC Ser	CTT Leu	AAA Lys	GAA Glu	AGC Ser	GCT Ala	TCG Ser	CCC Pro	TAT Tyr	AAG Lys	AAC Asn	1251

395	400	405	410	
ATG CTC TCT TTA ACC CTC AAT GCG GCT AAT GGC ACA ATC AGC GTG AGC				1299
Met Leu Ser Leu Thr Leu Asn Ala Ala Asn Gly Thr Ile Ser Val Ser	415	420	425	
GGC ACG GTG TTT GAA GAA GAT ATT TTA AAA CTC ACT GAG ATT GAT GGG				1347
Gly Thr Val Phe Glu Glu Asp Ile Leu Lys Leu Thr Glu Ile Asp Gly	430	435	440	
TTT CAT ATT GAT ATA GAG CCA AAG GGT AAA ATG CTT TTA TTC AGG AAT				1395
Phe His Ile Asp Ile Glu Pro Lys Gly Lys Met Leu Leu Phe Arg Asn	445	450	455	
ACG GAT ATT CCA GGC GTT ATT GGG AGT GTG GGG AAT GCG TTC GCT AGG				1443
Thr Asp Ile Pro Gly Val Ile Gly Ser Val Gly Asn Ala Phe Ala Arg	460	465	470	
CAT GGC ATT AAC ATC GCT GAT TTT CGT TTG GGG CGT AAC ACG CAA AAA				1491
His Gly Ile Asn Ile Ala Asp Phe Arg Leu Gly Arg Asn Thr Gln Lys	475	480	485	490
GAA GCC CTA GCA CTC ATT ATT GTA GAT GAA GAA GTT TCT TTG GAA GTT				1539
Glu Ala Leu Ala Leu Ile Ile Val Asp Glu Glu Val Ser Leu Glu Val	495	500	505	
TTA GAA GAG CTT AAA AAC ATT CCT GCG TGC TTA AGC GTT CAT TAT GTG				1587
Leu Glu Glu Leu Lys Asn Ile Pro Ala Cys Leu Ser Val His Tyr Val	510	515	520	
GTT ATT TAAGGTAGTT GGATGCGAGA TTTTAAATA CTTTAAATA				1633
Val Ile				

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

Met Tyr Gln Val Ala Ile Cys Asp Pro Ile His Ala Lys Gly Ile Gln	
1 5 10 15	
Ile Leu Glu Ala Gln Lys Asp Ile Val Leu His Asp Tyr Ser Lys Cys	
20 25 30	
Pro Lys Lys Glu Leu Leu Glu Lys Leu Thr Pro Met Asp Ala Leu Ile	
35 40 45	
Thr Arg Ser Met Thr Pro Ile Thr Ser Asp Phe Leu Lys Pro Leu Thr	
50 55 60	
His Leu Lys Ser Ile Val Arg Ala Gly Val Gly Val Asp Asn Ile Asp	
65 70 75 80	
Leu Glu Ser Cys Ser Gln Lys Gly Ile Val Val Met Asn Ile Pro Thr	

85															90					95				
Ala	Asn	Thr	Ile	Ala	Ala	Val	Glu	Leu	Thr	Met	Ala	His	Leu	Ile	Asn									
			100					105					110											
Ala	Val	Arg	Ser	Phe	Pro	Cys	Ala	Asn	Asp	Gln	Ile	Lys	His	Gln	Arg									
		115					120					125												
Leu	Trp	Lys	Arg	Glu	Asp	Trp	Tyr	Gly	Thr	Glu	Leu	Lys	Asn	Lys	Lys									
	130					135					140													
Leu	Gly	Ile	Ile	Gly	Phe	Gly	Asn	Ile	Gly	Ser	Arg	Val	Gly	Ile	Arg									
145					150					155					160									
Ala	Lys	Ala	Phe	Glu	Met	Glu	Val	Leu	Ala	Tyr	Asp	Pro	Tyr	Ile	Pro									
				165					170						175									
Ser	Ser	Lys	Ala	Thr	Asp	Leu	Gly	Val	Ile	Tyr	Thr	Lys	Asn	Phe	Glu									
			180					185					190											
Asp	Ile	Leu	Gln	Cys	Asp	Met	Ile	Thr	Ile	His	Thr	Pro	Lys	Asn	Lys									
		195				200						205												
Glu	Thr	Ile	Asn	Met	Ile	Gly	Ala	Lys	Glu	Ile	Glu	Arg	Met	Lys	Lys									
	210					215					220													
Gly	Val	Ile	Leu	Leu	Asn	Cys	Ala	Arg	Gly	Gly	Leu	Tyr	Asn	Glu	Asp									
225					230					235					240									
Ala	Leu	Tyr	Glu	Ala	Leu	Glu	Thr	Lys	Lys	Val	Arg	Trp	Leu	Gly	Ile									
				245					250					255										
Asp	Val	Phe	Ser	Lys	Glu	Pro	Gly	Ile	His	Asn	Lys	Leu	Leu	Asp	Leu									
			260					265					270											
Pro	Asn	Val	Tyr	Ala	Thr	Pro	His	Ile	Gly	Ala	Asn	Thr	Leu	Glu	Ser									
		275					280					285												
Gln	Glu	Glu	Ile	Ser	Lys	Gln	Ala	Ala	Gln	Gly	Val	Met	Glu	Ser	Leu									
	290				295					300														
Arg	Gly	Ser	Ser	His	Pro	His	Ala	Leu	Asn	Leu	Pro	Met	Gln	Ala	Phe									
305					310					315					320									
Asp	Ala	Ser	Ala	Lys	Ala	Tyr	Leu	Asn	Leu	Ala	Gln	Lys	Leu	Gly	Tyr									
				325					330					335										
Phe	Ser	Ser	Gln	Ile	His	Lys	Gly	Val	Cys	Gln	Lys	Ile	Glu	Leu	Ser									
			340					345					350											
Leu	Cys	Gly	Glu	Ile	Asn	Gln	Phe	Lys	Asp	Ala	Leu	Val	Ala	Phe	Met									
		355																						

-774-

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1701
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GGATTTTATA TTTATTTTAT AGTAAGGCAG TCA ATG AGC AAG ATA GCA GAT GAT	54
Met Ser Lys Ile Ala Asp Asp	
1 5	
CAG AAC TTT AAT GAC GAG GAG GAA AAC TTC GCA AAA CTC TTT AAA AAA	102
Gln Asn Phe Asn Asp Glu Glu Asn Phe Ala Lys Leu Phe Lys Lys	
10 15 20	
GAA TTA GAA AAA GAA GAA ACC CTA GAA AAA GGC ACT ATC AAA GAA GGG	150
Glu Leu Glu Lys Glu Glu Thr Leu Glu Lys Gly Thr Ile Lys Glu Gly	
25 30 35	
CTA GTC GTT TCC ATC AAT GAG AAT GAT GGT TAT GCC ATG GTG AGC GTG	198
Leu Val Val Ser Ile Asn Glu Asn Asp Gly Tyr Ala Met Val Ser Val	
40 45 50 55	
GGC GGT AAG ACA GAA GGC CGT TTG GCT TTG AAT GAG ATC ACC GAT GAA	246
Gly Gly Lys Thr Glu Gly Arg Leu Ala Leu Asn Glu Ile Thr Asp Glu	
60 65 70	
AAG GGG CAG TTG CTG TAT CAA AAA AAT GAC CCC ATT ATC GTG CAT GTG	294
Lys Gly Gln Leu Leu Tyr Gln Lys Asn Asp Pro Ile Ile Val His Val	
75 80 85	
TCC GAA AAA GGT GAA CAC CCT AGC GTT TCC TAC AAA AAG GCC ATT TCC	342
Ser Glu Lys Gly Glu His Pro Ser Val Ser Tyr Lys Lys Ala Ile Ser	
90 95 100	
CAA CAA AAG ATT CAA GCT AAA ATT GAA GAA TTA GGC GAA AAC TAT GAA	390
Gln Gln Lys Ile Gln Ala Lys Ile Glu Glu Leu Gly Glu Asn Tyr Glu	
105 110 115	
AAC GCC ATT ATT GAA GGC AAG ATT GTA GGC AAG AAT AAA GGG GGT TAT	438
Asn Ala Ile Ile Glu Gly Lys Ile Val Gly Lys Asn Lys Gly Gly Tyr	
120 125 130 135	
ATC GTG GAG TCT CAA GGC GTG GAG TAT TTC CTC TCC CGC TCG CAC TCT	486
Ile Val Glu Ser Gln Gly Val Glu Tyr Phe Leu Ser Arg Ser His Ser	
140 145 150	
TCT TTA AAG AAT GAC GCA AAC CAT ATC GGC AAA CGC GTT AAA GCG TGC	534
Ser Leu Lys Asn Asp Ala Asn His Ile Gly Lys Arg Val Lys Ala Cys	

155										160										165																			
ATC	ATT	CGT	GTG	GAT	AAG	GAA	AAC	CAT	TCT	ATC	AAT	ATT	TCT	CGC	AAA	582																							
Ile	Ile	Arg	Val	Asp	Lys	Glu	Asn	His	Ser	Ile	Asn	Ile	Ser	Arg	Lys																								
170										175										180																			
CGA	TTC	TTT	GAA	GTC	AAT	GAC	AAA	CGA	CAA	CTT	GAG	GTT	TCT	AAG	GAA	630																							
Arg	Phe	Phe	Glu	Val	Asn	Asp	Lys	Arg	Gln	Leu	Glu	Val	Ser	Lys	Glu																								
185										190										195																			
TTG	TTA	GAA	GCC	ACA	GAG	CCG	GTG	TTA	GGG	GTT	GTG	CGC	CAG	ATC	ACC	678																							
Leu	Leu	Glu	Ala	Thr	Glu	Pro	Val	Leu	Gly	Val	Val	Arg	Gln	Ile	Thr																								
200										205										210										215									
CCT	TTT	GGC	ATT	TTT	GTA	GAA	GCT	AAG	GGG	ATT	GAG	GGC	TTG	GTC	CAT	726																							
Pro	Phe	Gly	Ile	Phe	Val	Glu	Ala	Lys	Gly	Ile	Glu	Gly	Leu	Val	His																								
220										225										230																			
TAT	TCT	GAA	ATC	AGC	CAT	AAG	GGA	CCA	GTC	AAT	CCT	GAA	AAA	TAC	TAC	774																							
Tyr	Ser	Glu	Ile	Ser	His	Lys	Gly	Pro	Val	Asn	Pro	Glu	Lys	Tyr	Tyr																								
235										240										245																			
AAA	GAG	GGC	GAT	GAA	GTC	TAT	GTC	AAA	GCC	ATC	GCT	TAT	GAT	GCA	GAA	822																							
Lys	Glu	Gly	Asp	Glu	Val	Tyr	Val	Lys	Ala	Ile	Ala	Tyr	Asp	Ala	Glu																								
250										255										260																			
AAA	AGA	CGC	CTT	TCA	CTC	TCC	ATA	AAA	GCG	ACT	ATA	GAA	GAC	CCA	TGG	870																							
Lys	Arg	Arg	Leu	Ser	Leu	Ser	Ile	Lys	Ala	Thr	Ile	Glu	Asp	Pro	Trp																								
265										270										275																			
GAA	GAG	ATT	CAA	GAC	AAG	CTA	AAA	CCC	GGA	TAC	GCC	ATT	AAG	GTA	GTG	918																							
Glu	Glu	Ile	Gln	Asp	Lys	Leu	Lys	Pro	Gly	Tyr	Ala	Ile	Lys	Val	Val																								
280										285										290										295									
GTG	AGC	AAC	ATT	GAA	CAT	TAT	GGG	GTG	TTT	GTG	GAT	ATT	GGT	AAT	GAT	966																							
Val	Ser	Asn	Ile	Glu	His	Tyr	Gly	Val	Phe	Val	Asp	Ile	Gly	Asn	Asp																								
300										305										310																			
ATT	GAA	GGC	TTT	TTG	CAT	GTT	TCT	GAA	ATC	TCT	TGG	GAT	AAA	AAT	GTC	1014																							
Ile	Glu	Gly	Phe	Leu	His	Val	Ser	Glu	Ile	Ser	Trp	Asp	Lys	Asn	Val																								
315										320										325																			
AGC	CAC	CCT	AAC	AAT	TAC	TTG	AGC	GTG	GGG	CAA	GAG	ATT	GAT	GTG	AAA	1062																							
Ser	His	Pro	Asn	Asn	Tyr	Leu	Ser	Val	Gly	Gln	Glu	Ile	Asp	Val	Lys																								
330										335										340																			
ATC	ATT	GAC	ATT	GAT	CCA	AAA	AAT	CGC	CGC	TTA	AGG	GTT	TCT	TTA	AAG	1110																							
Ile	Ile	Asp	Ile	Asp	Pro	Lys	Asn	Arg	Arg	Leu	Arg	Val	Ser	Leu	Lys																								
345										350										355																			
CAA	CTC	ACT	AAC	AGG	CCT	TTT	GAT	GTT	TTT	GAA	TCT	AAA	CAC	CAA	GTG	1158																							
Gln	Leu	Thr	Asn	Arg	Pro	Phe	Asp	Val	Phe	Glu	Ser	Lys	His	Gln	Val																								
360										365										370										375									
GGG	GAT	GTT	TTA	GAA	GGC	AAA	GTG	GCG	ACT	TTA	ACG	GAT	TTT	GGG	GCG	1206																							
Gly	Asp	Val	Leu	Glu	Gly	Lys	Val	Ala	Thr	Leu	Thr	Asp	Phe	Gly	Ala																								
380										385										390																			

[illegible]

Met	Ser	Lys	Ile	Ala	Asp	Asp	Gln	Asn	Phe	Asn	Asp	Glu	Glu	Glu	Asn
1				5					10					15	
Phe	Ala	Lys	Leu	Phe	Lys	Lys	Glu	Leu	Glu	Lys	Glu	Glu	Thr	Leu	Glu
			20					25					30		
Lys	Gly	Thr	Ile	Lys	Glu	Gly	Leu	Val	Val	Ser	Ile	Asn	Glu	Asn	Asp
		35					40					45			
Gly	Tyr	Ala	Met	Val	Ser	Val	Gly	Gly	Lys	Thr	Glu	Gly	Arg	Leu	Ala
	50					55					60				
Leu	Asn	Glu	Ile	Thr	Asp	Glu	Lys	Gly	Gln	Leu	Leu	Tyr	Gln	Lys	Asn
65					70					75					80
Asp	Pro	Ile	Ile	Val	His	Val	Ser	Glu	Lys	Gly	Glu	His	Pro	Ser	Val
			85						90					95	
Ser	Tyr	Lys	Lys	Ala	Ile	Ser	Gln	Gln	Lys	Ile	Gln	Ala	Lys	Ile	Glu
			100					105					110		
Glu	Leu	Gly	Glu	Asn	Tyr	Glu	Asn	Ala	Ile	Ile	Glu	Gly	Lys	Ile	Val
		115					120					125			
Gly	Lys	Asn	Lys	Gly	Gly	Tyr	Ile	Val	Glu	Ser	Gln	Gly	Val	Glu	Tyr
	130					135					140				
Phe	Leu	Ser	Arg	Ser	His	Ser	Ser	Leu	Lys	Asn	Asp	Ala	Asn	His	Ile
145					150					155					160
Gly	Lys	Arg	Val	Lys	Ala	Cys	Ile	Ile	Arg	Val	Asp	Lys	Glu	Asn	His
			165						170					175	
Ser	Ile	Asn	Ile	Ser	Arg	Lys	Arg	Phe	Phe	Glu	Val	Asn	Asp	Lys	Arg
		180						185					190		
Gln	Leu	Glu	Val	Ser	Lys	Glu	Leu	Leu	Glu	Ala	Thr	Glu	Pro	Val	Leu
		195					200					205			
Gly	Val	Val	Arg	Gln	Ile	Thr	Pro	Phe	Gly	Ile	Phe	Val	Glu	Ala	Lys
	210					215					220				
Gly	Ile	Glu	Gly	Leu	Val	His	Tyr	Ser	Glu	Ile	Ser	His	Lys	Gly	Pro
225					230					235					240
Val	Asn	Pro	Glu	Lys	Tyr	Tyr	Lys	Glu	Gly	Asp	Glu	Val	Tyr	Val	Lys
			245						250					255	
Ala	Ile	Ala	Tyr	Asp	Ala	Glu	Lys	Arg	Arg	Leu	Ser	Leu	Ser	Ile	Lys
		260						265					270		
Ala	Thr	Ile	Glu	Asp	Pro	Trp	Glu	Glu	Ile	Gln	Asp	Lys	Leu	Lys	Pro
		275					280					285			
Gly	Tyr	Ala	Ile	Lys	Val	Val	Val	Ser	Asn	Ile	Glu	His	Tyr	Gly	Val
	290					295					300				
Phe	Val	Asp	Ile	Gly	Asn	Asp	Ile	Glu	Gly	Phe	Leu	His	Val	Ser	Glu
305					310					315					320
Ile	Ser	Trp	Asp	Lys	Asn	Val	Ser	His	Pro	Asn	Asn	Tyr	Leu	Ser	Val
			325						330					335	
Gly	Gln	Glu	Ile	Asp	Val	Lys	Ile	Ile	Asp	Ile	Asp	Pro	Lys	Asn	Arg
			340					345					350		
Arg	Leu	Arg	Val	Ser	Leu	Lys	Gln	Leu	Thr	Asn	Arg	Pro	Phe	Asp	Val
		355					360					365			
Phe	Glu	Ser	Lys	His	Gln	Val	Gly	Asp	Val	Leu	Glu	Gly	Lys	Val	Ala
	370					375					380				
Thr	Leu	Thr	Asp	Phe	Gly	Ala	Phe	Leu	Asn	Leu	Gly	Gly	Val	Asp	Gly
385					390					395					400
Leu	Leu	His	Asn	His	Asp	Ala	Phe	Trp	Asp	Lys	Asp	Lys	Lys	Cys	Lys
			405						410					415	
Asp	His	Tyr	Lys	Ile	Gly	Asp	Val	Ile	Lys	Val	Lys	Ile	Leu	Lys	Ile
			420					425					430		
Asn	Lys	Lys	Asp	Lys	Lys	Ile	Ser	Leu	Ser	Ala	Lys	His	Leu	Val	Thr
		435					440					445			
Ser	Pro	Thr	Glu	Glu	Phe	Ala	Gln	Lys	His	Lys	Thr	Asp	Ser	Val	Ile
	450					455					460				

CGC Arg	GGG Gly	AGA Arg	GAA Glu	GAG Glu	TTT Phe	GTG Val	CGT Arg	GTG Val	AGT Ser	TGG Trp	GAT Asp	GTG Val	GCG Ala	TTG Leu	GAT Asp	390
105																
TTA Leu	GCG Ala	GCT Ala	AAA Lys	AAG Lys	CTT Leu	AAA Lys	GAA Glu	ATC Ile	CCT Pro	AAA Lys	GAA Glu	AAC Asn	ATT Ile	TAT Tyr	AAT Asn	438
120																
GCC Ala	AGT Ser	TAT Tyr	GGT Gly	GGC Gly	TGG Trp	GGG Gly	CAT His	GCG Ala	GGC Gly	AGC Ser	TTG Leu	CAT His	CGT Arg	TGC Cys	CAT His	486
140																
CAT His	TTA Leu	GCA Ala	TGG Trp	CGT Arg	TTT Phe	TTT Phe	AAC Asn	ACG Thr	ACT Thr	TTA Leu	GGA Gly	GGG Gly	GCT Ala	ATT Ile	GGC Gly	534
155																
ACT Thr	GAT Asp	GGG Gly	GAA Glu	TAT Tyr	AGT Ser	AAT Asn	GGC Gly	GCG Ala	GCC Ala	GCA Ala	AGA Arg	ATA Ile	AAC Asn	CCT Pro	ATG Met	582
170																
ATT Ile	GTA Val	GGG Gly	GAT Asp	ATG Met	GAA Glu	GTT Val	TAT Tyr	TCG Ser	CAA Gln	CAA Gln	ACC Thr	ACG Thr	CAT His	GAA Glu	GAG Glu	630
185																
ATG Met	ATT Ile	AAA Lys	AAT Asn	TGT Cys	AAG Lys	GTG Val	TAT Tyr	GTC Val	ATG Met	TGG Trp	GGG Gly	GCG Ala	GAT Asp	TTA Leu	CTC Leu	678
200																
AAG Lys	TGC Cys	AAC Asn	CGC Arg	ATT Ile	GAT Asp	TAT Tyr	TTT Phe	GTG Val	CCA Pro	AAC Asn	CAT His	GTC Val	AAT Asn	GAC Asp	AGC Ser	726
220																
TAC Tyr	TAC Tyr	CCC Pro	AAG Lys	TAT Tyr	AAA Lys	AGA Arg	GCT Ala	GGT Gly	ATT Ile	AAA Lys	TTC Phe	ATT Ile	AGT Ser	ATC Ile	GAT Asp	774
230																
CCC Pro	ATT Ile	TAT Tyr	ACC Thr	GAA Glu	ACC Thr	GCT Ala	CAA Gln	GCC Ala	TTT Phe	AGT Ser	GCT Ala	GAA Glu	TGG Trp	ATA Ile	CCC Pro	822
240																
ATT Ile	CGC Arg	CCT Pro	AAC Asn	ACT Thr	GAT Asp	GTA Val	GCG Ala	TTA Leu	ATG Met	CTA Leu	GGC Gly	ATG Met	ATG Met	CAT His	TAT Tyr	870
255																
CTT Leu	TAT Tyr	ACG Thr	AGC Ser	AAT Asn	CAA Gln	TAT Tyr	GAT Asp	AAA Lys	GCG Ala	TTT Phe	ATC Ile	GCT Ala	AAA Lys	TAC Tyr	ACT Thr	918
265																
GAT Asp	GGT Gly	TTT Phe	GAT Asp	AAA Lys	TTT Phe	TTA Leu	CCC Pro	TAT Tyr	TTG Leu	CTA Leu	GGA Gly	GAG Glu	AGC Ser	GAT Asp	AAT Asn	966
270																
GCG Ala	CCT Pro	AAG Lys	ACT Thr	TTA Leu	GAA Glu	TGG Trp	GCG Ala	TCT Ser	CAA Gln	ATC Ile	ACT Thr	GGA Gly	GTG Val	AGC Ser	GCA Ala	1014
280																
GAA Glu	AAA Lys	ATC Ile	AAA Lys	GAA Glu	TTA Leu	GCG Ala	GAT Asp	TTG Leu	TTT Phe	GTT Val	TCT Ser	AAA Lys	CGC Arg	ACT Thr	TTT Phe	1062
295																

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

Met	Ser	Ile	Ser	Arg	Arg	Ser	Ile	Leu	Thr	Lys	Ile	Pro	Ile	Ala	Leu
1				5					10					15	
Ala	Ser	Ala	Asn	Val	Leu	Lys	Ala	Val	Gly	Val	Phe	Glu	Lys	Val	Glu
			20					25					30		
Ser	Ile	Pro	His	Ala	Thr	His	Phe	Gly	Pro	Phe	Ile	Ala	Lys	Val	Gln
	35						40					45			
Asn	Gly	Val	Ile	Lys	Asp	Ile	Val	Pro	Gln	Lys	Ser	Asp	Tyr	Asn	Pro
	50					55					60				
Thr	Met	Met	Leu	Lys	Ala	Met	Val	Asp	Arg	Val	Tyr	Ser	Asp	Ser	Arg
65					70				75						80
Val	Lys	Tyr	Pro	Cys	Val	Arg	Lys	Ser	Phe	Leu	Glu	Asn	Lys	Lys	Asn
				85					90					95	
His	Lys	Glu	Leu	Arg	Gly	Arg	Glu	Glu	Phe	Val	Arg	Val	Ser	Trp	Asp
			100					105					110		
Val	Ala	Leu	Asp	Leu	Ala	Ala	Lys	Lys	Leu	Lys	Glu	Ile	Pro	Lys	Glu
		115						120				125			
Asn	Ile	Tyr	Asn	Ala	Ser	Tyr	Gly	Gly	Trp	Gly	His	Ala	Gly	Ser	Leu
	130					135					140				
His	Arg	Cys	His	His	Leu	Ala	Trp	Arg	Phe	Phe	Asn	Thr	Thr	Leu	Gly
145					150					155					160
Gly	Ala	Ile	Gly	Thr	Asp	Gly	Glu	Tyr	Ser	Asn	Gly	Ala	Ala	Ala	Arg
				165					170					175	
Ile	Asn	Pro	Met	Ile	Val	Gly	Asp	Met	Glu	Val	Tyr	Ser	Gln	Gln	Thr
			180					185					190		
Thr	His	Glu	Glu	Met	Ile	Lys	Asn	Cys	Lys	Val	Tyr	Val	Met	Trp	Gly
		195					200					205			
Ala	Asp	Leu	Leu	Lys	Cys	Asn	Arg	Ile	Asp	Tyr	Phe	Val	Pro	Asn	His
	210					215					220				
Val	Asn	Asp	Ser	Tyr	Tyr	Pro	Lys	Tyr	Lys	Arg	Ala	Gly	Ile	Lys	Phe
225					230					235					240
Ile	Ser	Ile	Asp	Pro	Ile	Tyr	Thr	Glu	Thr	Ala	Gln	Ala	Phe	Ser	Ala
				245					250					255	
Glu	Trp	Ile	Pro	Ile	Arg	Pro	Asn	Thr	Asp	Val	Ala	Leu	Met	Leu	Gly
			260					265					270		
Met	Met	His	Tyr	Leu	Tyr	Thr	Ser	Asn	Gln	Tyr	Asp	Lys	Ala	Phe	Ile
		275					280					285			
Ala	Lys	Tyr	Thr	Asp	Gly	Phe	Asp	Lys	Phe	Leu	Pro	Tyr	Leu	Leu	Gly
	290					295					300				
Glu	Ser	Asp	Asn	Ala	Pro	Lys	Thr	Leu	Glu	Trp	Ala	Ser	Gln	Ile	Thr
305					310					315					320
Gly	Val	Ser	Ala	Glu	Lys	Ile	Lys	Glu	Leu	Ala	Asp	Leu	Phe	Val	Ser
				325					330					335	
Lys	Arg	Thr	Phe	Leu	Ala	Gly	Asn	Trp	Ala	Met	Gln	Arg	Ala	Gln	Tyr
			340					345					350		
Gly	Glu	Gln	Pro	Asp	Trp	Ala	Leu	Ile	Val	Leu	Ala	Ser	Met	Ile	Gly
		355					360					365			
Gln	Val	Gly	Leu	Ser	Gly	Gly	Gly	Phe	Gly	Phe	Ser	Met	His	Tyr	Gly
	370					375					380				
Gly	Asn	Ala	Gln	Ala	Ser	Ser	Gly	Ala	Arg	Ile	Val	Pro	Met	Ile	Ser
385					390					395					400
Gln	Gly	His	Asn	Ser	Val	Lys	Ser	Val	Ile	Pro	Ala	Ser	Arg	Val	Ser
				405					410					415	
Glu	Ala	Ile	Leu	Asn	Pro	Asp	Lys	Glu	Ile	Asp	Phe	Met	Gly	Lys	Lys
			420					425				430			
Leu	Lys	Leu	Pro	Lys	Ile	Lys	Met	Ile	Tyr	Asn	Cys	Gly	Ala	Asp	Leu
		435					440					445			

Leu Gly His Glu Thr Asp Thr Asn Glu Leu Ile Arg Ala Leu Arg Thr
 450 455 460
 Leu Asp Cys Val Ile Val His Glu Pro Trp Trp Arg Leu Arg Gln Asn
 465 470 475 480
 Leu Leu Ile Leu Ser Leu Leu Pro Leu Ala Leu Trp Lys Glu Met Ile
 485 490 495
 Leu Leu Leu Glu Gly Val Ile Leu Arg Met Trp Phe Met Pro Cys Val
 500 505 510
 Arg Trp

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24...509
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

ATTGACGCTT ATAAGGATAA AAG ATG AAT ATT TTT CAA ACG AGT TTG AAA TGT	53
Met Asn Ile Phe Gln Thr Ser Leu Lys Cys	
1 5 10	
TGC GTG GGG TTG GTT TTG TCT GTG GGG GTC TTA TTA GGG GAT TCT AAA	101
Cys Val Gly Leu Val Leu Ser Val Gly Val Leu Leu Gly Asp Ser Lys	
15 20 25	
GCT TTT AAG GTT AGG GTG GAT AAA AGT TTA ACC CCG CCT TTT TTG AAT	149
Ala Phe Lys Val Arg Val Asp Lys Ser Leu Thr Pro Pro Phe Leu Asn	
30 35 40	
GTG CTT TCA TTA GCT TTT AAA CAA GAC ATG AAA AAA GAG GTC ATT TTT	197
Val Leu Ser Leu Ala Phe Lys Gln Asp Met Lys Lys Glu Val Ile Phe	
45 50 55	
GTG ATT ACC AAA AGC AAT AAG TTG AGT AAA AAA GTG CTT TGT GAT TTT	245
Val Ile Thr Lys Ser Asn Lys Leu Ser Lys Lys Val Leu Cys Asp Phe	
60 65 70	
GAC GCT TTT TTA TTG CCT GAG ACT CTG ATG AGC GGC ATG CCT AAA AAA	293
Asp Ala Phe Leu Leu Pro Glu Thr Leu Met Ser Gly Met Pro Lys Lys	
75 80 85 90	
GCA CTA TTC CAT AAA GAG TTT TTA TTC CAA TCT AAA GAA AAT AAA ACG	341
Ala Leu Phe His Lys Glu Phe Leu Phe Gln Ser Lys Glu Asn Lys Thr	
95 100 105	
CTC TAT GCG TTT TCG CTG ATT GAT TCT CAA TAT TGC TCA AAA GGT GGA	389

Leu	Tyr	Ala	Phe	Ser	Leu	Ile	Asp	Ser	Gln	Tyr	Cys	Ser	Lys	Gly	Gly		
			110					115					120				
AAT	TAC	AGA	TAC	GAA	CTA	GAA	AAA	TTA	GAA	CGC	TGG	TTT	GTG	CAA	AAA	437	
Asn	Tyr	Arg	Tyr	Glu	Leu	Glu	Lys	Leu	Glu	Arg	Trp	Phe	Val	Gln	Lys		
		125					130					135					
GCA	CCT	GAG	TTG	GCT	GAA	AGC	TAT	AGG	GTG	AAT	TAC	AAA	AAT	CAA	TAC	485	
Ala	Pro	Glu	Leu	Ala	Glu	Ser	Tyr	Arg	Val	Asn	Tyr	Lys	Asn	Gln	Tyr		
	140					145				150							
AAT	AAA	ACA	CAG	ATC	TCA	CAA	AAA	TAAAGAATGA	GCGATGATTT	TAGTATTAGA	539						
Asn	Lys	Thr	Gln	Ile	Ser	Gln	Lys										
155					160												
T																540	

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

Met	Asn	Ile	Phe	Gln	Thr	Ser	Leu	Lys	Cys	Cys	Val	Gly	Leu	Val	Leu		
1				5					10				15				
Ser	Val	Gly	Val	Leu	Leu	Gly	Asp	Ser	Lys	Ala	Phe	Lys	Val	Arg	Val		
			20					25					30				
Asp	Lys	Ser	Leu	Thr	Pro	Pro	Phe	Leu	Asn	Val	Leu	Ser	Leu	Ala	Phe		
		35					40					45					
Lys	Gln	Asp	Met	Lys	Lys	Glu	Val	Ile	Phe	Val	Ile	Thr	Lys	Ser	Asn		
	50					55					60						
Lys	Leu	Ser	Lys	Lys	Val	Leu	Cys	Asp	Phe	Asp	Ala	Phe	Leu	Leu	Pro		
65					70				75						80		
Glu	Thr	Leu	Met	Ser	Gly	Met	Pro	Lys	Lys	Ala	Leu	Phe	His	Lys	Glu		
			85					90						95			
Phe	Leu	Phe	Gln	Ser	Lys	Glu	Asn	Lys	Thr	Leu	Tyr	Ala	Phe	Ser	Leu		
			100					105					110				
Ile	Asp	Ser	Gln	Tyr	Cys	Ser	Lys	Gly	Gly	Asn	Tyr	Arg	Tyr	Glu	Leu		
	115						120					125					
Glu	Lys	Leu	Glu	Arg	Trp	Phe	Val	Gln	Lys	Ala	Pro	Glu	Leu	Ala	Glu		
	130					135				140							
Ser	Tyr	Arg	Val	Asn	Tyr	Lys	Asn	Gln	Tyr	Asn	Lys	Thr	Gln	Ile	Ser		
145					150					155					160		
Gln	Lys																

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 25...1548

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

TCTCACAAAA ATAAAGAATG AGCG ATG ATT TTA GTA TTA GAT TTT GGG AGT	51
Met Ile Leu Val Leu Asp Phe Gly Ser	
1 5	
CAA TAC ACA CAG CTG ATT GCT AGA AGA TTG AGA GAG AGA GGG ATT TAT	99
Gln Tyr Thr Gln Leu Ile Ala Arg Arg Leu Arg Glu Arg Gly Ile Tyr	
10 15 20 25	
ACA GAA ATA GTC CCT TTT TTT GAA AGC ATA GAA AAC ATT CAA AAA AAA	147
Thr Glu Ile Val Pro Phe Phe Glu Ser Ile Glu Asn Ile Gln Lys Lys	
30 35 40	
GCC CCC AAA GGT TTG ATT TTG AGT GGG GGG CCA GCG AGC GTG TAT GCT	195
Ala Pro Lys Gly Leu Ile Leu Ser Gly Gly Pro Ala Ser Val Tyr Ala	
45 50 55	
AAA GAC GCT TAC AAG CCT AGT GGG AAA ATC TTT GAT TTG AAT GTG CCG	243
Lys Asp Ala Tyr Lys Pro Ser Gly Lys Ile Phe Asp Leu Asn Val Pro	
60 65 70	
ATT TTA GGG ATT TGC TAC GGC ATG CAG TAT TTG GTG GAT TTT TTT GGG	291
Ile Leu Gly Ile Cys Tyr Gly Met Gln Tyr Leu Val Asp Phe Phe Gly	
75 80 85	
GGG GTA GTG GTT GGT GCG AAT GAG CAA GAA TTT GGT AAG GCT GTT TTA	339
Gly Val Val Val Gly Ala Asn Glu Gln Glu Phe Gly Lys Ala Val Leu	
90 95 100 105	
GAA ATC ACT CAA AAT TCT GTG ATT TTT GAA GGC GTG AAG ATT AAA AGC	387
Glu Ile Thr Gln Asn Ser Val Ile Phe Glu Gly Val Lys Ile Lys Ser	
110 115 120	
CTT GTG TGG ATG AGC CAT ATG GAT AAA GTC ATA GAA CTG CCT AAA GGC	435
Leu Val Trp Met Ser His Met Asp Lys Val Ile Glu Leu Pro Lys Gly	
125 130 135	
TTT ACT ACC CTT GCA AAA AGC CCT AAT TCC CCC CAT TGC GCG ATT GAA	483
Phe Thr Thr Leu Ala Lys Ser Pro Asn Ser Pro His Cys Ala Ile Glu	
140 145 150	
AAC GGC AAG ATT TTT GGC TTG CAA TTC CAC CCA GAA GTC GTT CAA AGC	531
Asn Gly Lys Ile Phe Gly Leu Gln Phe His Pro Glu Val Val Gln Ser	
155 160 165	
GAA GAA GGG GGT AAG ATT TTA GAA AAT TTT GCC CTT TTA GTT TGC GGC	579
Glu Glu Gly Gly Lys Ile Leu Glu Asn Phe Ala Leu Leu Val Cys Gly	

170	175	180	185	
TGT GAA AAA ACT	TGG GGG ATG CAG CAT	TTC GCT CAA AGA GAA ATC GCA	627	
Cys Glu Lys Thr	Trp Gly Met Gln His	Phe Ala Gln Arg Glu Ile Ala		
	190	195 200		
CGA TTG AAA GAA AAA ATC	GCT AAC GCT AAG GTT TTG TGC GCG GTG AGT	675		
Arg Leu Lys Glu Lys Ile Ala Asn Ala Lys Val Leu Cys Ala Val Ser				
	205 210	215		
GGG GGC GTG GAT TCT ACG GTG GTC GCT ACG CTG TTG CAC AGA GCC ATT	723			
Gly Gly Val Asp Ser Thr Val Val Ala Thr Leu Leu His Arg Ala Ile				
	220 225 230			
AAG GAT AAT TTG ATC GCT GTT TTT GTG GAT CAT GGC TTG TTG CGT AAA	771			
Lys Asp Asn Leu Ile Ala Val Phe Val Asp His Gly Leu Leu Arg Lys				
	235 240 245			
AAT GAA AAA GAA AGG GTG CAA GCG ATG TTT AAG GAC TTG AAA ATC CCT	819			
Asn Glu Lys Glu Arg Val Gln Ala Met Phe Lys Asp Leu Lys Ile Pro				
	250 255 260 265			
TTA AAC ACG ATA GAC GCT AAA GAA GTC TTT TTG TCT AAA TTA AAG GGC	867			
Leu Asn Thr Ile Asp Ala Lys Glu Val Phe Leu Ser Lys Leu Lys Gly				
	270 275 280			
GTG AGC GAG CCT GAA TTG AAG CGA AAA ATC ATC GGC GAG ACC TTT ATT	915			
Val Ser Glu Pro Glu Leu Lys Arg Lys Ile Ile Gly Glu Thr Phe Ile				
	285 290 295			
GAA GTG TTT GAA AAA GAA GCC AAA AAG CAC CAT TTA AAA GGC AAA ATT	963			
Glu Val Phe Glu Lys Glu Ala Lys Lys His His Leu Lys Gly Lys Ile				
	300 305 310			
GAA TTT TTA GCC CAA GGC ACT TTA TAC CCT GAT GTG ATT GAA TCC GTG	1011			
Glu Phe Leu Ala Gln Gly Thr Leu Tyr Pro Asp Val Ile Glu Ser Val				
	315 320 325			
AGC GTT AAA GGG CCT TCA AAA GTG ATC AAA ACC CAT CAT AAT GTG GGC	1059			
Ser Val Lys Gly Pro Ser Lys Val Ile Lys Thr His His Asn Val Gly				
	330 335 340 345			
GGA CTG CCT GAA TGG ATG GAT TTT AAA CTC ATA GAG CCT TTA AGG GAG	1107			
Gly Leu Pro Glu Trp Met Asp Phe Lys Leu Ile Glu Pro Leu Arg Glu				
	350 355 360			
TTG TTT AAA GAT GAG GTG CGC TTA CTG GGT AAA GAA TTG GGC GTT AGT	1155			
Leu Phe Lys Asp Glu Val Arg Leu Leu Gly Lys Glu Leu Gly Val Ser				
	365 370 375			
CAG GAT TTT TTA ATG CGC CAC CCT TTT CCA GGG CCT GGG CTT GCT GTA	1203			
Gln Asp Phe Leu Met Arg His Pro Phe Pro Gly Pro Gly Leu Ala Val				
	380 385 390			
AGG ATT TTA GGC GAA ATC AGT GAG AGT AAG ATC AAA CGC TTG CAA GAA	1251			
Arg Ile Leu Gly Glu Ile Ser Glu Ser Lys Ile Lys Arg Leu Gln Glu				
	395 400 405			

GCG GAT TTT ATT TTT ATA GAG GAA CTT AAA AAA GCC AAT TTG TAT GAC	1299
Ala Asp Phe Ile Phe Ile Glu Glu Leu Lys Lys Ala Asn Leu Tyr Asp	
410 415 420 425	
AAG GTT TGG CAA GCT TTT TGC GTG CTG TTG AAT GTC AAT TCT GTG GGG	1347
Lys Val Trp Gln Ala Phe Cys Val Leu Leu Asn Val Asn Ser Val Gly	
430 435 440	
GTT ATG GGG GAT AAC CGC ACT TAT GAA AAC GCT ATT TGC TTA AGA GCG	1395
Val Met Gly Asp Asn Arg Thr Tyr Glu Asn Ala Ile Cys Leu Arg Ala	
445 450 455	
GTA AAT GCG AGC GAT GGC ATG ACG GCG AGC TTT TCA TTT TTA GAG CAT	1443
Val Asn Ala Ser Asp Gly Met Thr Ala Ser Phe Ser Phe Leu Glu His	
460 465 470	
TCT TTT TTA GAA AAG GTT TCT AAC CGT ATC ACT AAT GAA GTG AGC GGT	1491
Ser Phe Leu Glu Lys Val Ser Asn Arg Ile Thr Asn Glu Val Ser Gly	
475 480 485	
ATC AAT AGG GTG GTG TAT GAC ATT ACC TCT AAA CCA CCA GGA ACG ATT	1539
Ile Asn Arg Val Val Tyr Asp Ile Thr Ser Lys Pro Pro Gly Thr Ile	
490 495 500 505	
GAA TGG GAA TGATTATCTT AAAAAATAGC ACTA	1572
Glu Trp Glu	

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

Met	Ile	Leu	Val	Leu	Asp	Phe	Gly	Ser	Gln	Tyr	Thr	Gln	Leu	Ile	Ala
1				5					10					15	
Arg	Arg	Leu	Arg	Glu	Arg	Gly	Ile	Tyr	Thr	Glu	Ile	Val	Pro	Phe	Phe
			20					25					30		
Glu	Ser	Ile	Glu	Asn	Ile	Gln	Lys	Lys	Ala	Pro	Lys	Gly	Leu	Ile	Leu
		35				40						45			
Ser	Gly	Gly	Pro	Ala	Ser	Val	Tyr	Ala	Lys	Asp	Ala	Tyr	Lys	Pro	Ser
	50					55				60					
Gly	Lys	Ile	Phe	Asp	Leu	Asn	Val	Pro	Ile	Leu	Gly	Ile	Cys	Tyr	Gly
65				70				75					80		
Met	Gln	Tyr	Leu	Val	Asp	Phe	Phe	Gly	Gly	Val	Val	Val	Gly	Ala	Asn
			85					90					95		
Glu	Gln	Glu	Phe	Gly	Lys	Ala	Val	Leu	Glu	Ile	Thr	Gln	Asn	Ser	Val
		100				105						110			
Ile	Phe	Glu	Gly	Val	Lys	Ile	Lys	Ser	Leu	Val	Trp	Met	Ser	His	Met
		115				120					125				
Asp	Lys	Val	Ile	Glu	Leu	Pro	Lys	Gly	Phe	Thr	Thr	Leu	Ala	Lys	Ser

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 26...808
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

AAAAACCCCC	ACGCTATGGT	AAATC	ATG	CTC	ATT	TGT	AAC	GAT	AAA	TCC	AAT	52
			Met	Leu	Ile	Cys	Asn	Asp	Lys	Ser	Asn	
			1				5					
CCA AAA ACC CTT TTA GAA GAA ATC ATG GCG TTA AGG CCA TGG CGT AAA	100											
Pro Lys Thr Leu Leu Glu Glu Ile Met Ala Leu Arg Pro Trp Arg Lys												
10 15 20 25												
GGC CCT TTT GAA ATT TCT CAA ATC AAG ATT GAT AGC GAA TGG GAT AGC	148											
Gly Pro Phe Glu Ile Ser Gln Ile Lys Ile Asp Ser Glu Trp Asp Ser												
30 35 40												
TCC ATT AAA TGG GAT CTA GTT AAA AAC GCC ACT CCT TTA AAA GAT AAG	196											
Ser Ile Lys Trp Asp Leu Val Lys Asn Ala Thr Pro Leu Lys Asp Lys												
45 50 55												
GTT GTG GCT GAT GTG GGT TGC AAT AAC GGC TAT TAC TTG TTT AAA ATG	244											
Val Val Ala Asp Val Gly Cys Asn Asn Gly Tyr Tyr Leu Phe Lys Met												
60 65 70												
CTA GAA CAT GGG CCT AAA AGT TTG GTG GGG TTT GAT CCG GGC GTT TTA	292											
Leu Glu His Gly Pro Lys Ser Leu Val Gly Phe Asp Pro Gly Val Leu												
75 80 85												
GTC AAA AAA CAA TTT GAA TTT TTA GCC CCC TTT TTT GAT AAA GAA AAA	340											
Val Lys Lys Gln Phe Glu Phe Leu Ala Pro Phe Phe Asp Lys Glu Lys												
90 95 100 105												
AAA ATC ATT TAT GAG TCT TTG GGG GTA GAG GAT TTG CAT GAA AAA TAC	388											
Lys Ile Ile Tyr Glu Ser Leu Gly Val Glu Asp Leu His Glu Lys Tyr												
110 115 120												
CCT AAC GCT TTT GAT GTC ATT TTT TGC TTA GGG GTG CTA TAC CAC AGA	436											
Pro Asn Ala Phe Asp Val Ile Phe Cys Leu Gly Val Leu Tyr His Arg												
125 130 135												
AAA AGC CCG CTA GAG GCT TTA AAA GCC TTG TAT CAC GCT TTG AAA ATA	484											
Lys Ser Pro Leu Glu Ala Leu Lys Ala Leu Tyr His Ala Leu Lys Ile												
140 145 150												
AAA GGG GAG CTG GTG TTG GAT ACC TTA ATC ATT GAT TCG CCC TTA GAC	532											
Lys Gly Glu Leu Val Leu Asp Thr Leu Ile Ile Asp Ser Pro Leu Asp												
155 160 165												
ATC GCC CTT TGC CCT AAA AAA ACT TAT GCT AAA ATG AAA AAT GTT TAT	580											
Ile Ala Leu Cys Pro Lys Lys Thr Tyr Ala Lys Met Lys Asn Val Tyr												
170 175 180 185												
TTT ATC CCC AGT GTT AGC GCG TTA AAA GGG TGG TGC GAA AGG GTA GGG	628											
Phe Ile Pro Ser Val Ser Ala Leu Lys Gly Trp Cys Glu Arg Val Gly												
190 195 200												

TTT GAA AAT TTT GAG ATT CTT AGC GTT TTA AAG ACC ACG CCT AAA GAA	676
Phe Glu Asn Phe Glu Ile Leu Ser Val Leu Lys Thr Thr Pro Lys Glu	
205 210 215	
CAG CGT AAA ACG GAT TTT ATT TTG GGG CAG AGT TTG GAA GAT TTT TTG	724
Gln Arg Lys Thr Asp Phe Ile Leu Gly Gln Ser Leu Glu Asp Phe Leu	
220 225 230	
GAT AAA ACA GAT CCC TCT AAA ACT TTA GAG GGG TAT GAC GCC CCT TTA	772
Asp Lys Thr Asp Pro Ser Lys Thr Leu Glu Gly Tyr Asp Ala Pro Leu	
235 240 245	
AGG GGG TAT TTT AAA ATG CTT AAA CCA AGC AAG CGT TAAATAAAGG ATTAAG	824
Arg Gly Tyr Phe Lys Met Leu Lys Pro Ser Lys Arg	
250 255 260	
ATAGTGCAAG	834

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

Met	Leu	Ile	Cys	Asn	Asp	Lys	Ser	Asn	Pro	Lys	Thr	Leu	Leu	Glu	Glu
1				5				10						15	
Ile	Met	Ala	Leu	Arg	Pro	Trp	Arg	Lys	Gly	Pro	Phe	Glu	Ile	Ser	Gln
			20					25					30		
Ile	Lys	Ile	Asp	Ser	Glu	Trp	Asp	Ser	Ser	Ile	Lys	Trp	Asp	Leu	Val
			35				40					45			
Lys	Asn	Ala	Thr	Pro	Leu	Lys	Asp	Lys	Val	Val	Ala	Asp	Val	Gly	Cys
			50			55				60					
Asn	Asn	Gly	Tyr	Tyr	Leu	Phe	Lys	Met	Leu	Glu	His	Gly	Pro	Lys	Ser
65					70					75				80	
Leu	Val	Gly	Phe	Asp	Pro	Gly	Val	Leu	Val	Lys	Lys	Gln	Phe	Glu	Phe
			85					90						95	
Leu	Ala	Pro	Phe	Phe	Asp	Lys	Glu	Lys	Lys	Ile	Ile	Tyr	Glu	Ser	Leu
			100					105					110		
Gly	Val	Glu	Asp	Leu	His	Glu	Lys	Tyr	Pro	Asn	Ala	Phe	Asp	Val	Ile
			115				120					125			
Phe	Cys	Leu	Gly	Val	Leu	Tyr	His	Arg	Lys	Ser	Pro	Leu	Glu	Ala	Leu
			130				135				140				
Lys	Ala	Leu	Tyr	His	Ala	Leu	Lys	Ile	Lys	Gly	Glu	Leu	Val	Leu	Asp
145					150					155				160	
Thr	Leu	Ile	Ile	Asp	Ser	Pro	Leu	Asp	Ile	Ala	Leu	Cys	Pro	Lys	Lys
				165				170						175	
Thr	Tyr	Ala	Lys	Met	Lys	Asn	Val	Tyr	Phe	Ile	Pro	Ser	Val	Ser	Ala
			180					185					190		
Leu	Lys	Gly	Trp	Cys	Glu	Arg	Val	Gly	Phe	Glu	Asn	Phe	Glu	Ile	Leu
			195				200					205			
Ser	Val	Leu	Lys	Thr	Thr	Pro	Lys	Glu	Gln	Arg	Lys	Thr	Asp	Phe	Ile
			210			215					220				

Leu Gly Gln Ser Leu Glu Asp Phe Leu Asp Lys Thr Asp Pro Ser Lys
 225 230 235 240
 Thr Leu Glu Gly Tyr Asp Ala Pro Leu Arg Gly Tyr Phe Lys Met Leu
 245 250 255
 Lys Pro Ser Lys Arg
 260

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...1197
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

TTAAATTCAA TTTTAAAGAA GAGTAGTTAA ATG GTT ATT GTT TTA GTC GTG GAT	54
Met Val Ile Val Leu Val Val Asp	
1 5	
AGT TTT AAA GAC ACC AGT AAT GGC ACT TCT ATG ACA GCG TTT CGT TTT	102
Ser Phe Lys Asp Thr Ser Asn Gly Thr Ser Met Thr Ala Phe Arg Phe	
10 15 20	
TTT GAA GCG CTG AAA AAA AGA GGG CAT GTG ATG AGA GTG GTC GCC CCT	150
Phe Glu Ala Leu Lys Lys Arg Gly His Val Met Arg Val Val Ala Pro	
25 30 35 40	
CAT GTG GAT AAT TTA GGG AGT GAA GAA GAG GGG TAT TAC AAC CTT AAA	198
His Val Asp Asn Leu Gly Ser Glu Glu Glu Gly Tyr Tyr Asn Leu Lys	
45 50 55	
GAG CGC TAC ATC CCC CTA GTT ACA GAA ATT TCA CAC AAA CAA CAC ATC	246
Glu Arg Tyr Ile Pro Leu Val Thr Glu Ile Ser His Lys Gln His Ile	
60 65 70	
CTT TTT GCT AAA CCC GAT GAA AAA ATC TTA AGA AAG GCT TTT AAG GGA	294
Leu Phe Ala Lys Pro Asp Glu Lys Ile Leu Arg Lys Ala Phe Lys Gly	
75 80 85	
GCG GAT ATG ATC CAT ACT TAT TTG CCT TTT TTG CTA GAA AAA ACA GCC	342
Ala Asp Met Ile His Thr Tyr Leu Pro Phe Leu Leu Glu Lys Thr Ala	
90 95 100	
GTA AAA ATC GCG CGA GAA ATG CAA GTG CCT TAT ATT GGC TCT TTC CAT	390
Val Lys Ile Ala Arg Glu Met Gln Val Pro Tyr Ile Gly Ser Phe His	
105 110 115 120	
TTA CAG CCA GAG CAT ATT TCT TAT AAC ATG AAA TTG GGG TGG TTT TCT	438

Leu	Gln	Pro	Glu	His	Ile	Ser	Tyr	Asn	Met	Lys	Leu	Gly	Trp	Phe	Ser		
				125						130						135	
TGG	TTC	AAC	ATG	ATG	CTT	TTT	TCG	TGG	TTT	AAA	TCT	TCG	CAT	TAC	CGC	486	
Trp	Phe	Asn	Met	Met	Leu	Phe	Ser	Trp	Phe	Lys	Ser	Ser	His	Tyr	Arg		
				140						145						150	
TAT	ATC	CAC	CAT	ATC	CAT	TGC	CCG	TCA	AAA	TTC	ATT	GTA	GAA	GAA	TTA	534	
Tyr	Ile	His	His	Ile	His	Cys	Pro	Ser	Lys	Phe	Ile	Val	Glu	Glu	Leu		
				155						160						165	
GAA	AAA	TAC	AAC	TAT	GGA	GGG	AAA	AAA	TAC	GCT	ATT	TCT	AAC	GGC	TTT	582	
Glu	Lys	Tyr	Asn	Tyr	Gly	Gly	Lys	Lys	Tyr	Ala	Ile	Ser	Asn	Gly	Phe		
				170						175						180	
GAT	CCC	ATG	TTT	AGA	TTT	GAA	CAC	CCG	CAA	AAA	AGC	CTT	TTT	GAC	ACC	630	
Asp	Pro	Met	Phe	Arg	Phe	Glu	His	Pro	Gln	Lys	Ser	Leu	Phe	Asp	Thr		
				185						190						195	
ACA	CCC	TTT	AAA	ATC	GCT	ATG	GTA	GGA	CGC	TAT	TCT	AAT	GAA	AAA	AAT	678	
Thr	Pro	Phe	Lys	Ile	Ala	Met	Val	Gly	Arg	Tyr	Ser	Asn	Glu	Lys	Asn		
				205						210						215	
CAA	AGC	GTT	TTA	ATC	AAA	GCG	GTT	GCT	TTA	AGC	AAA	TAC	AAA	CAA	GAT	726	
Gln	Ser	Val	Leu	Ile	Lys	Ala	Val	Ala	Leu	Ser	Lys	Tyr	Lys	Gln	Asp		
				220						225						230	
ATT	GTA	TTA	TTG	CTC	AAA	GGC	AAA	GGG	CCT	GAT	GAG	AAA	AAA	ATC	AAA	774	
Ile	Val	Leu	Leu	Leu	Lys	Gly	Lys	Gly	Pro	Asp	Glu	Lys	Lys	Ile	Lys		
				235						240						245	
CTT	TTA	GCC	CAA	AAA	CTA	GGC	GTA	AAA	GCG	GAG	TTT	GGG	TTT	GTC	AAT	822	
Leu	Leu	Ala	Gln	Lys	Leu	Gly	Val	Lys	Ala	Glu	Phe	Gly	Phe	Val	Asn		
				250						255						260	
TCC	AAT	GAA	TTG	TTA	GAG	ATC	TTA	AAA	ACT	TGC	ACC	CTT	TAT	GTG	CAT	870	
Ser	Asn	Glu	Leu	Leu	Glu	Ile	Leu	Lys	Thr	Cys	Thr	Leu	Tyr	Val	His		
				265						270						275	
GCA	GCC	AAT	GTG	GAA	AGC	GAA	GCG	ATT	GCG	TGC	TTA	GAG	GCC	ATT	AGC	918	
Ala	Ala	Asn	Val	Glu	Ser	Glu	Ala	Ile	Ala	Cys	Leu	Glu	Ala	Ile	Ser		
				285						290						295	
GTG	GGG	ATT	GTG	CCT	GTT	ATC	GCT	AAT	AGC	CCT	TTA	AGC	GCG	ACC	AGG	966	
Val	Gly	Ile	Val	Pro	Val	Ile	Ala	Asn	Ser	Pro	Leu	Ser	Ala	Thr	Arg		
				300						305						310	
CAA	TTT	GCG	CTA	GAT	GAA	CGA	TCG	CTA	TTT	GAA	CCT	AAT	AAC	GCT	AAA	1014	
Gln	Phe	Ala	Leu	Asp	Glu	Arg	Ser	Leu	Phe	Glu	Pro	Asn	Asn	Ala	Lys		
				315						320						325	
GAT	TTG	AGC	GCT	AAA	ATA	GAT	TGG	TGG	TTA	GAA	AAC	AAG	CTT	GAA	AGA	1062	
Asp	Leu	Ser	Ala	Lys	Ile	Asp	Trp	Trp	Leu	Glu	Asn	Lys	Leu	Glu	Arg		
				330						335						340	
GAA	AGG	ATG	CAA	AAC	GAA	TAC	GCT	AAA	AGC	GCT	TTA	AAT	TAC	ACT	TTA	1110	
Glu	Arg	Met	Gln	Asn	Glu	Tyr	Ala	Lys	Ser	Ala	Leu	Asn	Tyr	Thr	Leu		
				345						350						355	

Ile Ala Cys Leu Glu Ala Ile Ser Val Gly Ile Val Pro Val Ile Ala
 290 295 300
 Asn Ser Pro Leu Ser Ala Thr Arg Gln Phe Ala Leu Asp Glu Arg Ser
 305 310 315 320
 Leu Phe Glu Pro Asn Asn Ala Lys Asp Leu Ser Ala Lys Ile Asp Trp
 325 330 335
 Trp Leu Glu Asn Lys Leu Glu Arg Glu Arg Met Gln Asn Glu Tyr Ala
 340 345 350
 Lys Ser Ala Leu Asn Tyr Thr Leu Glu Asn Ser Val Ile Gln Ile Glu
 355 360 365
 Lys Val Tyr Glu Glu Ala Ile Arg Asp Phe Lys Asn Asn Pro His Leu
 370 375 380
 Phe Lys Thr Leu Ser
 385

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...903
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

TAGAAAAGGT AGTTT ATG GAG TTA GAA GAA ATT GTT GAT AGT GAG AGG AAT	51
Met Glu Leu Glu Glu Ile Val Asp Ser Glu Arg Asn	
1 5 10	
ATC CAT AAG ACT ATA GAA GTT TTA GGA AAA GGC GGA CAG GGT ATA GTG	99
Ile His Lys Thr Ile Glu Val Leu Gly Lys Gly Gly Gln Gly Ile Val	
15 20 25	
TAT CGC TGT TTG GAT AAG GAT GTG GCT ATT AAG GTA GTA TTG AGG GAT	147
Tyr Arg Cys Leu Asp Lys Asp Val Ala Ile Lys Val Val Leu Arg Asp	
30 35 40	
GGA GAT TTT ATT AAA GAC AAA GAA TCC CTC AAA CAA TAT GAA AAA AGC	195
Gly Asp Phe Ile Lys Asp Lys Glu Ser Leu Lys Gln Tyr Glu Lys Ser	
45 50 55 60	
GTT CTA AAC TTA TCT TTT AAG CCG ATA GAG AGT CAT TTC CCT ATG TCA	243
Val Leu Asn Leu Ser Phe Lys Pro Ile Glu Ser His Phe Pro Met Ser	
65 70 75	
ATT CCA CTG GTA ACT TTG AAA GAA AAA CAA GGC TAT GTG ATG AAA ATG	291
Ile Pro Leu Val Thr Leu Lys Glu Lys Gln Gly Tyr Val Met Lys Met	
80 85 90	
GCT GAG GGC TAT GAA CCA CTA AAA ACT TTT TTA AAG AAG CCC AGC ATT	339

Ala	Glu	Gly	Tyr	Glu	Pro	Leu	Lys	Thr	Phe	Leu	Lys	Lys	Pro	Ser	Ile		
		95					100					105					
TTA	GAA	AAC	GAA	GAA	AAA	GAT	GGG	ATT	TTT	AGG	ATC	AAT	AAT	GCC	ATT	387	
Leu	Glu	Asn	Glu	Glu	Lys	Asp	Gly	Ile	Phe	Arg	Ile	Asn	Asn	Ala	Ile		
	110					115					120						
CAA	GAA	CTT	TGC	AAA	GAT	AAC	CAT	TAT	ATG	ACT	TTA	AGT	TTA	AGT	TAT	435	
Gln	Glu	Leu	Cys	Lys	Asp	Asn	His	Tyr	Met	Thr	Leu	Ser	Leu	Ser	Tyr		
	125				130					135					140		
TAC	TCA	CAA	ACA	CAA	GGA	TTG	AGA	TCA	CGA	TTA	AAA	ATA	CTC	ACC	CAT	483	
Tyr	Ser	Gln	Thr	Gln	Gly	Leu	Arg	Ser	Arg	Leu	Lys	Ile	Leu	Thr	His		
				145					150					155			
TTA	GCA	AAA	CTT	CTA	TTC	AGA	TTG	CAA	AGT	AAG	GGT	TTG	GTG	TAT	GGG	531	
Leu	Ala	Lys	Leu	Leu	Phe	Arg	Leu	Gln	Ser	Lys	Gly	Leu	Val	Tyr	Gly		
			160					165					170				
GAC	TTG	AAT	TTA	AAC	AAT	GTT	TTT	TAT	AAA	GAC	AAT	TCA	GCG	TTT	TTA	579	
Asp	Leu	Asn	Leu	Asn	Asn	Val	Phe	Tyr	Lys	Asp	Asn	Ser	Ala	Phe	Leu		
	175						180					185					
ATT	GAT	GCG	GAT	AAT	GTG	CGT	TAT	GAG	AGC	GAA	AAA	GCC	CTG	TGT	GTT	627	
Ile	Asp	Ala	Asp	Asn	Val	Arg	Tyr	Glu	Ser	Glu	Lys	Ala	Leu	Cys	Val		
	190					195					200						
ATT	TTT	ACG	CCT	AAC	TAT	GGG	GCT	TTA	GAG	ATT	AGC	CAA	ACC	TCT	AAA	675	
Ile	Phe	Thr	Pro	Asn	Tyr	Gly	Ala	Leu	Glu	Ile	Ser	Gln	Thr	Ser	Lys		
	205				210					215					220		
AAT	AGC	GAT	ACA	ACC	AAT	TAC	AAC	ACC	ATG	CTT	AGC	GAT	ACC	TTT	TCT	723	
Asn	Ser	Asp	Thr	Thr	Asn	Tyr	Asn	Thr	Met	Leu	Ser	Asp	Thr	Phe	Ser		
				225					230					235			
TTT	GCT	ATC	ATA	ACT	TAT	GAA	CTT	TTA	AAT	ATG	GTT	CAT	CCT	TTT	GAT	771	
Phe	Ala	Ile	Ile	Thr	Tyr	Glu	Leu	Leu	Asn	Met	Val	His	Pro	Phe	Asp		
			240					245					250				
GGG	AAT	AAG	GCA	GAT	GAT	AGT	GTA	GAA	AAT	TTT	ATA	GAA	TTG	CCT	TGG	819	
Gly	Asn	Lys	Ala	Asp	Asp	Ser	Val	Glu	Asn	Phe	Ile	Glu	Leu	Pro	Trp		
	255						260					265					
ATT	GAA	GAT	AGA	AAG	GAT	GAT	AGC	AAT	CGT	TCT	TGT	GGC	TTA	CTG	CCT	867	
Ile	Glu	Asp	Arg	Lys	Asp	Asp	Ser	Asn	Arg	Ser	Cys	Gly	Leu	Leu	Pro		
	270					275					280						
TTT	TTC	TTA	ACA	AGG	GAT	TTA	AAA	AAT	TTA	TTA	GCG	TAATGCTTTG	AAGAAG			919	
Phe	Phe	Leu	Thr	Arg	Asp	Leu	Lys	Asn	Leu	Leu	Ala						
	285				290				295								
GCAAAAAAGA	TCCTTTGAAA	CGCCCTAC														947	

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

Met	Glu	Leu	Glu	Glu	Ile	Val	Asp	Ser	Glu	Arg	Asn	Ile	His	Lys	Thr
1				5					10					15	
Ile	Glu	Val	Leu	Gly	Lys	Gly	Gly	Gln	Gly	Ile	Val	Tyr	Arg	Cys	Leu
			20					25					30		
Asp	Lys	Asp	Val	Ala	Ile	Lys	Val	Val	Leu	Arg	Asp	Gly	Asp	Phe	Ile
		35					40					45			
Lys	Asp	Lys	Glu	Ser	Leu	Lys	Gln	Tyr	Glu	Lys	Ser	Val	Leu	Asn	Leu
	50					55					60				
Ser	Phe	Lys	Pro	Ile	Glu	Ser	His	Phe	Pro	Met	Ser	Ile	Pro	Leu	Val
65					70				75					80	
Thr	Leu	Lys	Glu	Lys	Gln	Gly	Tyr	Val	Met	Lys	Met	Ala	Glu	Gly	Tyr
				85					90					95	
Glu	Pro	Leu	Lys	Thr	Phe	Leu	Lys	Lys	Pro	Ser	Ile	Leu	Glu	Asn	Glu
			100					105					110		
Glu	Lys	Asp	Gly	Ile	Phe	Arg	Ile	Asn	Asn	Ala	Ile	Gln	Glu	Leu	Cys
		115					120					125			
Lys	Asp	Asn	His	Tyr	Met	Thr	Leu	Ser	Leu	Ser	Tyr	Tyr	Ser	Gln	Thr
	130					135					140				
Gln	Gly	Leu	Arg	Ser	Arg	Leu	Lys	Ile	Leu	Thr	His	Leu	Ala	Lys	Leu
145					150					155				160	
Leu	Phe	Arg	Leu	Gln	Ser	Lys	Gly	Leu	Val	Tyr	Gly	Asp	Leu	Asn	Leu
				165					170					175	
Asn	Asn	Val	Phe	Tyr	Lys	Asp	Asn	Ser	Ala	Phe	Leu	Ile	Asp	Ala	Asp
		180					185						190		
Asn	Val	Arg	Tyr	Glu	Ser	Glu	Lys	Ala	Leu	Cys	Val	Ile	Phe	Thr	Pro
		195					200					205			
Asn	Tyr	Gly	Ala	Leu	Glu	Ile	Ser	Gln	Thr	Ser	Lys	Asn	Ser	Asp	Thr
	210					215					220				
Thr	Asn	Tyr	Asn	Thr	Met	Leu	Ser	Asp	Thr	Phe	Ser	Phe	Ala	Ile	Ile
225					230					235				240	
Thr	Tyr	Glu	Leu	Leu	Asn	Met	Val	His	Pro	Phe	Asp	Gly	Asn	Lys	Ala
				245					250					255	
Asp	Asp	Ser	Val	Glu	Asn	Phe	Ile	Glu	Leu	Pro	Trp	Ile	Glu	Asp	Arg
			260					265					270		
Lys	Asp	Asp	Ser	Asn	Arg	Ser	Cys	Gly	Leu	Leu	Pro	Phe	Phe	Leu	Thr
	275						280					285			
Arg	Asp	Leu	Lys	Asn	Leu	Leu	Ala								
290						295									

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 44...469
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

ATGCTTTGAA GAAGGCAAAA AAGATCCTTT GAAACGCCCT ACT	ATG CCC TTA TTT	55
	Met Pro Leu Phe	
	1	
ATA GAG AGC TTA GAA AAA GCT AGC TTG CAA GTG TTA GAA TGT GAA AAT	103	
Ile Glu Ser Leu Glu Lys Ala Ser Leu Gln Val Leu Glu Cys Glu Asn		
5 10 15 20		
TGT TCA ATG ACT TAT TAT GAT AGA GAT TAT AAT AGA GAA TGT GAG ATT	151	
Cys Ser Met Thr Tyr Tyr Asp Arg Asp Tyr Asn Arg Glu Cys Glu Ile		
25 30 35		
TGC CCT TAT TGC GAT GCT AAA AAA CCT GTC AGA CTT GTA GCA ACA AGT	199	
Cys Pro Tyr Cys Asp Ala Lys Lys Pro Val Arg Leu Val Ala Thr Ser		
40 45 50		
TAT TAC CAA AAG AGC GAA GTT TTT TAT TTT GTC TCG AAT TTT ACA GAC	247	
Tyr Tyr Gln Lys Ser Glu Val Phe Tyr Phe Val Ser Asn Phe Thr Asp		
55 60 65		
CCT ATT TTT TTA CCG ACA ACC TTA TTT AAG GGG ATT GAA GTG GTT AAA	295	
Pro Ile Phe Leu Pro Thr Thr Leu Phe Lys Gly Ile Glu Val Val Lys		
70 75 80		
AGC GAA TGG GAG TTT GCA GAG ATT GCT AAT AAT ATA TTG ATT TTT CAT	343	
Ser Glu Trp Glu Phe Ala Glu Ile Ala Asn Asn Ile Leu Ile Phe His		
85 90 95 100		
CAT GAC ATA CAA CAA GAA AAG ATT CTC ATT AAT AAT AAA AGA TTG GAT	391	
His Asp Ile Gln Gln Glu Lys Ile Leu Ile Asn Asn Lys Arg Leu Asp		
105 110 115		
CAC TAT AGG ATA GAA ATA GAT TTA GAA AAA GAA TTG ACT ATT TCA TAC	439	
His Tyr Arg Ile Glu Ile Asp Leu Glu Lys Glu Leu Thr Ile Ser Tyr		
120 125 130		
AAT GGT TTT TTA ATT AAG GTT CAA AAA TGC TGAGTTTAT CAAAGAAGAT AGC	492	
Asn Gly Phe Leu Ile Lys Val Gln Lys Cys		
135 140		
ATCATCAAGG CTTATAA	509	

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

Met	Pro	Leu	Phe	Ile	Glu	Ser	Leu	Glu	Lys	Ala	Ser	Leu	Gln	Val	Leu
1				5					10					15	
Glu	Cys	Glu	Asn	Cys	Ser	Met	Thr	Tyr	Tyr	Asp	Arg	Asp	Tyr	Asn	Arg
			20					25					30		
Glu	Cys	Glu	Ile	Cys	Pro	Tyr	Cys	Asp	Ala	Lys	Lys	Pro	Val	Arg	Leu
		35					40					45			
Val	Ala	Thr	Ser	Tyr	Tyr	Gln	Lys	Ser	Glu	Val	Phe	Tyr	Phe	Val	Ser
		50				55					60				
Asn	Phe	Thr	Asp	Pro	Ile	Phe	Leu	Pro	Thr	Thr	Leu	Phe	Lys	Gly	Ile
65					70				75						80
Glu	Val	Val	Lys	Ser	Glu	Trp	Glu	Phe	Ala	Glu	Ile	Ala	Asn	Asn	Ile
			85					90					95		
Leu	Ile	Phe	His	His	Asp	Ile	Gln	Gln	Glu	Lys	Ile	Leu	Ile	Asn	Asn
			100				105						110		
Lys	Arg	Leu	Asp	His	Tyr	Arg	Ile	Glu	Ile	Asp	Leu	Glu	Lys	Glu	Leu
		115					120					125			
Thr	Ile	Ser	Tyr	Asn	Gly	Phe	Leu	Ile	Lys	Val	Gln	Lys	Cys		
		130				135					140				

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 27...1193
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

AATGGTTTTT TAATTAAGGT TCAAAA ATG CTG AGT TTT ATC AAA GAA GAT AGC	53
Met Leu Ser Phe Ile Lys Glu Asp Ser	
1 5	
ATC ATC AAG GCT TAT AAC CTC AAT ACC GCA AAA CTA GAG CCA AAA GAT	101
Ile Ile Lys Ala Tyr Asn Leu Asn Thr Ala Lys Leu Glu Pro Lys Asp	
10 15 20 25	
AGA GAA AAA TTG GGA TTA TTA AAG ATT GAA AAA AAT AAA ATA TAT TTT	149
Arg Glu Lys Leu Gly Leu Leu Lys Ile Glu Lys Asn Lys Ile Tyr Phe	
30 35 40	
CAT CTA GAT GAA AAG CGT TAT TTG AAA TTA GAG ATC ATA GGC AAA ACC	197
His Leu Asp Glu Lys Arg Tyr Leu Lys Leu Glu Ile Ile Gly Lys Thr	
45 50 55	
AAA GAA AAA GAA ATT AAA AAC GCT TTT TGC AGT AAT GCT TTT CTT GCA	245
Lys Glu Lys Glu Ile Lys Asn Ala Phe Cys Ser Asn Ala Phe Leu Ala	
60 65 70	

GCT Ala	CAA Gln	GTC Val	CTA Leu	AAT Asn	TTA Leu	AAC Asn	CAA Gln	GAA Glu	AGA Arg	CAA Gln	GTT Val	TTA Leu	GAA Glu	TTG Leu	AAG Lys	293
758085																
TGC Cys	CAT His	TTC Phe	TTC Phe	AAG Lys	CAC His	CCT Pro	ATA Ile	AAA Lys	ATT Ile	CTT Leu	CCT Pro	GAA Glu	CCA Pro	TTA Leu	AAC Asn	341
9095100																
ATT Ile	AAT Asn	TTC Phe	AAA Lys	GAC Asp	ACA Thr	ATC Ile	ATA Ile	AAA Lys	AAG Lys	TTA Leu	CTA Leu	AAA Lys	GAT Asp	ATG Met	GGC Gly	389
110115120																
AAA Lys	GAT Asp	AAA Lys	AAA Lys	ATA Ile	GAA Glu	GAT Asp	TTT Phe	AAA Lys	GAA Glu	ACT Thr	TGT Cys	ATT Ile	TTA Leu	AAA Lys	ATA Ile	437
125130135																
GCT Ala	GGT Gly	TTT Phe	ACT Thr	TAT Tyr	TTT Phe	GTG Val	TGC Cys	GTA Val	TTG Leu	CCT Pro	TAT Tyr	GAA Glu	TAT Tyr	GAG Glu	AAT Asn	485
140145150																
AAA Lys	GAG Glu	GAT Asp	AAA Lys	GAG Glu	AAT Asn	AGT Ser	GAA Glu	GAG Glu	ATT Ile	TTA Leu	AAA Lys	GAA Glu	GAT Asp	TTC Phe	AGG Arg	533
155160165																
CTG Leu	TTA Leu	AAT Asn	ACC Thr	AAG Lys	GGG Gly	GGA Gly	TTA Leu	AGC Ser	GTT Val	AAG Lys	CGT Arg	GCT Ala	TTG Leu	ATA Ile	AAT Asn	581
170175180185																
AAC Asn	AGG Arg	CAT His	TCT Ser	TAT Tyr	GAA Glu	GCG Ala	ATA Ile	AAA Lys	TTA Leu	AGA Arg	CCC Pro	ATT Ile	AAA Lys	CAA Gln	GAG Glu	629
190195200																
TTA Leu	GTG Val	CCT Pro	GGT Gly	TTG Leu	TGT Cys	TTG Leu	TTT Phe	TTT Phe	CAA Gln	GGT Gly	TCA Ser	TTA Leu	GAA Glu	TTT Phe	AAT Asn	677
205210215																
GAT Asp	AAA Lys	ACC Thr	ACA Thr	AAA Lys	ACC Thr	ATG Met	CGA Arg	ACG Thr	AGC Ser	CTT Leu	TTA Leu	GAC Asp	CAG Gln	ATC Ile	CAG Gln	725
220225230																
CAA Gln	GAT Asp	GAC Asp	AAA Lys	TCT Ser	TAT Tyr	TTA Leu	AAA Lys	ATT Ile	TGG Trp	GAA Glu	AAA Lys	TAT Tyr	CTC Leu	ATC Ile	AAA Lys	773
235240245																
AGC Ser	GCT Ala	CAA Gln	AAA Lys	AGT Ser	TTT Phe	AAT Asn	GAG Glu	GCA Ala	AAA Lys	GAA Glu	GTG Val	GGG Gly	GTT Val	TTA Leu	GAG Glu	821
250255260265																
ATT Ile	GAA Glu	AGC Ser	GTG Val	AGT Ser	AAA Lys	GAA Glu	GGA Gly	GGG Gly	AAT Asn	TTA Leu	AGA Arg	ATT Ile	CGT Arg	TTT Phe	AAG Lys	869
270275280																
CCA Pro	GCT Ala	TTA Leu	GGC Gly	AAG Lys	AAT Asn	AAA Lys	ATG Met	GAA Glu	ATC Ile	TTA Leu	AAG Lys	AAA Lys	TCA Ser	CAA Gln	TTT Phe	917
285290295																
AAA Lys	AAG Lys	GGG Gly	AGT Ser	GAT Asp	TTA Leu	GGG Gly	GTT Val	TTA Leu	GAG Glu	GAT Asp	TTA Leu	GAC Asp	CCA Pro	CAA Gln	AAT Asn	965

ATT Ile 45	GAA Glu	AAT Asn	GAA Glu	TTA Leu	AAG Lys 50	CAA Gln	TTA Leu	GAA Glu	AAC Asn	AAA Lys 55	GAA Glu	AAT Asn	CTT Leu	AAA Lys	GCA Ala 60	195
GAC Asp	AAC Asn	AAC Asn	ACA Thr	GAA Glu 65	TTT Phe	AAA Lys	GAA Glu	GAA Glu	AAT Asn 70	CAA Gln	GAC Asp	ACT Thr	AAA Lys	GAA Glu 75	AAC Asn	243
CAG Gln	CCT Pro	AAC Asn	GAT Asp 80	TTG Leu	TTT Phe	TCT Ser	TTG Leu	CCA Pro 85	TTG Leu	CCC Pro	ACT Thr	CAA Gln 90	ACC Thr	ACC Thr	ATC Ile	291
AAT Asn	GGA Gly	ATT Ile 95	AAA Lys	GAA Glu	TTT Phe	GTA Val 100	GAA Glu	GAG Glu	CCT Pro	GTG Val	ATA Ile	GAA Glu 105	ACA Thr	GAG Glu	AAA Lys	339
AAA Lys 110	GAA Glu	ACA Thr	TCC Ser	CAA Gln	AAT Asn	GAG Glu 115	CCA Pro	ATC Ile	CAA Gln	GAA Glu 120	AAA Lys	AAA Lys	GAA Glu	AGA Arg	ATT Ile	387
TTT Phe 125	AAA Lys	AAC Asn	TTT Phe	TTC Phe	TCC Ser 130	AGA Arg	ATA Ile	GGC Gly	TTT Phe	GAT Asp 135	AAA Lys	AGT Ser	ATT Ile	GCC Ala	CCT Pro 140	435
ACA Thr	ATG Met	CTT Leu	TTT Phe	GAA Glu 145	GAA Glu	GTG Val	AGA Arg	GAT Asp	GCA Ala 150	AGC Ser	GTT Val	ATC Ile	TAT Tyr	CAT His 155	TTA Leu	483
GAG Glu	AAA Lys	AAA Lys	TTA Leu 160	GGC Gly	GAT Asp	TAT Tyr	ATC Ile	TTT Phe 165	TAT Tyr	GTA Val	GCG Ala	TGT Cys	TTC Phe 170	TTC Phe	TTT Phe	531
GGC Gly	ACA Thr	ACG Thr 175	GCA Ala	TTG Leu	CTT Leu	ATT Ile	ATC Ile 180	TTA Leu	CTG Leu	ACT Thr	ATT Ile	CTG Leu 185	TTG Leu	CCC Pro	TTA Leu	579
AAA Lys 190	CAA Gln	AAA Lys	GAG Glu	CCG Pro	TAT Tyr	TTA Leu 195	GTG Val	CAA Gln	TTT Phe	TCT Ser	AAC Asn 200	AAT Asn	AAA Lys	GAA Glu	AAT Asn	627
TTT Phe 205	GCT Ala	TTA Leu	GTT Val	CAA Gln 210	AAG Lys	GCA Ala	GAT Asp	AGC Ser	AGC Ser	ATT Ile 215	ACA Thr	GCC Ala	AAT Asn	AAA Lys	GCT Ala 220	675
CTT Leu	ATT Ile	CGT Arg	TCA Ser	TTA Leu 225	GTG Val	GGA Gly	GCG Ala	TAT Tyr	GTG Val 230	CTA Leu	AAC Asn	AGG Arg	GAA Glu 235	AGC Ser	ATT Ile	723
ACT Thr	CAT His	ATT Ile	GAG Glu 240	CAA Gln	CAT His	GAA Glu	AAA Lys	ATG Met 245	CGT Arg	CAA Gln	AAC Asn	ACC Thr	ATT Ile 250	AAA Lys	GAG Glu	771
CAA Gln	AGT Ser	TCC Ser 255	AAT Asn	GAA Glu	GTA Val	TGG Trp	TAT Tyr 260	GAA Glu	TTT Phe	GAA Glu	AAA Lys	CTC Leu 265	ATC Ile	GCT Ala	CAT His	819
TAT Tyr	GAC Asp	AGC Ser	ATT Ile	TAC Tyr	ACT Thr	AAT Asn	CCT Pro	TTA Leu	CTC Leu	ACA Thr	AGA Arg	AAA Lys	GTA Val	AAG Lys	ATT Ile	867

270	275	280	
GCA AAT ATT TAC TTA GAT AAA GAT TTA GCC TAT ATT GAC ATT GAA GTG			915
Ala Asn Ile Tyr Leu Asp Lys Asp Leu Ala Tyr Ile Asp Ile Glu Val			
285	290	295	300
AGC TTG TAT CAT AGT GGA GAA TTA GAG AGC TTG AAG CGC TAT AAA GTG			963
Ser Leu Tyr His Ser Gly Glu Leu Glu Ser Leu Lys Arg Tyr Lys Val			
	305	310	315
GTG ATG AGT TTT GAA TTT AAA AAA CAA GAA ATC AAT TTT GAC TCC ATG			1011
Val Met Ser Phe Glu Phe Lys Lys Gln Glu Ile Asn Phe Asp Ser Met			
	320	325	330
TCT TTA AAT CCT ACA GGC TTT ATG GTT ACA AGT TAT GAT GTA ACT GAA			1059
Ser Leu Asn Pro Thr Gly Phe Met Val Thr Ser Tyr Asp Val Thr Glu			
	335	340	345
ATT GCG ATT GTG AAT TAC CCA ACC GCT AAA GCG ATT GGG CTT TTT CTT			1107
Ile Ala Ile Val Asn Tyr Pro Thr Ala Lys Ala Ile Gly Leu Phe Leu			
	350	355	360
GCT TCA TAGCTCCATA ACTAGCTAGA TCCAATATGT TTCCATATTT AGAACTAACC CC			1165
Ala Ser			
365			
GTTAGAGGAA GCTCCACAAG			1185

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

Met	Ser	Lys	Arg	Ser	Glu	Val	Leu	Glu	Gln	Phe	His	Gly	Gly	Leu	Lys
1				5					10					15	
Asn	Leu	Glu	Leu	Gln	Thr	Lys	Arg	Arg	Met	Gly	Leu	Trp	Gly	Asp	Pro
			20					25					30		
Lys	Glu	Asn	Glu	Glu	Gln	Thr	Leu	Phe	Leu	Glu	Glu	Ile	Glu	Asn	Glu
		35					40					45			
Leu	Lys	Gln	Leu	Glu	Asn	Lys	Glu	Asn	Leu	Lys	Ala	Asp	Asn	Asn	Thr
		50				55				60					
Glu	Phe	Lys	Glu	Glu	Asn	Gln	Asp	Thr	Lys	Glu	Asn	Gln	Pro	Asn	Asp
65					70				75					80	
Leu	Phe	Ser	Leu	Pro	Leu	Pro	Thr	Gln	Thr	Thr	Ile	Asn	Gly	Ile	Lys
			85					90						95	
Glu	Phe	Val	Glu	Glu	Pro	Val	Ile	Glu	Thr	Glu	Lys	Lys	Glu	Thr	Ser
			100					105					110		
Gln	Asn	Glu	Pro	Ile	Gln	Glu	Lys	Lys	Glu	Arg	Ile	Phe	Lys	Asn	Phe
		115				120						125			
Phe	Ser	Arg	Ile	Gly	Phe	Asp	Lys	Ser	Ile	Ala	Pro	Thr	Met	Leu	Phe
		130				135					140				

GGG CAT TCT ATT AGC GTT CAT TCT ACC GAT GAA TAT TTC ATC CAA ACA	198
Gly His Ser Ile Ser Val His Ser Thr Asp Glu Tyr Phe Ile Gln Thr	
40 45 50	
GAT GAA GAG GGT ATC AGG CAT TAT GTT GTT GAT AAA AAG AAA CTC AAT	246
Asp Glu Glu Gly Ile Arg His Tyr Val Val Asp Lys Lys Lys Leu Asn	
55 60 65 70	
GAA TAC CAC CAA AAC AAT CAA GAA GCC TTC AAA CAA GCT TTA GAA AAT	294
Glu Tyr His Gln Asn Asn Gln Glu Ala Phe Lys Gln Ala Leu Glu Asn	
75 80 85	
CGT ATA GAT ATT GTA GTG TGC GAT AAC ACC AAT TTT GAA TCG TGG CAA	342
Arg Ile Asp Ile Val Val Cys Asp Asn Thr Asn Phe Glu Ser Trp Gln	
90 95 100	
AGC AAA CCA TAT ACA GAT ATG GCT AGA GAA TTT GGC TAT AAA ATT TTG	390
Ser Lys Pro Tyr Thr Asp Met Ala Arg Glu Phe Gly Tyr Lys Ile Leu	
105 110 115	
TTG ATT GAT TTT AAG AAT AGA CAC TTA GAA ACC CCC ATG GAT TAT GGA	438
Leu Ile Asp Phe Lys Asn Arg His Leu Glu Thr Pro Met Asp Tyr Gly	
120 125 130	
TGG GAT GTT GCG CAA TGC ATC AAG AAG CCA CGA GGT ATT GCA AAG CAT	486
Trp Asp Val Ala Gln Cys Ile Lys Lys Pro Arg Gly Ile Ala Lys His	
135 140 145 150	
TAT GAC TAT GAT TTT TAT TTG GAG AGG GTT TTG GTT GAG CCA CAG GAT	534
Tyr Asp Tyr Asp Phe Tyr Leu Glu Arg Val Leu Val Glu Pro Gln Asp	
155 160 165	
TAT GAG AAA CAA AAT AGA GAG TTG AGC TTA AAA GCC TTA GAA TTT TTG	582
Tyr Glu Lys Gln Asn Arg Glu Leu Ser Leu Lys Ala Leu Glu Phe Leu	
170 175 180	
AAA TAC AAT TTT GAT TTT GAT GTG ATT TTT TAT TCT TTT GGG GAG CAA	630
Lys Tyr Asn Phe Asp Phe Asp Val Ile Phe Tyr Ser Phe Gly Glu Gln	
185 190 195	
TTA ATG CCT ATT CTT ACT AGA ATG TTA GTT TCT GTC TCT AAG TCT CAT	678
Leu Met Pro Ile Leu Thr Arg Met Leu Val Ser Val Ser Lys Ser His	
200 205 210	
AGA AAG AGA CTT GAA AAC TAT GGC AAA GAC ATT AAA ACC TAATTTAGAT AA	729
Arg Lys Arg Leu Glu Asn Tyr Gly Lys Asp Ile Lys Thr	
215 220 225	
AGATGAGTTA AACACA	745

(2) INFORMATION FOR SEQ ID NO:584:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 227 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

```

Met Gly Gln Lys Arg Met Asn Lys Ser Asn Lys Leu Val Ile Ile Asn
 1           5           10           15
Arg Ala Ile Pro Gly Gly Gly Lys Thr Ser Leu Ile Lys Gln Ile Glu
          20           25           30
Glu Leu Ala Lys Ser Leu Gly His Ser Ile Ser Val His Ser Thr Asp
          35           40           45
Glu Tyr Phe Ile Gln Thr Asp Glu Glu Gly Ile Arg His Tyr Val Val
          50           55           60
Asp Lys Lys Lys Leu Asn Glu Tyr His Gln Asn Asn Gln Glu Ala Phe
65          70          75          80
Lys Gln Ala Leu Glu Asn Arg Ile Asp Ile Val Val Cys Asp Asn Thr
          85          90          95
Asn Phe Glu Ser Trp Gln Ser Lys Pro Tyr Thr Asp Met Ala Arg Glu
          100         105         110
Phe Gly Tyr Lys Ile Leu Leu Ile Asp Phe Lys Asn Arg His Leu Glu
          115         120         125
Thr Pro Met Asp Tyr Gly Trp Asp Val Ala Gln Cys Ile Lys Lys Pro
          130         135         140
Arg Gly Ile Ala Lys His Tyr Asp Tyr Asp Phe Tyr Leu Glu Arg Val
145         150         155         160
Leu Val Glu Pro Gln Asp Tyr Glu Lys Gln Asn Arg Glu Leu Ser Leu
          165         170         175
Lys Ala Leu Glu Phe Leu Lys Tyr Asn Phe Asp Phe Asp Val Ile Phe
          180         185         190
Tyr Ser Phe Gly Glu Gln Leu Met Pro Ile Leu Thr Arg Met Leu Val
          195         200         205
Ser Val Ser Lys Ser His Arg Lys Arg Leu Glu Asn Tyr Gly Lys Asp
210         215         220
Ile Lys Thr
225

```

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...468
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

```

ATTTACTAAA GGAAAACA ATG ATT AAA CTA ATC TTA CAC AAG AAG TCC ATA      51
      Met Ile Lys Leu Ile Leu His Lys Lys Ser Ile
        1           5           10

CAA ATT GAT GAA ACA TTG CTG AAT GTA AAA GAG CAT TTA GAA AAG TTT      99

```

Gln	Ile	Asp	Glu	Thr	Leu	Leu	Asn	Val	Lys	Glu	His	Leu	Glu	Lys	Phe		
			15					20					25				
TAT	TCA	AAT	AAA	GAA	CAA	GAG	ACA	ATC	GCT	CAA	ACT	TTA	GAG	AAT	GAA		147
Tyr	Ser	Asn	Lys	Glu	Gln	Glu	Thr	Ile	Ala	Gln	Thr	Leu	Glu	Asn	Glu		
		30					35					40					
ACA	GAA	ATT	TCT	TGT	AGC	TAT	TTT	TGG	GAC	AAA	GAC	TTC	TTG	TTG	TTA		195
Thr	Glu	Ile	Ser	Cys	Ser	Tyr	Phe	Trp	Asp	Lys	Asp	Phe	Leu	Leu	Leu		
	45					50					55						
GAG	CAA	CTT	TTA	GAA	AAT	RAT	TTA	GGT	CAT	TTT	ACC	TTT	GAG	AGC	GAG		243
Glu	Gln	Leu	Leu	Glu	Asn	Xaa	Leu	Gly	His	Phe	Thr	Phe	Glu	Ser	Glu		
60					65					70					75		
TTT	GCC	CTA	CTA	AAA	GAT	AAA	GAG	ACT	TTA	AAC	CTA	TCT	CAA	ATC	AAA		291
Phe	Ala	Leu	Leu	Lys	Asp	Lys	Glu	Thr	Leu	Asn	Leu	Ser	Gln	Ile	Lys		
				80					85					90			
CAA	ATC	GGT	GTC	TTA	AAG	GTT	CTT	ACC	TAT	GAR	ATG	ATA	CAA	ACC	TTA		339
Gln	Ile	Gly	Val	Leu	Lys	Val	Leu	Thr	Tyr	Xaa	Met	Ile	Gln	Thr	Leu		
			95					100					105				
AAA	AAT	CAA	ATC	ATT	CAT	TTA	GCA	CAA	GTT	GTC	AAT	GAA	GAA	AAT	TTA		387
Lys	Asn	Gln	Ile	Ile	His	Leu	Ala	Gln	Val	Val	Asn	Glu	Glu	Asn	Leu		
		110				115						120					
GAA	AAA	GAT	GAA	GAA	CTT	GTT	GTC	TAC	CAC	CTA	AAT	TTC	ACG	TCA	CGC		435
Glu	Lys	Asp	Glu	Glu	Leu	Val	Val	Tyr	His	Leu	Asn	Phe	Thr	Ser	Arg		
	125					130					135						
AAC	AAT	CTT	ACA	AAA	TAT	TAT	CCA	AGT	TCT	GTG	TGATTAAAAA	AGAAAGAAAT					488
Asn	Asn	Leu	Thr	Lys	Tyr	Tyr	Pro	Ser	Ser	Val							
140					145					150							
ATCGCATGAA	AAAATTAAGT	CATTTTAGAA	AGCTTATCGC	CTT													531

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

Met	Ile	Lys	Leu	Ile	Leu	His	Lys	Lys	Ser	Ile	Gln	Ile	Asp	Glu	Thr		
1				5					10					15			
Leu	Leu	Asn	Val	Lys	Glu	His	Leu	Glu	Lys	Phe	Tyr	Ser	Asn	Lys	Glu		
		20						25					30				
Gln	Glu	Thr	Ile	Ala	Gln	Thr	Leu	Glu	Asn	Glu	Thr	Glu	Ile	Ser	Cys		
		35					40					45					
Ser	Tyr	Phe	Trp	Asp	Lys	Asp	Phe	Leu	Leu	Leu	Glu	Gln	Leu	Leu	Glu		
	50					55					60						
Asn	Xaa	Leu	Gly	His	Phe	Thr	Phe	Glu	Ser	Glu	Phe	Ala	Leu	Leu	Lys		

65		70		75		80
Asp	Lys	Glu	Thr	Leu	Asn	Leu
		85		90		95
Lys	Val	Leu	Thr	Xaa	Met	Ile
		100		105		110
His	Leu	Ala	Gln	Val	Val	Asn
		115		120		125
Leu	Val	Val	Tyr	His	Leu	Asn
		130		135		140
Tyr	Tyr	Pro	Ser	Ser	Val	
145					150	

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...294
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

CTGGTTTATG AGTATTTTTT AAAAGAAGTC CCC ATG CAA TTA GTT GGT ATT TCA	54
Met Gln Leu Val Gly Ile Ser	
1 5	
GTT TCT AAT CTC AAA GAA ATC AGC TCC AAA GAA AAA TTT CTT TGG CTC	102
Val Ser Asn Leu Lys Glu Ile Ser Ser Lys Glu Lys Phe Leu Trp Leu	
10 15 20	
AAT GCT AAG AGT TTT TTA CTC TCA GGA TTT GTG CCT TTT ATT ATG ATA	150
Asn Ala Lys Ser Phe Leu Leu Ser Gly Phe Val Pro Phe Ile Met Ile	
25 30 35	
CCT TGG CTA GAT ATA TTG AAC TCT TTT GTG CTT TAT GTG TGC TTT CTC	198
Pro Trp Leu Asp Ile Leu Asn Ser Phe Val Leu Tyr Val Cys Phe Leu	
40 45 50 55	
TTA ATT TTT AGC ATA GCG GAG TTC TTT GAT GAA GAT ATA AGT GAC ATT	246
Leu Ile Phe Ser Ile Ala Glu Phe Phe Asp Glu Asp Ile Ser Asp Ile	
60 65 70	
TTA ATC GCT CAT TCC AAA ATT AAA ACC AAA GCT AAT TCA TTT TAC GCT T	295
Leu Ile Ala His Ser Lys Ile Lys Thr Lys Ala Asn Ser Phe Tyr Ala	
75 80 85	
AAAAGGAAAA AATATGCAAA AAGAAGTCTT AGTAGAAAA	334

(2) INFORMATION FOR SEQ ID NO:588:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

```

Met Gln Leu Val Gly Ile Ser Val Ser Asn Leu Lys Glu Ile Ser Ser
 1           5           10           15
Lys Glu Lys Phe Leu Trp Leu Asn Ala Lys Ser Phe Leu Leu Ser Gly
      20           25           30
Phe Val Pro Phe Ile Met Ile Pro Trp Leu Asp Ile Leu Asn Ser Phe
      35           40           45
Val Leu Tyr Val Cys Phe Leu Leu Ile Phe Ser Ile Ala Glu Phe Phe
      50           55           60
Asp Glu Asp Ile Ser Asp Ile Leu Ile Ala His Ser Lys Ile Lys Thr
      65           70           75           80
Lys Ala Asn Ser Phe Tyr Ala
                        85
  
```

(2) INFORMATION FOR SEQ ID NO:589:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 995 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 37...948
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

```

TAAAAACACC CCTAAAAGAA AAAGAAAGTC TTCTTA ATG TTA GAA AGC GCC CTT      54
                        Met Leu Glu Ser Ala Leu
                        1           5

AAA TAT TGC AAG GAA AAA GCC ATA GAC CTT TTA GTA GGG TTT GTG CCA      102
Lys Tyr Cys Lys Glu Lys Ala Ile Asp Leu Leu Val Gly Phe Val Pro
      10           15           20

AAA ACC TAT TCT ATG GCA CAA GAG TGC AAT ATT TTA GGC TTG TAT GAT      150
Lys Thr Tyr Ser Met Ala Gln Glu Cys Asn Ile Leu Gly Leu Tyr Asp
      25           30           35

GAT GCT TTC ATT ATT ACC AAA CAA GAA AAT CTA GTA GGC ATT ATA TCC      198
Asp Ala Phe Ile Ile Thr Lys Gln Glu Asn Leu Val Gly Ile Ile Ser
      40           45           50

TTA CAA GGA CTA AGC TAT TCT AAT TTA ATG CAA AAA GAC TTA GAG GGC      246
  
```

Leu 55	Gln	Gly	Leu	Ser	Tyr 60	Ser	Asn	Leu	Met	Gln 65	Lys	Asp	Leu	Glu	Gly 70	
TAT Tyr	TTT Phe	GAT Asp	GCT Ala	AGA Arg	CAA Gln	AAT Asn	GTT Val	CTC Leu	AAC Asn	ACC Thr	ATT Ile	AGT Ser	AAA Lys	GAC Asp	ATT Ile	294
CAA Gln	TTA Leu	AGA Arg	ATT Ile	GTG Val	GCT Ala	AAA Lys	AGG Arg	CGT Arg	AAG Lys	GAA Glu	TTT Phe	ATC Ile	AAT Asn	CAA Gln	AGT Ser	342
CCA Pro	AAT Asn	ATT Ile	GAC Asp	AAT Asn	ATT Ile	TAT Tyr	GCC Ala	AAA Lys	GCT Ala	ATT Ile	ATC Ile	ACA Thr	CAA Gln	TTT Phe	GAA Glu	390
AGC Ser	AAG Lys	GGA Gly	ATC Ile	TAT Tyr	AAA Lys	ACA Thr	GAG Glu	TAT Tyr	TTT Phe	TTA Leu	GTG Val	TTT Phe	GAA Glu	ACT Thr	ATC Ile	438
ACT Thr	TCT Ser	AAT Asn	GTC Val	AAG Lys	TCT Ser	TTC Phe	TTT Phe	GAA Glu	AAA Lys	AAG Lys	AAA Lys	TTG Leu	GAA Glu	ATG Met	ACT Thr	486
ACT Thr	TCA Ser	ATT Ile	AAT Asn	GAA Glu	GAG Glu	TTA Leu	GAA Glu	GAA Glu	AGC Ser	TCT Ser	AAA Lys	GAA Glu	GAT Asp	AAA Lys	CAA Gln	534
GAG Glu	AAT Asn	GAA Glu	AAT Asn	MGC Xaa	TCC Ser	AAT Asn	GAA Glu	ACT Thr	CAT His	TCA Ser	AAC Asn	ACA Thr	AGC Ser	TCT Ser	AAA Lys	582
AAA Lys	GAC Asp	AAG Lys	AAA Lys	AAC Asn	AAG Lys	TTC Phe	AAA Lys	AAA Lys	AAG Lys	ATA Ile	ACC Thr	TTT Phe	AGC Ser	ACC Thr	AAA Lys	630
AGT Ser	AAA Lys	AGA Arg	GCC Ala	TTA Leu	CTC Leu	ATT Ile	CAA Gln	ACC Thr	ATA Ile	GAA Glu	AGA Arg	GTA Val	AAA Lys	AAC Asn	GCT Ala	678
CTT Leu	AAA Lys	GAA Glu	TTT Phe	AAA Lys	CCC Pro	ACT Thr	TTA Leu	CTA Leu	AAT Asn	TCT Ser	AAA Lys	GAA Glu	GTA Val	TTA Leu	AAT Asn	726
TTC Phe	TAC Tyr	GCA Ala	GAA Glu	TAC Tyr	ATC Ile	AAT Asn	GGC Gly	AAA Lys	TAC Tyr	ATC Ile	GCC Ala	TTT Phe	AAT Asn	CCT Pro	AAA Lys	774
TTA Leu	AAG Lys	CGA Arg	TTA Leu	AGC Ser	GAT Asp	ACT Thr	ATA Ile	TTG Leu	CAT His	CTA Leu	ATG Met	TGC Cys	ATT Ile	TTA Leu	AGA Arg	822
AAG Lys	ATT Ile	ACT Thr	TTG Leu	TCA Ser	TTG Leu	AAT Asn	TTC Phe	AAA Lys	ATC Ile	AAA Lys	ACA Thr	CCT Pro	TTT Phe	GTG Val	CGT Arg	870
GTG Val	TGG Trp	GGA Gly	TTA Leu	AGG Arg	CTT Leu	ATG Met	AGA Arg	GCG Ala	AAG Lys	AAA Lys	TTT Phe	CTT Leu	CGC Arg	TCC Ser	CTA Leu	918

TAT CTA CTC TTT TAC ACA CCC AAA TTG AAC TAGATTTAAT CTTTCATATC CGC 971
 Tyr Leu Leu Phe Tyr Thr Pro Lys Leu Asn
 295 300

TCTTTAGGGC AATTTGAAAG CCTG

995

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

Met	Leu	Glu	Ser	Ala	Leu	Lys	Tyr	Cys	Lys	Glu	Lys	Ala	Ile	Asp	Leu
1				5					10					15	
Leu	Val	Gly	Phe	Val	Pro	Lys	Thr	Tyr	Ser	Met	Ala	Gln	Glu	Cys	Asn
			20					25					30		
Ile	Leu	Gly	Leu	Tyr	Asp	Asp	Ala	Phe	Ile	Ile	Thr	Lys	Gln	Glu	Asn
		35					40					45			
Leu	Val	Gly	Ile	Ile	Ser	Leu	Gln	Gly	Leu	Ser	Tyr	Ser	Asn	Leu	Met
		50				55					60				
Gln	Lys	Asp	Leu	Glu	Gly	Tyr	Phe	Asp	Ala	Arg	Gln	Asn	Val	Leu	Asn
65					70					75				80	
Thr	Ile	Ser	Lys	Asp	Ile	Gln	Leu	Arg	Ile	Val	Ala	Lys	Arg	Arg	Lys
				85					90					95	
Glu	Phe	Ile	Asn	Gln	Ser	Pro	Asn	Ile	Asp	Asn	Ile	Tyr	Ala	Lys	Ala
			100					105					110		
Ile	Ile	Thr	Gln	Phe	Glu	Ser	Lys	Gly	Ile	Tyr	Lys	Thr	Glu	Tyr	Phe
		115					120					125			
Leu	Val	Phe	Glu	Thr	Ile	Thr	Ser	Asn	Val	Lys	Ser	Phe	Phe	Glu	Lys
		130				135					140				
Lys	Lys	Leu	Glu	Met	Thr	Thr	Ser	Ile	Asn	Glu	Glu	Leu	Glu	Glu	Ser
145					150					155				160	
Ser	Lys	Glu	Asp	Lys	Gln	Glu	Asn	Glu	Asn	Xaa	Ser	Asn	Glu	Thr	His
				165					170					175	
Ser	Asn	Thr	Ser	Ser	Lys	Lys	Asp	Lys	Lys	Asn	Lys	Phe	Lys	Lys	Lys
			180					185					190		
Ile	Thr	Phe	Ser	Thr	Lys	Ser	Lys	Arg	Ala	Leu	Leu	Ile	Gln	Thr	Ile
		195					200						205		
Glu	Arg	Val	Lys	Asn	Ala	Leu	Lys	Glu	Phe	Lys	Pro	Thr	Leu	Leu	Asn
		210				215					220				
Ser	Lys	Glu	Val	Leu	Asn	Phe	Tyr	Ala	Glu	Tyr	Ile	Asn	Gly	Lys	Tyr
225					230					235				240	
Ile	Ala	Phe	Asn	Pro	Lys	Leu	Lys	Arg	Leu	Ser	Asp	Thr	Ile	Leu	His
				245					250					255	
Leu	Met	Cys	Ile	Leu	Arg	Lys	Ile	Thr	Leu	Ser	Leu	Asn	Phe	Lys	Ile
			260					265					270		
Lys	Thr	Pro	Phe	Val	Arg	Val	Trp	Gly	Leu	Arg	Leu	Met	Arg	Ala	Lys
		275					280					285			
Lys	Phe	Leu	Arg	Ser	Leu	Tyr	Leu	Leu	Phe	Tyr	Thr	Pro	Lys	Leu	Asn
		290				295					300				

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...1556
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

ATAATTATAT AGAATTAGTG CAAGCCAATC GTTTGAGC ATG CAA GAG TGT GCT TTA	56
Met Gln Glu Cys Ala Leu	
1 5	
AAC TTA GTT ATA AGG GCT AAA AGT AAA GCT AAA TTA GAC AAG TCT TTA	104
Asn Leu Val Ile Arg Ala Lys Ser Lys Ala Lys Leu Asp Lys Ser Leu	
10 15 20	
AAA GAG ATT TTA TCC TTG CTT AAT AAT GCT GGA CTA GGC AGT GTT ACA	152
Lys Glu Ile Leu Ser Leu Leu Asn Asn Ala Gly Leu Gly Ser Val Thr	
25 30 35	
GAA ACT ATA GGG CTA AAA CCA TCT TAT TTT TCA TTC TTC CCA AAT AAC	200
Glu Thr Ile Gly Leu Lys Pro Ser Tyr Phe Ser Phe Phe Pro Asn Asn	
40 45 50	
GCC AAT ATC AAC CCT AGA ATG AGA CAT CAA ACT TCC CAA GTC ATA GCA	248
Ala Asn Ile Asn Pro Arg Met Arg His Gln Thr Ser Gln Val Ile Ala	
55 60 65 70	
TCT TTG ATT TTG TTT GAG AAA AAT AAT ACA GGT TTT AGA GCA AAT TCT	296
Ser Leu Ile Leu Phe Glu Lys Asn Asn Thr Gly Phe Arg Ala Asn Ser	
75 80 85	
TGG GGG GAT ATG CCC TTA TCT GTG TTT AAG AAC CTA GAC CAT AGC CCT	344
Trp Gly Asp Met Pro Leu Ser Val Phe Lys Asn Leu Asp His Ser Pro	
90 95 100	
TAT TTG TTT AAT TTT CAT AAT CAA GAA GTC AAA CAT AAG GGC GTG TTA	392
Tyr Leu Phe Asn Phe His Asn Gln Glu Val Lys His Lys Gly Val Leu	
105 110 115	
GCC CAC AAT GTC GCA CGA GTA GTG GGA CAT ACC ATG ATT ATA GGA GCA	440
Ala His Asn Val Ala Arg Val Val Gly His Thr Met Ile Ile Gly Ala	
120 125 130	
ACA GGT GCT GGT AAA ACC ACA CTC ATT AGC TAT TTG ATG ATG AGT GCC	488
Thr Gly Ala Gly Lys Thr Thr Leu Ile Ser Tyr Leu Met Met Ser Ala	
135 140 145 150	
TTA AAA TAT TCT AAC ATT GAT ATT TTA GCT CTT GAT AGA CTA AAT GGT	536
Leu Lys Tyr Ser Asn Ile Asp Ile Leu Ala Leu Asp Arg Leu Asn Gly	

																584
																632
																680
																728
																776
																824
																872
																920
																968
																1016
																1064
																1112
																1160
																1208

			100					105					110			
Lys	His	Lys	Gly	Val	Leu	Ala	His	Asn	Val	Ala	Arg	Val	Val	Gly	His	
		115					120					125				
Thr	Met	Ile	Ile	Gly	Ala	Thr	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Ile	Ser	
	130					135					140					
Tyr	Leu	Met	Met	Ser	Ala	Leu	Lys	Tyr	Ser	Asn	Ile	Asp	Ile	Leu	Ala	
145					150					155					160	
Leu	Asp	Arg	Leu	Asn	Gly	Leu	Tyr	Ser	Phe	Thr	Lys	Tyr	Phe	Asp	Gly	
				165					170					175		
Ile	Tyr	Asn	Gln	Gly	Glu	Asn	Phe	His	Ile	Asn	Pro	Phe	Ser	Leu	Glu	
		180						185					190			
Asp	Ser	Ala	Thr	Asn	Arg	Ala	Phe	Leu	Leu	His	Phe	Tyr	Ala	Gln	Met	
		195					200					205				
Ala	Lys	Val	Asp	Ser	Tyr	Asp	Asp	His	Lys	Asp	Lys	Val	Glu	Asp	Arg	
	210					215					220					
Thr	Ala	Leu	Leu	Asn	Ala	Ile	Asp	Thr	Met	Tyr	Arg	Asn	Tyr	Asn	Asp	
225					230					235					240	
Glu	Val	Lys	Gln	Ala	Lys	Phe	Ser	Asn	Gln	Glu	Leu	Pro	Leu	Pro	Phe	
				245					250					255		
Asp	Leu	Lys	Glu	Phe	Val	Asn	Ala	Ile	Ala	Lys	Thr	Asn	Thr	Asp	Ile	
		260						265					270			
Leu	Asp	Ser	Ser	Phe	Glu	Asp	Tyr	Leu	Lys	Ser	Ser	Leu	Phe	Ser	Ser	
		275					280					285				
Arg	Met	Asp	Ser	Leu	Asp	Phe	Lys	Thr	Arg	Ile	Ser	Thr	Ile	Asn	Thr	
	290					295					300					
Asp	Ser	Ile	Leu	His	Asn	Asp	Asp	Asp	Ala	Gly	Leu	Leu	Ala	Tyr	Tyr	
305					310					315					320	
Val	Phe	His	Lys	Met	Ile	Asp	Arg	Ala	Leu	Lys	Ile	Asn	Arg	Gly	Phe	
				325					330					335		
Leu	Cys	Phe	Ile	Asp	Glu	Phe	Lys	Ser	Tyr	Ala	Gln	Asn	Glu	Met	Met	
			340					345					350			
Asn	Lys	Lys	Ile	Asn	Glu	Ile	Ile	Thr	Gln	Ala	Arg	Lys	Ala	Asn	Gly	
		355					360					365				
Val	Ile	Val	Leu	Ala	Leu	Gln	Asp	Ile	Asn	Gln	Leu	Ser	Glu	Val	Arg	
	370					375					380					
Asn	Ala	Gln	Ser	Phe	Ile	Lys	Asn	Met	Gly	Gln	Leu	Ile	Leu	Tyr	Pro	
385					390					395					400	
Gln	Arg	Asn	Ile	Asp	Thr	Lys	Asp	Leu	Asn	Asp	Lys	Phe	Gly	Ile	Arg	
				405					410					415		
Leu	Ser	Asp	Thr	Glu	Lys	His	Phe	Leu	Glu	Asn	Thr	Ala	Val	Asn	Glu	
			420					425					430			
Tyr	Lys	Val	Leu	Leu	Lys	Asn	Met	Asn	Asp	Gly	Ser	Ser	Asn	Ile	Ile	

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 563 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 24...509

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

CAACTCTTTT TTAAGGGGGA CAC ATG TCT AAT TTG CAA GAA CTT AGA GAG CAT	53
Met Ser Asn Leu Gln Glu Leu Arg Glu His	
1 5 10	
TTA AAA GAA TTA GAA AAT TCC TTT GAA ATA GGC TCT TTT ACT AAA GAA	101
Leu Lys Glu Leu Glu Asn Ser Phe Glu Ile Gly Ser Phe Thr Lys Glu	
15 20 25	
AAT ATT AAA GAA TAC GCT AAA TGC TTT TTT ATG AGT TTA AGC ATG TTT	149
Asn Ile Lys Glu Tyr Ala Lys Cys Phe Phe Met Ser Leu Ser Met Phe	
30 35 40	
TTA GAA GAA CAA GAA AAA AAC CAA CAA GAA GAG TTT TTA GAA CAA GAT	197
Leu Glu Glu Gln Glu Lys Asn Gln Gln Glu Glu Phe Leu Glu Gln Asp	
45 50 55	
ACC AAA GAA AAT CAA GAA GAG CTC ATT AAA AAC ATT CAA ACA AGC ATT	245
Thr Lys Glu Asn Gln Glu Glu Leu Ile Lys Asn Ile Gln Thr Ser Ile	
60 65 70	
GCT AAA AAC CAA GAG TTA GAA AAA ATC TCT TTT GAA AAA TGG GAG AAT	293
Ala Lys Asn Gln Glu Leu Glu Lys Ile Ser Phe Glu Lys Trp Glu Asn	
75 80 85 90	
AAA ATT CAA GAA AGG GTT TTG CCT AAG TTA AAA CGC ATT GTT ACG CAT	341
Lys Ile Gln Glu Arg Val Leu Pro Lys Leu Lys Arg Ile Val Thr His	
95 100 105	
AAG TTG CAA GAA AGT ATC ACA TCT AGC ATA AAC ACG CAA TTA GAG AGT	389
Lys Leu Gln Glu Ser Ile Thr Ser Ser Ile Asn Thr Gln Leu Glu Ser	
110 115 120	
TTT AAA AAA GAT GAG TTA GAT TTA TCT AGC GTG TTT GAA ATC CAA AGA	437
Phe Lys Lys Asp Glu Leu Asp Leu Ser Ser Val Phe Glu Ile Gln Arg	
125 130 135	
AAG AAC ACT CAA ATA GCG TAT AGA TTA GCT ATA GGG GGG CTT ATA GGT	485
Lys Asn Thr Gln Ile Ala Tyr Arg Leu Ala Ile Gly Gly Leu Ile Gly	
140 145 150	
ATC ATT GCT TTA AGC TCG CAA ATT TGATTATTAA CTCTATACTT CACGCTTTTT	539
Ile Ile Ala Leu Ser Ser Gln Ile	
155 160	
AGCCTTTGTG TGTTCCTTTTG TAAA	563

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

```

Met Ser Asn Leu Gln Glu Leu Arg Glu His Leu Lys Glu Leu Glu Asn
 1          5          10          15
Ser Phe Glu Ile Gly Ser Phe Thr Lys Glu Asn Ile Lys Glu Tyr Ala
 20          25          30
Lys Cys Phe Phe Met Ser Leu Ser Met Phe Leu Glu Glu Gln Glu Lys
 35          40          45
Asn Gln Gln Glu Glu Phe Leu Glu Gln Asp Thr Lys Glu Asn Gln Glu
 50          55          60
Glu Leu Ile Lys Asn Ile Gln Thr Ser Ile Ala Lys Asn Gln Glu Leu
 65          70          75          80
Glu Lys Ile Ser Phe Glu Lys Trp Glu Asn Lys Ile Gln Glu Arg Val
 85          90          95
Leu Pro Lys Leu Lys Arg Ile Val Thr His Lys Leu Gln Glu Ser Ile
100          105          110
Thr Ser Ser Ile Asn Thr Gln Leu Glu Ser Phe Lys Lys Asp Glu Leu
115          120          125
Asp Leu Ser Ser Val Phe Glu Ile Gln Arg Lys Asn Thr Gln Ile Ala
130          135          140
Tyr Arg Leu Ala Ile Gly Leu Ile Gly Ile Ile Ala Leu Ser Ser
145          150          155          160
Gln Ile

```

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...3186
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

```

CCTTAAATCT AAGGGGTGTG C ATG CCA TAC AAT GAA ATC ACA AGG GTT CAA      51
      Met Pro Tyr Asn Glu Ile Thr Arg Val Gln
      1          5          10

ATC CCT GCC TTA ATG CAT TTA GCC AAG TTG GGC TAT GAT TTT ATC CCC      99

```

Ile	Pro	Ala	Leu	Met	His	Leu	Ala	Lys	Leu	Gly	Tyr	Asp	Phe	Ile	Pro	
				15					20					25		
ACT	AAT	TCT	AAA	GAA	AAT	AAG	CCC	AAC	CTA	GAC	ACC	GCC	ACC	AAC	ATT	147
Thr	Asn	Ser	Lys	Glu	Asn	Lys	Pro	Asn	Leu	Asp	Thr	Ala	Thr	Asn	Ile	
			30					35					40			
TTA	ACC	AAT	AGT	TTC	ACT	AAA	TCC	TTT	GAG	CGG	TTA	AAC	CCC	ACT	AAA	195
Leu	Thr	Asn	Ser	Phe	Thr	Lys	Ser	Phe	Glu	Arg	Leu	Asn	Pro	Thr	Lys	
			45				50					55				
AAC	GCA	CAA	GAA	ACG	CTT	GCT	GAA	ATG	AAA	AAA	CGC	TTG	AAT	TGC	GAT	243
Asn	Ala	Gln	Glu	Thr	Leu	Ala	Glu	Met	Lys	Lys	Arg	Leu	Asn	Cys	Asp	
			60			65					70					
GAT	TTG	GGC	AAA	AGC	TTT	TAT	GAA	TAC	TTG	CTC	AAA	AGC	GAG	AAT	CAA	291
Asp	Leu	Gly	Lys	Ser	Phe	Tyr	Glu	Tyr	Leu	Leu	Lys	Ser	Glu	Asn	Gln	
					80					85					90	
ATC	ATA	GAC	TTT	GAT	AAC	CCT	AAC	AAC	AAT	CTT	TAT	GAA	ATG	ATG	ACT	339
Ile	Ile	Asp	Phe	Asp	Asn	Pro	Asn	Asn	Asn	Leu	Tyr	Glu	Met	Met	Thr	
				95					100					105		
GAA	TTA	CCC	TAC	AAA	TCT	TTT	AGG	CCT	GAC	ACC	ACC	CTT	TTT	ATC	AAT	387
Glu	Leu	Pro	Tyr	Lys	Ser	Phe	Arg	Pro	Asp	Thr	Thr	Leu	Phe	Ile	Asn	
				110				115					120			
GGC	TTG	CCT	TTG	GTG	AAT	ATA	GAA	GTT	AAA	CAG	CCT	TAC	GCC	AAA	AAA	435
Gly	Leu	Pro	Leu	Val	Asn	Ile	Glu	Val	Lys	Gln	Pro	Tyr	Ala	Lys	Lys	
			125				130					135				
GGC	ATT	AAA	GAA	GAA	AGA	GAT	CGC	CAC	ATC	AAA	CGC	TAT	GAA	AAC	CCT	483
Gly	Ile	Lys	Glu	Glu	Arg	Asp	Arg	His	Ile	Lys	Arg	Tyr	Glu	Asn	Pro	
			140			145					150					
GAA	AAC	AAA	GTT	TTT	TAT	AAT	CTC	GCG	CAA	ATC	TGG	CTT	TTT	AGC	GAT	531
Glu	Asn	Lys	Val	Phe	Tyr	Asn	Leu	Ala	Gln	Ile	Trp	Leu	Phe	Ser	Asp	
					160					165					170	
AAC	TTA	CCC	TAT	GAT	GAA	AAC	AAA	CCC	GAT	CAA	GGC	GCG	TTT	TAT	AGC	579
Asn	Leu	Pro	Tyr	Asp	Glu	Asn	Lys	Pro	Asp	Gln	Gly	Ala	Phe	Tyr	Ser	
				175					180					185		
GCT	TCT	TAT	TCG	CCC	ATT	TTC	CAA	CGC	TTT	GTT	GAA	GCT	CAT	AGG	CTA	627
Ala	Ser	Tyr	Ser	Pro	Ile	Phe	Gln	Arg	Phe	Val	Glu	Ala	His	Arg	Leu	
				190				195					200			
GAT	ATT	WCC	CCC	SSN	CCC	CSC	CAA	AAA	AAT	GAT	CAA	AAT	CAT	CAA	AAC	675
Asp	Ile	Xaa	Pro	Xaa	Pro	Xaa	Gln	Lys	Asn	Asp	Gln	Asn	His	Gln	Asn	
			205				210					215				
GAT	CAA	AAT	CAT	CGA	TCG	CTT	GAA	GAA	ATT	CAA	AAA	AGC	GTC	TTA</		

		115					120					125			
Ile	Glu	Val	Lys	Gln	Pro	Tyr	Ala	Lys	Lys	Gly	Ile	Lys	Glu	Glu	Arg
	130					135					140				
Asp	Arg	His	Ile	Lys	Arg	Tyr	Glu	Asn	Pro	Glu	Asn	Lys	Val	Phe	Tyr
145					150					155					160
Asn	Leu	Ala	Gln	Ile	Trp	Leu	Phe	Ser	Asp	Asn	Leu	Pro	Tyr	Asp	Glu
				165					170					175	
Asn	Lys	Pro	Asp	Gln	Gly	Ala	Phe	Tyr	Ser	Ala	Ser	Tyr	Ser	Pro	Ile
			180					185					190		
Phe	Gln	Arg	Phe	Val	Glu	Ala	His	Arg	Leu	Asp	Ile	Xaa	Pro	Xaa	Pro
		195					200					205			
Xaa	Gln	Lys	Asn	Asp	Gln	Asn	His	Gln	Asn	Asp	Gln	Asn	His	Arg	Ser
	210					215					220				
Leu	Glu	Glu	Ile	Gln	Lys	Ser	Val	Leu	Asn	Glu	Phe	Asn	Leu	Lys	Asp
225					230					235					240
Thr	Asp	Thr	Pro	Lys	Ser	Pro	Lys	Asp	Thr	Pro	Thr	Asn	Ser	Leu	Leu
				245					250					255	
Thr	Ser	Phe	Cys	Ser	Pro	Lys	Arg	Leu	Cys	Phe	Ile	Leu	Lys	Tyr	Gly
			260					265					270		
Ile	Ser	Phe	Leu	Lys	Glu	Lys	Ser	Glu	Phe	Lys	Lys	His	Val	Trp	Arg
		275					280					285			
Tyr	Ala	Gln	Met	Phe	Ala	Ser	Leu	Asn	Val	Leu	Lys	Glu	Leu	Gln	Lys
	290					295					300				
His	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	Lys	Asp	Pro	Leu	Lys	Gly	Ile	Ile
305					310					315					320
Trp	His	Thr	Gln	Gly	Ser	Gly	Lys	Thr	Ala	Leu	Thr	Tyr	His	Leu	Thr
				325					330					335	
Lys	Leu	Ile	Arg	Asp	Phe	Phe	Ser	Arg	Ser	Asn	Leu	Asn	Lys	Lys	Thr
			340					345					350		
Lys	Phe	Tyr	Phe	Ile	Val	Asp	Arg	Leu	Asp	Leu	Leu	Glu	Gln	Ala	Lys
		355					360					365			
Asn	Glu	Phe	Leu	Lys	Arg	Gly	Leu	Cys	Val	His	Glu	Ala	Glu	Asn	Lys
	370					375					380				
Glu	Asp	Leu	Ser	Gln	Lys	Leu	Lys	Ser	Ser	Ser	Val	Phe	Glu	Gly	Ser
385					390					395					400
Gln	Gly	Asn	Asp	Glu	Ile	Ile	Val	Val	Asn	Ile	Gln	Lys	Phe	Lys	Ala
				405					410					415	
Pro	Asn	Glu	Glu	Lys	Ser	Pro	Asn	Glu	Asp	Pro	Ser	Asn	Ser	Ala	Pro
			420					425					430		
Lys	Glu	Ile	Ile	Ser	Lys	Thr	Glu	Leu	Gln	Glu	Ser	Ile	Gln	Asn	Ser
		435					440					445			
Arg	Asn	Leu	Gln	Arg	Val	Phe	Ile	Ile	Asp	Glu	Ala	His	Arg	Ser	Tyr
	450					455					460				
Asp	Pro	Lys	Gly	Cys	Phe	Tyr	Ala	Asn							

1045

1050

1055

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...511
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

TAGAAGAATT TGAAAGGTTG CTCGC ATG CAA AGA GAA TTA AGG CTT TTA AAT	52
Met Gln Arg Glu Leu Arg Leu Leu Asn	
1 5	
AAC AAG CAT TGC ATG GAA TAC TTG CAA TTT CTG TCC AAA AAC CAT TTG	100
Asn Lys His Cys Met Glu Tyr Leu Gln Phe Leu Ser Lys Asn His Leu	
10 15 20 25	
AGT TTT AAC CTT TTG TGC GAA AGA GAT GCG ATT GAT TTT TCC CCC AAG	148
Ser Phe Asn Leu Leu Cys Glu Arg Asp Ala Ile Asp Phe Ser Pro Lys	
30 35 40	
CTC CCT AAA GAA ATT CAT GAA AAA TTC GGC GCG TTA GTG CTA TTT GTT	196
Leu Pro Lys Glu Ile His Glu Lys Phe Gly Ala Leu Val Leu Phe Val	
45 50 55	
TTA GCC GGA TAC ACC TTA GAA AGC TTG ATA ATT GAT ACA AAA AGC GTG	244
Leu Ala Gly Tyr Thr Leu Glu Ser Leu Ile Ile Asp Thr Lys Ser Val	
60 65 70	
CAA TTT GAA GCC GGG TTT GGC CCT AAT AAC ATT GGC AGT GTG GTT CAA	292
Gln Phe Glu Ala Gly Phe Gly Pro Asn Asn Ile Gly Ser Val Val Gln	
75 80 85	
GTA AAA CTT CCT GGC ATC ATT CAA ATC CTT ATC AAA GAA AAA AAT GAA	340
Val Lys Leu Pro Gly Ile Ile Gln Ile Leu Ile Lys Glu Lys Asn Glu	
90 95 100 105	
AAT GCC GTT TTA TTC AAT CGT TGC GAT TCG CTT GAA TTG TTT CAA AAA	388
Asn Ala Val Leu Phe Asn Arg Cys Asp Ser Leu Glu Leu Phe Gln Lys	
110 115 120	
GAA GAT TCA ATC GCG CAA GAG CCA AAA AAA GAC GAG CGG GAG TCT AAA	436
Glu Asp Ser Ile Ala Gln Glu Pro Lys Lys Asp Glu Arg Glu Ser Lys	
125 130 135	
GAA TGG CTG GAT TCT AAA GAG GCT CTT TTT TCC AAT TCC AAA AAC CGC	484
Glu Trp Leu Asp Ser Lys Glu Ala Leu Phe Ser Asn Ser Lys Asn Arg	

140

145

150

GCG ATT TTA GAA AAT CTG CAC AAA AGC TAAAGGAATC ATTGATGAGC GTTTTGA 538
Ala Ile Leu Glu Asn Leu His Lys Ser
155 160

AATTGCATGT AAAAGTCTTT CGTTTTGAAA CCAATA 574

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

Met	Gln	Arg	Glu	Leu	Arg	Leu	Leu	Asn	Asn	Lys	His	Cys	Met	Glu	Tyr
1				5					10					15	
Leu	Gln	Phe	Leu	Ser	Lys	Asn	His	Leu	Ser	Phe	Asn	Leu	Leu	Cys	Glu
			20					25					30		
Arg	Asp	Ala	Ile	Asp	Phe	Ser	Pro	Lys	Leu	Pro	Lys	Glu	Ile	His	Glu
		35					40					45			
Lys	Phe	Gly	Ala	Leu	Val	Leu	Phe	Val	Leu	Ala	Gly	Tyr	Thr	Leu	Glu
	50					55					60				
Ser	Leu	Ile	Ile	Asp	Thr	Lys	Ser	Val	Gln	Phe	Glu	Ala	Gly	Phe	Gly
65					70				75					80	
Pro	Asn	Asn	Ile	Gly	Ser	Val	Val	Gln	Val	Lys	Leu	Pro	Gly	Ile	Ile
			85					90						95	
Gln	Ile	Leu	Ile	Lys	Glu	Lys	Asn	Glu	Asn	Ala	Val	Leu	Phe	Asn	Arg
			100					105					110		
Cys	Asp	Ser	Leu	Glu	Leu	Phe	Gln	Lys	Glu	Asp	Ser	Ile	Ala	Gln	Glu
		115					120					125			
Pro	Lys	Lys	Asp	Glu	Arg	Glu	Ser	Lys	Glu	Trp	Leu	Asp	Ser	Lys	Glu
	130					135					140				
Ala	Leu	Phe	Ser	Asn	Ser	Lys	Asn	Arg	Ala	Ile	Leu	Glu	Asn	Leu	His
145					150					155				160	
Lys	Ser														

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1697 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 14...1648
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

TTTAGGGGGG	TAA	ATG	CCT	TCA	AAC	GCT	CTT	TTG	ATT	GAA	GAA	ATC	ACT	49
	Met	Pro	Ser	Asn	Ala	Leu	Leu	Ile	Glu	Glu	Ile	Thr		
	1					5					10			
CAT	TTA	ATC	AAT	GTT	TCT	CAT	AGT	AGC	GTG	CAT	AAT	TGG	ATC	97
His	Leu	Ile	Asn	Val	Ser	His	Ser	Ser	Val	His	Asn	Trp	Ile	
	15					20					25			
AAT	CTT	TTA	GAG	AAA	CTA	GAA	ATT	GAT	CAT	AAA	ATT	TAT	GTG	145
Asn	Leu	Leu	Glu	Lys	Leu	Glu	Ile	Asp	His	Lys	Ile	Tyr	Val	
	30					35					40			
AGT	TCT	TTT	TTA	GAT	TTT	TGC	CGC	AAC	CAT	TTA	GGG	AAA	AAC	193
Ser	Ser	Phe	Leu	Asp	Phe	Cys	Arg	Asn	His	Leu	Gly	Lys	Asn	
45					50					55			Lys	
													Leu	
													60	
AAC	AAA	TAC	GCT	AAC	AAA	TCC	TTA	AAA	GGC	GTG	CAT	AAC	CAT	241
Asn	Lys	Tyr	Ala	Asn	Lys	Ser	Leu	Lys	Gly	Val	His	Asn	His	
				65					70				Gln	
													Glu	
													75	
TTG	ATT	TTA	AAA	TAC	CTA	GAA	ATA	TTA	GAA	AAT	AGC	TCT	GAT	289
Leu	Ile	Leu	Lys	Tyr	Leu	Glu	Ile	Leu	Glu	Asn	Ser	Ser	Asp	
			80					85					Leu	
													Glu	
													90	
AAG	TTG	GGT	TCT	TAT	TAT	GAA	GAA	GAG	CTT	TCT	AAC	GCC	ACC	337
Lys	Leu	Gly	Ser	Tyr	Tyr	Glu	Glu	Glu	Leu	Ser	Asn	Ala	Thr	
		95					100					105	Arg	
													Asn	
TTA	GAA	GGC	ATT	TAC	TAC	ACT	CCT	AAC	AGG	ATA	GTA	GAA	CAA	385
Leu	Glu	Gly	Ile	Tyr	Tyr	Thr	Pro	Asn	Arg	Ile	Val	Glu	Gln	
	110					115					120		Leu	
													Phe	
ACC	CTC	CCT	AAA	GAT	TTT	GAT	GTC	TCT	CAA	GCG	ATT	TTT	TGC	433
Thr	Leu	Pro	Lys	Asp	Phe	Asp	Val	Ser	Gln	Ala	Ile	Phe	Cys	
125					130					135			Asp	
													Pro	
													140	
GCT	GTG	GGG	AGT	GGG	AAT	TTT	ATC	ATG	CAT	GCT	TTA	AAA	CTG	481
Ala	Val	Gly	Ser	Gly	Asn	Phe	Ile	Met	His	Ala	Leu	Lys	Leu	
				145					150				Gly	
													Phe	
													155	
AAG	GTT	GAA	AAC	ATT	TAT	GGC	TAT	GAT	ACG	GAC	GCT	TTT	GCT	529
Lys	Val	Glu	Asn	Ile	Tyr	Gly	Tyr	Asp	Thr	Asp	Ala	Phe	Ala	
			160					165					Val	
													Ala	
TTG	ACT	AAA	AAG	CGT	ATT	AAA	GAG	CGT	TAT	CAT	TTA	GAT	TGC	577
Leu	Thr	Lys	Lys	Arg	Ile	Lys	Glu	Arg	Tyr	His	Leu	Asp	Cys	
		175					180					185	Leu	
													Asn	
ATT	GTG	CAA	AAA	GAT	TTT	TTA	AAT	TTA	AAA	CAC	ACC	CCG	CAA	625
Ile	Val	Gln	Lys	Asp	Phe	Leu	Asn	Leu	Lys	His	Thr	Pro	Gln	
	190					195					200		Phe	
													Asp	
TGC	ATT	TTC	ACT	AAC	CCG	CCA	TGG	GGC	AAG	AAA	TAC	AAT	CAA	673
Cys	Ile	Phe	Thr	Asn	Pro	Pro	Trp	Gly	Lys	Lys	Tyr	Asn	Gln	
205					210					215			Asn	
													Gln	
													220	

AAA Lys	GAA Glu	AAT Asn	TTT Phe	AAA Lys 225	CAG Gln	CAA Gln	TTC Phe	AAC Asn	CTC Leu 230	TCT Ser	CAA Gln	AGC Ser	CTA Leu	GAT Asp 235	AGC Ser	721
GCG Ala	TCG Ser	CTC Leu	TTT Phe 240	TTT Phe	ATA Ile	GCG Ala	AGT Ser	TTG Leu	AAT Asn 245	TGT Cys	TTA Leu	AAA Lys	GAA Glu 250	AAC Asn	GCT Ala	769
CAT His	TTG Leu	GGG Gly 255	TTA Leu	TTA Leu	TTA Leu	CCC Pro	GAA Glu 260	AGT Ser	TGT Cys	TTG Leu	AAT Asn	ATT Ile 265	GAT Asp	GCG Ala	TTT Phe	817
AAA Lys	AAA Lys 270	ATG Met	CGA Arg	GAA Glu	ATG Met	GCT Ala 275	TTA Leu	AAG Lys	TTT Phe	CAC His	ATT Ile 280	AGA Arg	AGC Ser	CTG Leu	ATT Ile	865
GAT Asp 285	TTT Phe	GAC Asp	AAA Lys	CCT Pro	TTT Phe 290	AAA Lys	AAT Asn	CTA Leu	ATG Met	ACT Thr 295	AAG Lys	GCT Ala	GTG Val	GGT Gly	TTG Leu 300	913
GCG Ala	CTT Leu	AAA Lys	AAA Lys	ACC Thr 305	CCT Pro	AAT Asn	AAG Lys	GAT Asp	CAA Gln 310	AAA Lys	ATC Ile	TCA Ser	TGC Cys	TTT Phe 315	TAT Tyr	961
CAA Gln	AAT Asn	AGC Ser	AAG Lys 320	TTC Phe	AAA Lys	CGC Arg	TCG Ser	CCC Pro 325	TCT Ser	TCT Ser	TTT Phe	TTT Phe	AAC Asn 330	AAC Asn	CCT Pro	1009
AAA Lys	AAG Lys	ATT Ile 335	TTT Phe	AAT Asn	ATC Ile	CAT His	TGC Cys 340	TCT Ser	AGC Ser	AAA Lys	GAA Glu	AAT Asn 345	AAA Lys	ATT Ile	TTA Leu	1057
GAC Asp	CAC His 350	CTT Leu	TTT Phe	TCC Ser	CTC Leu	CCT Pro 355	CAT His	ATG Met	ACT Thr	TTA Leu	AAA Lys 360	AAT Asn	AAC Asn	GCT Ala	CAT His	1105
TTT Phe 365	GCT Ala	TTA Leu	GGG Gly	ATT Ile	GTT Val 370	ACA Thr	GGC Gly	AAC Asn	AAT Asn	AAA Lys 375	GAA Glu	AAA Lys	TTA Leu	CAC His	CCC Pro 380	1153
AAA Lys	CAA Gln	GAA Glu	AAA Lys	AAT Asn 385	ACC Thr	ATT Ile	CCC Pro	ATT Ile	TTT Phe 390	AGG Arg	GGT Gly	TCA Ser	GAT Asp	ATT Ile 395	TTA Leu	1201
AAA Lys	GAC Asp	GGA Gly	TTA Leu 400	AAA Lys	GCC Ala	CCT Pro	AGC Ser	CAA Gln 405	TTC Phe	ATT Ile	AAC Asn	GCT Ala	GGT Gly 410	TTA Leu	AAA Lys	1249
GAC Asp	TGC Cys	CAG Gln 415	CAA Gln	GTC Val	GCC Ala	CCC Pro	TTA Leu 420	AGC Ser	CTT Leu	TAT Tyr	CAA Gln	GCT Ala 425	AGA Arg	GAA Glu	AAA Lys	1297
ATC Ile	GTG Val 430	TAT Tyr	AAA Lys	TTC Phe	ATT Ile	TCT Ser 435	TCA Ser	AAG Lys	CTT Leu	GTC Val	TTT Phe 440	TTT Phe	TAT Tyr	GAC Asp	AAT Asn	1345
AAG Lys	CAA Gln	CGC Arg	CTT Leu	TTT Phe	TTA Leu	AAC Asn	AGC Ser	GCG Ala	AAC Asn	ATG Met	TTT Phe	GTT Val	TTA Leu	AAA Lys	GAA Glu	1393

445	450	455	460	
AAT TTC CCT ATC AAC GCT CAT GCA TTA AAA GAA TTG TTA AAC AGC GAT				1441
Asn Phe Pro Ile Asn Ala His Ala Leu Lys Glu Leu Leu Asn Ser Asp	465	470	475	
TTA ATG CAA TTC ATT TTT GAA TCG CTT TTT AAA ACG CAT AAA ATC TTA				1489
Leu Met Gln Phe Ile Phe Glu Ser Leu Phe Lys Thr His Lys Ile Leu	480	485	490	
AGA AAA GAT TTG GAA TGT TTG CCC CTA TTT GTG CAA TTT ATT AAC GAT				1537
Arg Lys Asp Leu Glu Cys Leu Pro Leu Phe Val Gln Phe Ile Asn Asp	495	500	505	
AAT TTT GAT GAA AAA TTT TAT TTA AAA AAT TTA GGG ATA GAA AAA AAA				1585
Asn Phe Asp Glu Lys Phe Tyr Leu Lys Asn Leu Gly Ile Glu Lys Lys	510	515	520	
GAC CCT AAA CAT TTC ACC ATC AGG AAA AAT CAT GCA TGT TGC TTG TCT				1633
Asp Pro Lys His Phe Thr Ile Arg Lys Asn His Ala Cys Cys Leu Ser	525	530	535	540
TTT GGC TTT AGG GGA TAATCTCATC ACGCTTAGCC TTTTAAAAGA AATCGCTTTC A				1689
Phe Gly Phe Arg Gly	545			
AACAGCAA				1697

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

Met	Pro	Ser	Asn	Ala	Leu	Leu	Ile	Glu	Glu	Ile	Thr	His	Leu	Ile	Asn
1				5				10					15		
Val	Ser	His	Ser	Ser	Val	His	Asn	Trp	Ile	Lys	Thr	Asn	Leu	Leu	Glu
			20					25					30		
Lys	Leu	Glu	Ile	Asp	His	Lys	Ile	Tyr	Val	Lys	Thr	Ser	Ser	Phe	Leu
		35					40					45			
Asp	Phe	Cys	Arg	Asn	His	Leu	Gly	Lys	Asn	Lys	Leu	Asn	Lys	Tyr	Ala
	50				55					60					
Asn	Lys	Ser	Leu	Lys	Gly	Val	His	Asn	His	Gln	Glu	Leu	Ile	Leu	Lys
65				70						75				80	
Tyr	Leu	Glu	Ile	Leu	Glu	Asn	Ser	Ser	Asp	Leu	Glu	Lys	Leu	Gly	Ser
			85					90					95		
Tyr	Tyr	Glu	Glu	Glu	Leu	Ser	Asn	Ala	Thr	Arg	Asn	Leu	Glu	Gly	Ile
		100					105					110			
Tyr	Tyr	Thr	Pro	Asn	Arg	Ile	Val	Glu	Gln	Leu	Phe	Thr	Leu	Pro	Lys
	115				120							125			
Asp	Phe	Asp	Val	Ser	Gln	Ala	Ile	Phe	Cys	Asp	Pro	Ala	Val	Gly	Ser
	130					135					140				

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 46...1842
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

TATTGTGTTA TACTTCTAAT TTCAATTTTG CTTGTTAGGA CATTT ATG AAA AAT ATT	57
Met Lys Asn Ile	
1	
AGA AAT ATC GCT GTA ATC GCG CAT GTT GAT CAT GGG AAA ACC ACT CTA	105
Arg Asn Ile Ala Val Ile Ala His Val Asp His Gly Lys Thr Thr Leu	
5 10 15 20	
GTA GAT GGC TTA CTT TCT CAA TCT GGC ACA TTT AGT GAG AGG GAA AAA	153
Val Asp Gly Leu Leu Ser Gln Ser Gly Thr Phe Ser Glu Arg Glu Lys	
25 30 35	
GTG GAT GAA AGG GTG ATG GAT AGC AAT GAT TTG GAA AGA GAA AGA GGG	201
Val Asp Glu Arg Val Met Asp Ser Asn Asp Leu Glu Arg Glu Arg Gly	
40 45 50	
ATT ACT ATC CTG TCT AAA AAC ACC GCT ATT TAT TAC AAA GAC ACT AAA	249
Ile Thr Ile Leu Ser Lys Asn Thr Ala Ile Tyr Tyr Lys Asp Thr Lys	
55 60 65	
ATC AAT ATC ATT GAC ACT CCC GGG CAT GCT GAT TTT GGG GGC GAA GTG	297
Ile Asn Ile Ile Asp Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val	
70 75 80	
GAG CGC GTT TTA AAA ATG GTG GAT GGG GTG TTG CTT TTA GTG GAC GCT	345
Glu Arg Val Leu Lys Met Val Asp Gly Val Leu Leu Leu Val Asp Ala	
85 90 95 100	
CAA GAA GGG GTC ATG CCT CAA ACT AAA TTC GTG GTT AAA AAG GCT TTG	393
Gln Glu Gly Val Met Pro Gln Thr Lys Phe Val Val Lys Lys Ala Leu	
105 110 115	
AGT TTT GGG ATT TGC CCT ATT GTG GTG GTG AAT AAA ATT GAT AAG CCT	441
Ser Phe Gly Ile Cys Pro Ile Val Val Val Asn Lys Ile Asp Lys Pro	
120 125 130	
GCC GCT GAA CCG GAC AGA GTG GTG GAT GAA GTT TTT GAC TTG TTC GTA	489
Ala Ala Glu Pro Asp Arg Val Val Asp Glu Val Phe Asp Leu Phe Val	
135 140 145	
GCC ATG GGG GCT AGC GAT AAG CAA TTG GAT TTC CCT GTG GTG TAT GCC	537
Ala Met Gly Ala Ser Asp Lys Gln Leu Asp Phe Pro Val Val Tyr Ala	
150 155 160	
GCC GCA CGA GAT GGC TAT GCG ATG AAA AGT TTA GAC GAT GAA AAG AAA	585

Ala	Ala	Arg	Asp	Gly	Tyr	Ala	Met	Lys	Ser	Leu	Asp	Asp	Glu	Lys	Lys	
165					170					175					180	
AAT	TTA	GAG	CCT	TTG	TTT	GAA	ACG	ATT	TTA	GAG	CAT	GTG	CCA	AGC	CCT	633
Asn	Leu	Glu	Pro	Leu	Phe	Glu	Thr	Ile	Leu	Glu	His	Val	Pro	Ser	Pro	
				185					190					195		
AGC	GGG	AGC	GTT	GAT	GAG	CCT	TTG	CAA	ATG	CAA	ATT	TTC	ACG	CTT	GAT	681
Ser	Gly	Ser	Val	Asp	Glu	Pro	Leu	Gln	Met	Gln	Ile	Phe	Thr	Leu	Asp	
			200					205					210			
TAT	GAC	AAT	TAT	GTG	GGC	AAA	ATC	GGT	ATC	GCT	AGG	GTG	TTT	AAT	GGC	729
Tyr	Asp	Asn	Tyr	Val	Gly	Lys	Ile	Gly	Ile	Ala	Arg	Val	Phe	Asn	Gly	
		215					220					225				
TCG	GTT	AAA	AAG	AAT	GAA	AGC	GTG	CTG	TTG	ATG	AAA	AGC	GAT	GGG	AGT	777
Ser	Val	Lys	Lys	Asn	Glu	Ser	Val	Leu	Leu	Met	Lys	Ser	Asp	Gly	Ser	
	230					235					240					
AAA	GAA	AAT	GGC	CGT	ATC	ACT	AAG	CTT	ATA	GGT	TTT	TTA	GGG	CTG	GCT	825
Lys	Glu	Asn	Gly	Arg	Ile	Thr	Lys	Leu	Ile	Gly	Phe	Leu	Gly	Leu	Ala	
245					250					255					260	
AGG	ACT	GAG	ATT	GAA	AAC	GCT	TAT	GCG	GGC	GAT	ATT	GTA	GCG	ATT	GCC	873
Arg	Thr	Glu	Ile	Glu	Asn	Ala	Tyr	Ala	Gly	Asp	Ile	Val	Ala	Ile	Ala	
				265					270					275		
GGG	TTT	AAT	GCA	ATG	GAT	GTG	GGC	GAT	AGC	GTC	GTT	GAT	CCT	GCT	AAC	921
Gly	Phe	Asn	Ala	Met	Asp	Val	Gly	Asp	Ser	Val	Val	Asp	Pro	Ala	Asn	
			280					285					290			
CCC	ATG	CCT	TTA	GAT	CCC	ATG	CAT	TTA	GAA	GAG	CCT	ACG	ATG	AGC	GTG	969
Pro	Met	Pro	Leu	Asp	Pro	Met	His	Leu	Glu	Glu	Pro	Thr	Met	Ser	Val	
		295					300					305				
TAT	TTT	GCT	GTC	AAT	GAT	TCA	CCC	TTA	GCC	GGG	TTA	GAA	GGA	AAG	CAT	1017
Tyr	Phe	Ala	Val	Asn	Asp	Ser	Pro	Leu	Ala	Gly	Leu	Glu	Gly	Lys	His	
	310					315					320					
GTT	ACT	GCT	AAT	AAA	TTG	AAA	GAC	AGG	CTC	TTA	AAA	GAA	ATG	CAA	ACC	1065
Val	Thr	Ala	Asn	Lys	Leu	Lys	Asp	Arg	Leu	Leu	Lys	Glu	Met	Gln	Thr	
325					330					335					340	
AAT	ATC	GCT	ATG	AAA	TGC	GAA	GAA	ATG	GGC	GAG	GGC	AAG	TTT	AAA	GTG	1113
Asn	Ile	Ala	Met	Lys	Cys	Glu	Glu	Met	Gly	Glu	Gly	Lys	Phe	Lys	Val	
				345					350					355		
AGT	GGG	CGT	GGG	GAA	TTG	CAA	ATC	ACT	ATT	TTA	GCT	GAA	AAC	TTG	CGC	1161
Ser	Gly	Arg	Gly	Glu	Leu	Gln	Ile	Thr	Ile	Leu	Ala	Glu	Asn	Leu	Arg	
			360					365					370			
CGT	GAA	GGG	TTT	GAA	TTT	AGC	ATT	TCA	CGC	CCT	GAA	GTC	ATC	ATT	AAA	1209
Arg	Glu	Gly	Phe	Glu	Phe	Ser	Ile	Ser	Arg	Pro	Glu	Val	Ile	Ile	Lys	
		375					380					385				
GAA	GAA	AAT	GGC	GTT	AAA	TGC	GAG	CCT	TTT	GAG	CAT	TTA	GTG	ATT	GAC	1257
Glu	Glu	Asn	Gly	Val	Lys	Cys	Glu	Pro	Phe	Glu	His	Leu	Val	Ile	Asp	
	390					395					400					

ACG Thr 405	CCC Pro	CAA Gln	GAT Asp	TTT Phe 410	AGT Ser 410	GGG Gly	GCT Ala	ATC Ile	ATT Ile	GAG Glu 415	AGA Arg	TTG Leu	GGC Gly	AAA Lys	AGA Arg 420	1305
AAA Lys	GCT Ala	GAG Glu	ATG Met	AAA Lys 425	GCG Ala	ATG Met	AAT Asn	CCC Pro	ATG Met	AGT Ser	GAT Asp	GGC Gly	TAT Tyr	ACA Thr	AGA Arg 435	1353
TTA Leu	GAA Glu	TTT Phe	GAA Glu 440	ATT Ile	CCT Pro	GCA Ala	AGA Arg	GGG Gly 445	CTT Leu	ATC Ile	GGT Gly	TAT Tyr	AGG Arg 450	AGC Ser	GAG Glu	1401
TTT Phe	TTA Leu	ACC Thr 455	GAC Asp	ACC Thr	AAG Lys	GGC Gly	GAA Glu 460	GGC Gly	GTG Val	ATG Met	AAT Asn	CAT His	AGC Ser	TTT Phe	TTA Leu	1449
GAA Glu 470	TTC Phe	CGC Arg	CCT Pro	TTC Phe	AGC Ser	GGG Gly 475	AGC Ser	GTG Val	GAA Glu	TCG Ser	CGC Arg	AAA Lys	AAT Asn	GGG Gly	GCG Ala	1497
CTA Leu 485	ATC Ile	AGC Ser	ATG Met	GAA Glu	AAT Asn 490	GGC Gly	GAA Glu	GCG Ala	ACC Thr	GCT Ala	TTT Phe	TCC Ser	CTT Leu	TTC Phe	AAT Asn 500	1545
ATC Ile	CAA Gln	GAA Glu	AGA Arg	GGC Gly 505	ACG Thr	CTT Leu	TTT Phe	ATC Ile	AAC Asn	CCC Pro	CAA Gln	ACG Thr	AAG Lys	GTT Val	TAT Tyr 515	1593
GTG Val	GGC Gly	ATG Met	GTC Val 520	ATT Ile	GGC Gly	GAG Glu	CAC His	AGC Ser	CGG Arg	GAT Asp	AAT Asn	GAT Asp	TTA Leu	GAT Asp	GTC Val 530	1641
AAT Asn	CCT Pro	ATT Ile	AAA Lys	TCC Ser	AAG Lys	CAT His	TTA Leu	ACC Thr	AAC Asn	ATG Met	AGA Arg	GCG Ala	AGC Ser	GGG Gly	AGC Ser 545	1689
GAT Asp 550	GAT Asp	GCG Ala	ATC Ile	AAA Lys	CTC Leu	ACC Thr 555	CCG Pro	CCT Pro	AGG Arg	ACT Thr	ATG Met	GTG Val	TTA Leu	GAA Glu	AGA Arg 560	1737
GCG Ala 565	TTA Leu	GAA Glu	TGG Trp	ATT Ile	GAA Glu	GAA Glu 570	GAT Asp	GAG Glu	ATT Ile	TTG Leu	GAA Glu	GTT Val	ACC Thr	CCC Pro	TTG Leu 580	1785
AAT Asn	TTA Leu	AGG Arg	ATC Ile	AGG Arg 585	AAA Lys	AAG Lys	ATT Ile	TTA Leu	GAC Asp	CCT Pro	AAC Asn	ATG Met	AGG Arg	AAA Lys	AGG Arg 595	1833
GCG Ala	AAA Lys	AAA Lys	TAAATAGAAT	TTTTTGAAT	GCATGCCAAT	TTATTCAACC	AA									1884

(2) INFORMATION FOR SEQ ID NO:602:

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

Met	Lys	Asn	Ile	Arg	Asn	Ile	Ala	Val	Ile	Ala	His	Val	Asp	His	Gly
1				5					10					15	
Lys	Thr	Thr	Leu	Val	Asp	Gly	Leu	Leu	Ser	Gln	Ser	Gly	Thr	Phe	Ser
			20					25					30		
Glu	Arg	Glu	Lys	Val	Asp	Glu	Arg	Val	Met	Asp	Ser	Asn	Asp	Leu	Glu
		35					40					45			
Arg	Glu	Arg	Gly	Ile	Thr	Ile	Leu	Ser	Lys	Asn	Thr	Ala	Ile	Tyr	Tyr
	50					55					60				
Lys	Asp	Thr	Lys	Ile	Asn	Ile	Ile	Asp	Thr	Pro	Gly	His	Ala	Asp	Phe
65					70					75					80
Gly	Gly	Glu	Val	Glu	Arg	Val	Leu	Lys	Met	Val	Asp	Gly	Val	Leu	Leu
			85						90					95	
Leu	Val	Asp	Ala	Gln	Glu	Gly	Val	Met	Pro	Gln	Thr	Lys	Phe	Val	Val
			100					105					110		
Lys	Lys	Ala	Leu	Ser	Phe	Gly	Ile	Cys	Pro	Ile	Val	Val	Val	Asn	Lys
		115					120					125			
Ile	Asp	Lys	Pro	Ala	Ala	Glu	Pro	Asp	Arg	Val	Val	Asp	Glu	Val	Phe
	130					135					140				
Asp	Leu	Phe	Val	Ala	Met	Gly	Ala	Ser	Asp	Lys	Gln	Leu	Asp	Phe	Pro
145					150					155					160
Val	Val	Tyr	Ala	Ala	Ala	Arg	Asp	Gly	Tyr	Ala	Met	Lys	Ser	Leu	Asp
				165					170					175	
Asp	Glu	Lys	Lys	Asn	Leu	Glu	Pro	Leu	Phe	Glu	Thr	Ile	Leu	Glu	His
			180					185					190		
Val	Pro	Ser	Pro	Ser	Gly	Ser	Val	Asp	Glu	Pro	Leu	Gln	Met	Gln	Ile
		195					200					205			
Phe	Thr	Leu	Asp	Tyr	Asp	Asn	Tyr	Val	Gly	Lys	Ile	Gly	Ile	Ala	Arg
	210					215					220				
Val	Phe	Asn	Gly	Ser	Val	Lys	Lys	Asn	Glu	Ser	Val	Leu	Leu	Met	Lys
225					230					235					240
Ser	Asp	Gly	Ser	Lys	Glu	Asn	Gly	Arg	Ile	Thr	Lys	Leu	Ile	Gly	Phe
				245					250					255	
Leu	Gly	Leu	Ala	Arg	Thr	Glu	Ile	Glu	Asn	Ala	Tyr	Ala	Gly	Asp	Ile
			260					265					270		
Val	Ala	Ile	Ala	Gly	Phe	Asn	Ala	Met	Asp	Val	Gly	Asp	Ser	Val	Val
		275					280					285			
Asp	Pro	Ala	Asn	Pro	Met	Pro	Leu	Asp	Pro	Met	His	Leu	Glu	Glu	Pro
	290					295					300				
Thr	Met	Ser	Val	Tyr	Phe	Ala	Val	Asn	Asp	Ser	Pro	Leu	Ala	Gly	Leu
305					310					315					320
Glu	Gly	Lys	His	Val	Thr	Ala	Asn	Lys	Leu	Lys	Asp	Arg	Leu	Leu	Lys
				325					330					335	
Glu	Met	Gln	Thr	Asn	Ile	Ala	Met	Lys	Cys	Glu	Glu	Met	Gly	Glu	Gly
			340					345					350		
Lys	Phe	Lys	Val	Ser	Gly	Arg	Gly	Glu	Leu	Gln	Ile	Thr	Ile	Leu	Ala
		355					360					365			
Glu	Asn	Leu	Arg	Arg	Glu	Gly	Phe	Glu	Phe	Ser	Ile	Ser	Arg	Pro	Glu
	370					375					380				
Val	Ile	Ile	Lys	Glu	Glu	Asn	Gly	Val	Lys	Cys	Glu	Pro	Phe	Glu	His
385					390					395					400
Leu	Val	Ile	Asp	Thr	Pro	Gln	Asp	Phe	Ser	Gly	Ala	Ile	Ile	Glu	Arg

35				40				45								
AGA Arg 50	GAT Asp	TAT Tyr	ATT Ile	TTA Leu	GAG Glu 55	CAT His	GCC Ala	ATT Ile	TTG Leu	AAC Asn 60	GCC Ala	CTA Leu	GAT Asp	TAT Tyr	GGT Gly 65	248
GTG Val	CCT Pro	CAA Gln	ATG Met	AGA Arg 70	GAA Glu	CGA Arg	GTG Val	ATT Ile	TTA Leu 75	GTG Val	GGC Gly	GTG Val	CTT Leu	AAA Lys 80	AGC Ser	296
TTT Phe	AAA Lys	CAA Gln	AAA Lys 85	TTT Phe	TAC Tyr	TTC Phe	CCT Pro	AAA Lys 90	CCC Pro	ATA Ile	AAA Lys	ACG Thr	CAT His 95	TTT Phe	TCT Ser	344
CTG Leu	AAA Lys	GAC Asp 100	GCT Ala	TTA Leu	GGG Gly	GAT Asp	TTA Leu 105	CCA Pro	CCC Pro	ATT Ile	CAA Gln	AGC Ser 110	GGT Gly	GAA Glu	AAT Asn	392
GGT Gly 115	GAT Asp	GCT Ala	TTA Leu	GGT Gly	TAT Tyr	CTT Leu 120	AAA Lys	AAT Asn	GCG Ala	GAT Asp	AAT Asn	GTT Val	TTT Phe	TTG Leu	GAA Glu	440
TTT Phe 130	GTG Val	CGA Arg	AAT Asn	TCT Ser	AAA Lys 135	GAA Glu	TTA Leu	AGC Ser	GAA Glu	CAT His 140	AGC Ser	AGT Ser	CCT Pro	AAA Lys	AAC Asn 145	488
AAT Asn	GAA Glu	AAA Lys	CTG Leu	ATA Ile 150	AAA Lys	ATC Ile	ATG Met	CAA Gln	ACG Thr 155	CTA Leu	AAA Lys	GAC Asp	GGA Gly	CAG Gln 160	AGT Ser	536
AAA Lys	GAT Asp	GAT Asp	TTG Leu 165	CCA Pro	GAA Glu	AGT Ser	CTG Leu	CGT Arg 170	CCC Pro	AAA Lys	AGT Ser	GGT Gly	TAT Tyr 175	ATT Ile	AAT Asn	584
ACC Thr	TAT Tyr	GCC Ala 180	AAA Lys	ATG Met	TGG Trp	TGG Trp	GAA Glu 185	AAA Lys	CCA Pro	GCC Ala	CCC Pro	ACC Thr 190	ATT Ile	ACA Thr	AGA Arg	632
AAT Asn 195	TTT Phe	TCT Ser	ACC Thr	CCA Pro	AGC Ser	AGT Ser 200	TCT Ser	AGG Arg	TGT Cys	ATC Ile	CAT His 205	CCA Pro	AGA Arg	GAC Asp	TCT Ser	680
AGA Arg 210	GCG Ala	TTA Leu	AGC Ser	ATT Ile	AGA Arg 215	GAG Glu	GGG Gly	GCA Ala	AGA Arg	TTG Leu 220	CAA Gln	AGC Ser	TTT Phe	CCT Pro	GAT Asp 225	728
AAT Asn	TAT Tyr	AAA Lys	TTC Phe	TGT Cys 230	GGG Gly	AGT Ser	GGT Gly	AGC Ser	GCT Ala 235	AAA Lys	AGA Arg	TTG Leu	CAA Gln	ATT Ile 240	GGC Gly	776
AAT Asn	GCC Ala	GTG Val	CCG Pro 245	CCT Pro	TTA Leu	TTG Leu	AGT Ser	GTA Val 250	GCG Ala	CTC Leu	GCG Ala	CAG Gln	GCG Ala 255	GTC Val	TTT Phe	824
GAC Asp	TTT Phe	TTA Leu 260	AAG Lys	GGG Gly	TAAGATGTTTT AACAAATAATG ACTTTAAGGA TTACAGAAAA T											880

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...1338
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

TGGTAGTTAA	GA	ATG	GGT	AAT	CAT	TTT	TCT	AAA	TTA	GGA	TTT	GTT	TTA	GCC	51	
	Met	Gly	Asn	His	Phe	Ser	Lys	Leu	Gly	Phe	Val	Leu	Ala			
	1				5					10						
GCA	TTA	GGA	AGC	GCG	ATA	GGT	TTA	GGG	CAT	ATC	TGG	CGT	TTC	CCC	TAC	99
Ala	Leu	Gly	Ser	Ala	Ile	Gly	Leu	Gly	His	Ile	Trp	Arg	Phe	Pro	Tyr	
	15					20				25						
ATG	ACT	GGG	GTG	AGT	GGT	GGG	GCT	TTT	GTT	TTA	TTG	TTT	TTA	TTT		147
Met	Thr	Gly	Val	Ser	Gly	Gly	Gly	Ala	Phe	Val	Leu	Leu	Phe	Leu	Phe	
	30				35				40					45		
TTA	TCT	TTA	AGC	GTT	GGC	GCG	GCG	ATG	TTT	ATC	GCT	GAA	ATG	CTA	TTA	195
Leu	Ser	Leu	Ser	Val	Gly	Ala	Ala	Met	Phe	Ile	Ala	Glu	Met	Leu	Leu	
				50					55					60		
GGA	CAA	AGC	ACT	CAA	AAA	AAT	GTA	ACA	GAA	GCT	TTT	AAA	GAG	CTT	GAC	243
Gly	Gln	Ser	Thr	Gln	Lys	Asn	Val	Thr	Glu	Ala	Phe	Lys	Glu	Leu	Asp	
			65				70					75				
ATT	AAC	CCC	AAA	AAA	CGC	TGG	AAA	TAC	GCA	GGG	CTT	TTG	CTT	GTT	TCT	291
Ile	Asn	Pro	Lys	Lys	Arg	Trp	Lys	Tyr	Ala	Gly	Leu	Leu	Leu	Val	Ser	
		80					85					90				
GGG	CCA	TTA	ATA	CTG	ACT	TTT	TAC	GGC	ACG	ATT	TTA	GGT	TGG	GTG	CTT	339
Gly	Pro	Leu	Ile	Leu	Thr	Phe	Tyr	Gly	Thr	Ile	Leu	Gly	Trp	Val	Leu	
	95					100					105					
TAT	TAT	TTG	GTG	AGT	GTT	AGT	TTT	AAT	TTG	CCT	AAC	AAT	ATC	CAA	GAA	387
Tyr	Tyr	Leu	Val	Ser	Val	Ser	Phe	Asn	Leu	Pro	Asn	Asn	Ile	Gln	Glu	
	110				115					120				125		
TCT	GAA	CAA	ATT	TTT	ACT	CAA	ACT	TTG	CAG	TCT	ATA	GGG	CTA	CAA	TCC	435
Ser	Glu	Gln	Ile	Phe	Thr	Gln	Thr	Leu	Gln	Ser	Ile	Gly	Leu	Gln	Ser	
				130					135					140		
ATA	GGG	CTT	TTT	AGC	GTT	TTA	TTG	ATA	ACC	GGA	TGG	ATT	GTT	TCT	AGG	483
Ile	Gly	Leu	Phe	Ser	Val	Leu	Leu	Ile	Thr	Gly	Trp	Ile	Val	Ser	Arg	
			145					150					155			
GGG	ATT	AAA	GAA	GGC	ATT	GAA	AAG	CTC	AAT	TTG	GTT	TTA	ATG	CCC	TTA	531
Gly	Ile	Lys	Glu	Gly	Ile	Glu	Lys	Leu	Asn	Leu	Val	Leu	Met	Pro	Leu	
		160					165					170				
CTC	TTT	GCT	ACT	TTT	TTT	GGT	TTG	CTT	TTC	TAT	GCG	ATG	AGC	ATG	GAT	579
Leu	Phe	Ala	Thr	Phe	Phe	Gly	Leu	Leu	Phe	Tyr	Ala	Met	Ser	Met	Asp	
	175					180					185					
TCT	TTT	TCT	AAA	GCT	TTT	CAT	TTC	ATG	TTT	GAT	TTC	AAA	CCA	AAA	GAT	627

Ser Phe Ser Lys Ala Phe His Phe Met Phe Asp Phe Lys Pro Lys Asp
190 195 200 205

TTG	ACC	TCT	CAA	GTG	TTC	ACT	TAT	TCC	TTG	GGG	CAG	GTT	TTC	TTT	TCC	675
Leu	Thr	Ser	Gln	Val	Phe	Thr	Tyr	Ser	Leu	Gly	Gln	Val	Phe	Phe	Ser	
				210					215					220		

TTA	AGC	ATC	GGT	TTA	GGG	ATC	AAT	ATC	ACT	TAC	GCT	GCG	GTT	ACG	GAT	723
Leu	Ser	Ile	Gly	Leu	Gly	Ile	Asn	Ile	Thr	Tyr	Ala	Ala	Val	Thr	Asp	
			225					230					235			

AAA ACG CAG AAT TTG CTT AAA AGC ACT ATT TGG GTG GTT TTA TCA GGA 771
Lys Thr Gln Asn Leu Leu Lys Ser Thr Ile Trp Val Val Leu Ser Gly
240 245 250

ATT CTA ATT TCT CTT GTG GCA GGA CTT ATG ATT TTC ACT TTT GTG TTT 819
Ile Leu Ile Ser Leu Val Ala Gly Leu Met Ile Phe Thr Phe Val Phe
255 260 265

GAA TAT GGG GCG AAT GTC TCA CAA GGC ACA GGG TTA ATC TTC ACT TCT 867
Glu Tyr Gly Ala Asn Val Ser Gln Gly Thr Gly Leu Ile Phe Thr Ser
270 275 280 285

TTA	CCG	GTG	GTT	TTT	GGC	CAA	ATG	GGA	GCG	ATA	GGC	ATT	CTT	GTT	TCG	915
Leu	Pro	Val	Val	Phe	Gly	Gln	Met	Gly	Ala	Ile	Gly	Ile	Leu	Val	Ser	
				290					295					300		

ATT CTT TTC TTG CTC GCG CTC GCT TTT GCT GGC ATC ACT TCT ACG GTG 963
Ile Leu Phe Leu Ala Leu Ala Phe Ala Gly Ile Thr Ser Thr Val
305 310 315

GCT TTA TTG GAG CCA AGC GTG ATG TAT CTT ACC GAA AGG TAT CAA TAC 1011
Ala Leu Leu Glu Pro Ser Val Met Tyr Leu Thr Glu Arg Tyr Gln Tyr
320 325 330

TCT CGT TTT AAG GTT ACT TGG GGT CTT GTA GCA CTA ATT TTT GTG GTA 1059
Ser Arg Phe Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val Val
335 340 345

GGC GTG GTG TTG ATT TTC TCG CTC CAT AAG GAT TAT AAA GAT TAT CTC 1107
Gly Val Val Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr Leu
350 355 360 365

ACT TTC TTT GAA AAA AGT CTT TTT GAT TGG TTG GAT TTT GCA TCA AGC 1155
Thr Phe Phe Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser Ser
370 380

ACC ATT ATC ATG CCT TTA GGC GGG ATG GCA ACC TTT ATT TTT ATG GGT 1203
Thr Ile Ile Met Pro Leu Gly Gly Met Ala Thr Phe Ile Phe Met Gly
385 390 395

TGG GTT TTG AAA AAA GAA AAA TTG CGT CTT TTG AGC GTG CAC TTT TTA 1251
Trp Val Leu Lys Lys Glu Lys Leu Arg Leu Leu Ser Val His Phe Leu
400 405 410

GGC CCT AAA TTG TTT GCA ACT TGG TAT TTC TTG CTT AAA TAT ATC ACC 1299
Gly Pro Lys Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile Thr
415 420 425

CCT TTA ATT GTG TTT TCC ATT TGG TTG AGC AAG ATT TAT TAAAATATTT GG 1350
 Pro Leu Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr
 430 435 440

CATGGGAAAA TTTTCTAAAT TAGGCT

1376

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

Met	Gly	Asn	His	Phe	Ser	Lys	Leu	Gly	Phe	Val	Leu	Ala	Ala	Leu	Gly
1				5					10					15	
Ser	Ala	Ile	Gly	Leu	Gly	His	Ile	Trp	Arg	Phe	Pro	Tyr	Met	Thr	Gly
			20					25					30		
Val	Ser	Gly	Gly	Ala	Phe	Val	Leu	Leu	Phe	Leu	Phe	Leu	Ser	Leu	
		35				40					45				
Ser	Val	Gly	Ala	Ala	Met	Phe	Ile	Ala	Glu	Met	Leu	Leu	Gly	Gln	Ser
	50					55					60				
Thr	Gln	Lys	Asn	Val	Thr	Glu	Ala	Phe	Lys	Glu	Leu	Asp	Ile	Asn	Pro
65					70					75				80	
Lys	Lys	Arg	Trp	Lys	Tyr	Ala	Gly	Leu	Leu	Val	Ser	Gly	Pro	Leu	
				85				90					95		
Ile	Leu	Thr	Phe	Tyr	Gly	Thr	Ile	Leu	Gly	Trp	Val	Leu	Tyr	Tyr	Leu
			100					105					110		
Val	Ser	Val	Ser	Phe	Asn	Leu	Pro	Asn	Asn	Ile	Gln	Glu	Ser	Glu	Gln
		115					120					125			
Ile	Phe	Thr	Gln	Thr	Leu	Gln	Ser	Ile	Gly	Leu	Gln	Ser	Ile	Gly	Leu
	130					135					140				
Phe	Ser	Val	Leu	Leu	Ile	Thr	Gly	Trp	Ile	Val	Ser	Arg	Gly	Ile	Lys
145					150					155				160	
Glu	Gly	Ile	Glu	Lys	Leu	Asn	Leu	Val	Leu	Met	Pro	Leu	Leu	Phe	Ala
				165					170					175	
Thr	Phe	Phe	Gly	Leu	Leu	Phe	Tyr	Ala	Met	Ser	Met	Asp	Ser	Phe	Ser
			180					185					190		
Lys	Ala	Phe	His	Phe	Met	Phe	Asp	Phe	Lys	Pro	Lys	Asp	Leu	Thr	Ser
		195					200					205			
Gln	Val	Phe	Thr	Tyr	Ser	Leu	Gly	Gln	Val	Phe	Phe	Ser	Leu	Ser	Ile
	210					215					220				
Gly	Leu	Gly	Ile	Asn	Ile	Thr	Tyr	Ala	Ala	Val	Thr	Asp	Lys	Thr	Gln
225					230					235				240	
Asn	Leu	Leu	Lys	Ser	Thr	Ile	Trp	Val	Val	Leu	Ser	Gly	Ile	Leu	Ile
				245					250					255	
Ser	Leu	Val	Ala	Gly	Leu	Met	Ile	Phe	Thr	Phe	Val	Phe	Glu	Tyr	Gly
			260					265					270		
Ala	Asn	Val	Ser	Gln	Gly	Thr	Gly	Leu	Ile	Phe	Thr	Ser	Leu	Pro	Val
		275					280					285			
Val	Phe	Gly	Gln	Met	Gly	Ala	Ile	Gly	Ile	Leu	Val	Ser	Ile	Leu	Phe
	290					295					300				
Leu	Leu	Ala	Leu	Ala	Phe	Ala	Gly	Ile	Thr	Ser	Thr	Val	Ala	Leu	Leu
305					310					315					320

Glu	Pro	Ser	Val	Met	Tyr	Leu	Thr	Glu	Arg	Tyr	Gln	Tyr	Ser	Arg	Phe	
				325					330					335		
Lys	Val	Thr	Trp	Gly	Leu	Val	Ala	Leu	Ile	Phe	Val	Val	Gly	Val	Val	
			340					345					350			
Leu	Ile	Phe	Ser	Leu	His	Lys	Asp	Tyr	Lys	Asp	Tyr	Leu	Thr	Phe	Phe	
		355					360					365				
Glu	Lys	Ser	Leu	Phe	Asp	Trp	Leu	Asp	Phe	Ala	Ser	Ser	Thr	Ile	Ile	
	370					375					380					
Met	Pro	Leu	Gly	Gly	Met	Ala	Thr	Phe	Ile	Phe	Met	Gly	Trp	Val	Leu	
385					390					395					400	
Lys	Lys	Glu	Lys	Leu	Arg	Leu	Leu	Ser	Val	His	Phe	Leu	Gly	Pro	Lys	
			405					410						415		
Leu	Phe	Ala	Thr	Trp	Tyr	Phe	Leu	Leu	Lys	Tyr	Ile	Thr	Pro	Leu	Ile	
			420					425					430			
Val	Phe	Ser	Ile	Trp	Leu	Ser	Lys	Ile	Tyr							
		435					440									

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 17...1081
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GAAATAAGGA	TGCTTG	ATG	AAA	AGC	ATT	TTG	CTC	TTT	ATG	ATT	TTT	GTA	GTT		52	
		Met	Lys	Ser	Ile	Leu	Leu	Phe	Met	Ile	Phe	Val	Val			
		1				5					10					
TGT	CAG	TTA	GAA	GGC	AAA	AAA	TTT	TCA	CAA	GAT	AAT	TTT	AAG	GTG	GAT	100
Cys	Gln	Leu	Glu	Gly	Lys	Lys	Phe	Ser	Gln	Asp	Asn	Phe	Lys	Val	Asp	
		15				20					25					
TAT	AAC	TAC	TAT	TTG	CGC	AAA	CAG	GAT	TTG	CAC	ATC	ATT	AAA	ACG	CAA	148
Tyr	Asn	Tyr	Tyr	Leu	Arg	Lys	Gln	Asp	Leu	His	Ile	Ile	Lys	Thr	Gln	
		30				35				40						
AAC	GAT	TTG	TCC	AAT	TCT	TGG	TAT	CTC	CCT	CCA	CAA	AAA	GCC	CCC	AAA	196
Asn	Asp	Leu	Ser	Asn	Ser	Trp	Tyr	Leu	Pro	Pro	Gln	Lys	Ala	Pro	Lys	
45					50					55				60		
GAA	CAT	TCT	TGG	GTG	GAT	TTT	GCT	AAA	AAA	TAT	TTA	AAC	ATG	ATG	GAT	244
Glu	His	Ser	Trp	Val	Asp	Phe	Ala	Lys	Lys	Tyr	Leu	Asn	Met	Met	Asp	
			65					70					75			
TAT	CTA	GGC	ACT	TAT	TTT	CTG	CCT	TTT	TAT	CAT	AGT	TTC	ACC	CCC	ATT	292
Tyr	Leu	Gly	Thr	Tyr	Phe	Leu	Pro	Phe	Tyr	His	Ser	Phe	Thr	Pro	Ile	
			80					85					90			

TTT	CAA	TGG	TAC	CAC	CCC	AAT	ATC	AAC	CCG	TAT	CAA	CGC	AAT	GAG	TTT	340
Phe	Gln	Trp	Tyr	His	Pro	Asn	Ile	Asn	Pro	Tyr	Gln	Arg	Asn	Glu	Phe	
		95														
AAG	TTC	CAA	ATT	AGT	TTT	AGA	GTG	CCT	GTA	TTT	AGG	CAT	ATT	CTT	TGG	388
Lys	Phe	Gln	Ile	Ser	Phe	Arg	Val	Pro	Val	Phe	Arg	His	Ile	Leu	Trp	
		110														
ACT	AAA	GGC	ACG	CTG	TAT	TTA	GCT	TAT	ACC	CAA	ACT	GAC	TGG	TTT	CAA	436
Thr	Lys	Gly	Thr	Leu	Tyr	Leu	Ala	Tyr	Thr	Gln	Thr	Asp	Trp	Phe	Gln	
		125														
ATT	TAC	AAT	GAC	CCC	CAA	TCC	GCT	CCC	ATG	CGA	ATG	ATG	AAT	TTC	ATG	484
Ile	Tyr	Asn	Asp	Pro	Gln	Ser	Ala	Pro	Met	Arg	Met	Met	Asn	Phe	Met	
CCT	GAA	CTC	ATT	TAT	GTT	TAT	CCT	ATC	AAT	TTT	AAA	CCT	TTT	GGG	GGT	532
Pro	Glu	Leu	Ile	Tyr	Val	Tyr	Pro	Ile	Asn	Phe	Lys	Pro	Phe	Gly	Gly	
AAA	ATA	GGG	AAT	TTT	TCT	GAA	ATT	TGG	ATA	GGT	TGG	CAG	CAC	ATT	TCT	580
Lys	Ile	Gly	Asn	Phe	Ser	Glu	Ile	Trp	Ile	Gly	Trp	Gln	His	Ile	Ser	
		175														
AAT	GGC	GTG	GGG	GGC	GCG	CAA	TGT	TAC	CAA	CCT	TTT	AAT	AAA	GAA	GGC	628
Asn	Gly	Val	Gly	Gly	Ala	Gln	Cys	Tyr	Gln	Pro	Phe	Asn	Lys	Glu	Gly	
		190														
AAT	CCT	GAA	AAC	CAG	TTT	CCA	GGA	CAA	CCT	GTA	ATC	GTT	AAA	GAT	TAT	676
Asn	Pro	Glu	Asn	Gln	Phe	Pro	Gly	Gln	Pro	Val	Ile	Val	Lys	Asp	Tyr	
		205														
AAT	GGG	CAA	AAA	GAT	GTG	CGC	TGG	GGG	GGG	TGT	CGT	TCG	GTG	AGC	GCG	724
Asn	Gly	Gln	Lys	Asp	Val	Arg	Trp	Gly	Gly	Cys	Arg	Ser	Val	Ser	Ala	
GGG	CAA	CGC	CCT	GTG	TTT	CGT	TTG	GTG	TGG	GAA	AAG	GGA	GGC	CTA	AAA	772
Gly	Gln	Arg	Pro	Val	Phe	Arg	Leu	Val	Trp	Glu	Lys	Gly	Gly	Leu	Lys	
ATC	ATG	GTC	GCT	TAT	TGG	CCC	TAT	GTC	CCT	TAT	GAT	CAA	TCC	AAT	CCT	820
Ile	Met	Val	Ala	Tyr	Trp	Pro	Tyr	Val	Pro	Tyr	Asp	Gln	Ser	Asn	Pro	
		255														
AAT	TTG	ATT	GAT	TAC	ATG	GGG	TAT	GGT	AAC	GCT	AAA	ATT	GAT	TAC	AGG	868
Asn	Leu	Ile	Asp	Tyr	Met	Gly	Tyr	Gly	Asn	Ala	Lys	Ile	Asp	Tyr	Arg	
		270														
AGA	GGG	CGC	CAC	CAT	TTT	GAA	TTG	CAG	CTT	TAT	GAT	ATT	TTC	ACG	CAA	916
Arg	Gly	Arg	His	His	Phe	Glu	Leu	Gln	Leu	Tyr	Asp	Ile	Phe	Thr	Gln	
		285														
TAC	TGG	CGT	TAT	GAT	CGC	TGG	CAT	GGA	GCT	TTC	CGC	TTA	GGC	TAT	ACC	964
Tyr	Trp	Arg	Tyr	Asp	Arg	Trp	His	Gly	Ala	Phe	Arg	Leu	Gly	Tyr	Thr	
TAT	CGC	ATT	AAC	CCT	TTT	GTG	GGG	ATT	TAT	GCG	CAG	TGG	TTT	AAC	GGC	1012
Tyr	Arg	Ile	Asn	Pro	Phe	Val	Gly	Ile	Tyr	Ala	Gln	Trp	Phe	Asn	Gly	

320 325 330
 TAT GGC GAT GGC TTG TAT GAA TAC GAT GTT TTT TCC AAT CGT ATA GGG 1060
 Tyr Gly Asp Gly Leu Tyr Glu Tyr Asp Val Phe Ser Asn Arg Ile Gly
 335 340 345
 GTA GGA ATA CGC TTA AAC CCT TAAAAAAGCG TTCTTTTAYG CTATAATTAA GACC 1115
 Val Gly Ile Arg Leu Asn Pro
 350 355
 AAAAA 1120

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

Met	Lys	Ser	Ile	Leu	Leu	Phe	Met	Ile	Phe	Val	Val	Cys	Gln	Leu	Glu
1				5					10					15	
Gly	Lys	Lys	Phe	Ser	Gln	Asp	Asn	Phe	Lys	Val	Asp	Tyr	Asn	Tyr	Tyr
			20					25					30		
Leu	Arg	Lys	Gln	Asp	Leu	His	Ile	Ile	Lys	Thr	Gln	Asn	Asp	Leu	Ser
		35					40					45			
Asn	Ser	Trp	Tyr	Leu	Pro	Pro	Gln	Lys	Ala	Pro	Lys	Glu	His	Ser	Trp
	50					55				60					
Val	Asp	Phe	Ala	Lys	Lys	Tyr	Leu	Asn	Met	Met	Asp	Tyr	Leu	Gly	Thr
65					70					75				80	
Tyr	Phe	Leu	Pro	Phe	Tyr	His	Ser	Phe	Thr	Pro	Ile	Phe	Gln	Trp	Tyr
			85						90				95		
His	Pro	Asn	Ile	Asn	Pro	Tyr	Gln	Arg	Asn	Glu	Phe	Lys	Phe	Gln	Ile
		100					105						110		
Ser	Phe	Arg	Val	Pro	Val	Phe	Arg	His	Ile	Leu	Trp	Thr	Lys	Gly	Thr
		115					120					125			
Leu	Tyr	Leu	Ala	Tyr	Thr	Gln	Thr	Asp	Trp	Phe	Gln	Ile	Tyr	Asn	Asp
	130					135					140				
Pro	Gln	Ser	Ala	Pro	Met	Arg	Met	Met	Asn	Phe	Met	Pro	Glu	Leu	Ile
145					150					155				160	
Tyr	Val	Tyr	Pro	Ile	Asn	Phe	Lys	Pro	Phe	Gly	Gly	Lys	Ile	Gly	Asn
			165						170				175		
Phe	Ser	Glu	Ile	Trp	Ile	Gly	Trp	Gln	His	Ile	Ser	Asn	Gly	Val	Gly
		180						185					190		
Gly	Ala	Gln	Cys	Tyr	Gln	Pro	Phe	Asn	Lys	Glu	Gly	Asn	Pro	Glu	Asn
		195					200					205			
Gln	Phe	Pro	Gly	Gln	Pro	Val	Ile	Val	Lys	Asp	Tyr	Asn	Gly	Gln	Lys
	210					215					220				
Asp	Val	Arg	Trp	Gly	Gly	Cys	Arg	Ser	Val	Ser	Ala	Gly	Gln	Arg	Pro
225				230						235				240	
Val	Phe	Arg	Leu	Val	Trp	Glu	Lys	Gly	Gly	Leu	Lys	Ile	Met	Val	Ala
			245						250				255		
Tyr	Trp	Pro	Tyr	Val	Pro	Tyr	Asp	Gln	Ser	Asn	Pro	Asn	Leu	Ile	Asp
			260					265					270		

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

GTG GAT AAA GCT AAT AAG AGT TTA GAA GAA ATC GCT TGC GAA GAA GCG	390
Val Asp Lys Ala Asn Lys Ser Leu Glu Glu Ile Ala Cys Glu Glu Ala	
105 110 115	
CTA GAA GAA TGC GGT TAT CAA ATT AGC CCT AAA AAT TTA GAA ACC ATA	438
Leu Glu Glu Cys Gly Tyr Gln Ile Ser Pro Lys Asn Leu Glu Thr Ile	
120 125 130 135	
GGC CAA TTT TAT AGC GCG ACT GGG TTG AGT GGG AGT TTG CAA ACG CTC	486
Gly Gln Phe Tyr Ser Ala Thr Gly Leu Ser Gly Ser Leu Gln Thr Leu	
140 145 150	
TAT TAC GCT GAA GTG CAT AAG AAT TTG AAA GTT TCA AAG GGT GGG GGG	534
Tyr Tyr Ala Glu Val His Lys Asn Leu Lys Val Ser Lys Gly Gly Gly	
155 160 165	
ATT GAT ACC GAA AGG ATT GAA GTG CTG TTT TTA GAG CGA TCA AAA GCT	582
Ile Asp Thr Glu Arg Ile Glu Val Leu Phe Leu Glu Arg Ser Lys Ala	
170 175 180	
CTT GAT TTT ATA ATG GAT TTT CAA TAC GCT AAA ACC ACC GGA TTG TCT	630
Leu Asp Phe Ile Met Asp Phe Gln Tyr Ala Lys Thr Thr Gly Leu Ser	
185 190 195	
TTA GCC ATT TTA TGG CAT TTA AAA AAG TTT AAA AAT GTT TAAAAGGAAT TT	681
Leu Ala Ile Leu Trp His Leu Lys Lys Phe Lys Asn Val	
200 205 210	
TATGTTAAGG CTTTTG	697

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

Met Ser Tyr Phe Lys Asn Ala Phe Asn Gln Lys Ser Leu Ile Asp Asp	
1 5 10 15	
Ser Ser Val Tyr Leu Glu Pro Cys Ser Ser Ser Asn Phe Ile Glu Leu	
20 25 30	
Lys Arg Met His Tyr Asn Glu Glu Asn Thr Lys Lys Thr Trp Asp Ile	
35 40 45	
Ile Lys Ser Leu Asp Ser Val Ala Val Leu Leu Tyr Glu Lys Glu Ser	
50 55 60	
Asp Cys Phe Val Ile Val Lys Gln Phe Arg Pro Ala Ile Tyr Ala Arg	
65 70 75 80	
Arg Phe His Phe Lys Cys Asp Gln Asp Gln Thr Ile Asp Gly Tyr Thr	
85 90 95	
Tyr Glu Leu Cys Ala Gly Leu Val Asp Lys Ala Asn Lys Ser Leu Glu	
100 105 110	
Glu Ile Ala Cys Glu Glu Ala Leu Glu Glu Cys Gly Tyr Gln Ile Ser	
115 120 125	

Pro Lys Asn Leu Glu Thr Ile Gly Gln Phe Tyr Ser Ala Thr Gly Leu
 130 135 140
 Ser Gly Ser Leu Gln Thr Leu Tyr Tyr Ala Glu Val His Lys Asn Leu
 145 150 155 160
 Lys Val Ser Lys Gly Gly Ile Asp Thr Glu Arg Ile Glu Val Leu
 165 170 175
 Phe Leu Glu Arg Ser Lys Ala Leu Asp Phe Ile Met Asp Phe Gln Tyr
 180 185 190
 Ala Lys Thr Thr Gly Leu Ser Leu Ala Ile Leu Trp His Leu Lys Lys
 195 200 205
 Phe Lys Asn Val
 210

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...2022
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

TGCGAACAAAT TATGGGATGA TATTATAAAAA ATTGGTGGGA ATGATAAG ATG AAC GGA	57
Met Asn Gly	
1	
CAT TTT ATC GGT TCT ATT TTG TAT GTG CTA GAT AGT AAT ACG CAC TCT	105
His Phe Ile Gly Ser Ile Leu Tyr Val Leu Asp Ser Asn Thr His Ser	
5 10 15	
AAC AAT ACA TTA CTC ATC ATT GAC GGC CAA CAA AGG CTC ACC ACT ATC	153
Asn Asn Thr Leu Leu Ile Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile	
20 25 30 35	
ACG CTT TTA CTC ATC GCT TTA AGG AAT CAT CTA AGC GAA GAA GTT GAA	201
Thr Leu Leu Leu Ile Ala Leu Arg Asn His Leu Ser Glu Glu Val Glu	
40 45 50	
ATT TTG GAG AAA TTT TCG CGT AAA GAA ATA GAG AGC TAT CTT ATC AAC	249
Ile Leu Glu Lys Phe Ser Arg Lys Glu Ile Glu Ser Tyr Leu Ile Asn	
55 60 65	
AGC AAT AAG GAC GGC GAT AAG AAA TTC AGG CTC ATT CTT TCA GAG TCC	297
Ser Asn Lys Asp Gly Asp Lys Lys Phe Arg Leu Ile Leu Ser Glu Ser	
70 75 80	
GAT AAA GAC ACC TTG CTG TCT TTG ATT GAT AAA AAC AAA AGA AAG CCG	345
Asp Lys Asp Thr Leu Leu Ser Leu Ile Asp Lys Asn Lys Arg Lys Pro	
85 90 95	

AGC Ser 100	GAG Glu 100	CCT Pro 100	TCG Ser 100	GTA Val 100	AAA Lys 105	ATA Ile 105	GTG Val 105	GAA Glu 105	AAT Asn 110	TTT Phe 110	GAA Glu 110	TTG Leu 110	TTT Phe 110	GAA Glu 115	AAA Lys 115	393
TGG Trp 120	ATC Ile 120	AGT Ser 120	GAA Glu 120	AAC Asn 120	ACC Thr 120	GAC Asp 120	AAA Lys 125	CTA Leu 125	GAA Glu 125	ACG Thr 125	ATT Ile 125	TTT Phe 125	AAA Lys 130	GGA Gly 130	TTA Leu 130	441
AAA Lys 135	AAA Lys 135	CTC Leu 135	ATG Met 135	ATA Ile 135	GTT Val 135	TGG Trp 140	ATT Ile 140	TCT Ser 140	TTA Leu 140	GAT Asp 140	AAA Lys 145	GGA Gly 145	AAA Lys 145	GAT Asp 145	GAT Asp 145	489
CCT Pro 150	CAA Gln 150	CTT Leu 150	ATT Ile 150	TTT Phe 150	GAG Glu 155	AGC Ser 155	ATG Met 155	AAC Asn 155	TCA Ser 155	AAA Lys 160	GAT Asp 160	ATC Ile 160	GAA Glu 160	CTC Leu 160	ACG Thr 160	537
CAA Gln 165	ACG Thr 165	GAT Asp 165	TTG Leu 165	ATC Ile 165	AGA Arg 170	AAT Asn 170	TAT Tyr 170	ATC Ile 170	GTA Val 170	ATG Met 175	GAA Glu 175	ACG Thr 175	GAG Glu 175	GTT Val 175	GAA Glu 175	585
AAA Lys 180	CAG Gln 180	GAA Glu 180	GAC Asp 180	TTT Phe 185	TAT Tyr 185	AAT Asn 185	CAA Gln 185	TAT Tyr 185	TGG Trp 190	AGG Arg 190	GCT Ala 190	ATG Met 190	GAG Glu 195	GAG Glu 195	AGA Arg 195	633
TTT Phe 200	GAA Glu 200	CAA Gln 200	AAT Asn 200	GAA Glu 200	ACA Thr 200	TTG Leu 205	TTT Phe 205	AAT Asn 205	CGG Arg 205	TTT Phe 205	GTC Val 205	CGG Arg 210	CAT His 210	TAT Tyr 210	CTC Leu 210	681
ACG Thr 215	ATC Ile 215	AAA Lys 215	ATA Ile 215	GGA Gly 215	AAG Lys 215	ATT Ile 220	CCC Pro 220	AAT Asn 220	GAG Glu 220	AAA Lys 225	AGA Arg 225	GTT Val 225	TAT Tyr 225	GAA Glu 225	GCT Ala 225	729
TTC Phe 230	AAG Lys 230	GAT Asp 230	TAC Tyr 230	CGG Arg 230	CAA Gln 235	AAA Lys 235	AAG Lys 235	GGG Gly 235	ATA Ile 240	GAA Glu 240	ATA Ile 240	GAG Glu 240	GAT Asp 240	TTA Leu 240	TTA Leu 240	777
AAA Lys 245	GAT Asp 245	TTA Leu 245	CAA Gln 245	AAA Lys 245	TAC Tyr 250	TGC Cys 250	GGG Gly 250	TAT Tyr 250	TTT Phe 255	TGC Cys 255	CAG Gln 255	ATT Ile 255	GCA Ala 255	TTC Phe 255	AAA Lys 255	825
AAA Lys 260	GAA Glu 260	GAC Asp 260	GAT Asp 265	AAA Lys 265	GAT Asp 265	TTA Leu 265	AAC Asn 265	AAG Lys 265	GCT Ala 270	TTA Leu 270	AGT Ser 270	TTT Phe 275	TTG Leu 275	GTG Val 275	AAT Asn 275	873
TTA Leu 280	GAG Glu 280	ATG Met 280	GAT Asp 280	GTG Val 280	ATC Ile 280	TAT Tyr 285	CCG Pro 285	CTA Leu 285	CTA Leu 285	CTA Leu 285	GAG Glu 285	CTT Leu 285	TAT Tyr 285	AGC Ser 290	GAT Asp 290	921
TAT Tyr 295	AAG Lys 295	GAT Asp 295	GGC Gly 295	GTT Val 295	TTA Leu 300	TCC Ser 300	AAG Lys 300	CAG Gln 300	GAT Asp 300	TTT Phe 305	ATC Ile 305	CCT Pro 305	ATT Ile 305	ATC Ile 305	TAT Tyr 305	969
TTA Leu 310	ATA Ile 310	GAG Glu 310	AGC Ser 310	TAT Tyr 310	ATT Ile 315	TGC Cys 315	AGA Arg 315	AGG Arg 315	GCG Ala 315	GTG Val 315	TGT Cys 315	GGG Gly 320	CTT Leu 320	GGC Gly 320	ACA Thr 320	1017
AAT Asn 1065	AGT Ser 1065	CTC Leu 1065	AAT Asn 1065	AAA Lys 1065	GTT Val 1065	TTT Phe 1065	CCC Pro 1065	TCT Ser 1065	TTT Phe 1065	ACA Thr 1065	AAG Lys 1065	CAC His 1065	ATC Ile 1065	CAA Gln 1065	AAA Lys 1065	1065

325				330				335								
GAT Asp 340	GAA Glu	TAT Tyr	TTT Phe	AAA Lys	AGC Ser	CTA Leu	AAG Lys	GCG Ala	CAT His	TTT Phe	GTC Val	TGT Cys	CTG Leu	ACA Thr	GAA Glu 355	1113
AAA Lys	CAA Gln	AGA Arg	TTT Phe	CCA Pro	AAC Asn	AAT Asn	GAC Asp	GAG Glu	TTT Phe	AAA Lys	AAG Lys	CTT Leu	TTT Phe	ATT Ile	ACG Thr 370	1161
ATA Ile	GAT Asp	TTT Phe	TAT Tyr	AAG Lys	TTT Phe	AAA Lys	AAA Lys	AAT Asn	AAA Lys	TAC Tyr	TTT Phe	CTT Leu	GAA Glu	AGG Arg	TTA Leu	1209
GAA Glu	AAT Asn	TTT Phe	GAC Asp	ACA Thr	AAA Lys	GAA Glu	CCG Pro	GTC Val	GAT Asp	ACT Thr	CAA Gln	AAA Lys	TGC Cys	AAT Asn	ATA Ile	1257
GAA Glu	CAT His	ATA Ile	ATG Met	CCT Pro	CAA Gln	ACC Thr	CTT Leu	ACT Thr	CCA Pro	GAA Glu	TGG Trp	CAA Gln	AGG Arg	GAT Asp	TTG Leu	1305
GGT Gly 420	GAA Glu	AAT Asn	TTT Phe	CAA Gln	GCA Ala	ATA Ile	CAC His	GAG Glu	AAA Lys	TAC Tyr	CTC Leu	CAC His	ACA Thr	ATA Ile	GGG Gly 435	1353
AAT Asn	CTC Leu	ACT Thr	CTA Leu	ACC Thr	GGT Gly	TAT Tyr	AAC Asn	TCT Ser	AAG Lys	TAT Tyr	AGC Ser	AAC Asn	AAT Asn	TCT Ser	TTC Phe 450	1401
CAA Gln	GAA Glu	AAA Lys	AGA Arg	GAT Asp	ATG Met	GAG Glu	AAG Lys	GGC Gly	TTT Phe	AAA Lys	CAA Gln	AGC Ser	TCA Ser	TTA Leu	AAA Lys	1449
CTC Leu	AAT Asn	CAA Gln	AGT Ser	TTG Leu	AAA Lys	GAT Asp	TTG Leu	GAA Glu	TCT Ser	TTT Phe	GGC Gly	GAA Glu	AAA Lys	GAG Glu	ATT Ile	1497
GAA Glu	AAA Lys	AGG Arg	GCT Ala	AGT Ser	GAT Asp	TTA Leu	GCG Ala	GAT Asp	TGG Trp	GCT Ala	TTA Leu	AAG Lys	ATT Ile	TGG Trp	ACT Thr	1545
TAC Tyr 500	CCA Pro	ATT Ile	CTA Leu	GAG Glu	GCA Ala	GAA Glu	ACA Thr	TTA Leu	GAG Glu	GAA Glu	TAT Tyr	AAA Lys	CCC Pro	AAA Lys	AAA Lys 515	1593
GAA Glu	AAG Lys	AAA Lys	GAA Glu	AAG Lys	AAA Lys	GAA Glu	AAA Lys	GAG Glu	GAG Glu	TAT Tyr	AAA Lys	CTC Leu	AAG Lys	AAA Lys	GAA Glu 530	1641
AAA Lys	AAG Lys	GTT Val	TAT Tyr	GAT Asp	TTA Leu	AGC Ser	TCT Ser	TAT Tyr	AAG Lys	TTT Phe	AGC Ser	TCT Ser	GAT Asp	TCA Ser	AGG Arg	1689
GAA Glu	TTG Leu	TTT Phe	GAT Asp	ATT Ile	TTA Leu	AGA Arg	GAA Glu	AAG Lys	ATT Ile	AAA Lys	GCT Ala	CTT Leu	GAT Asp	GAA Glu	AGG Arg	1737

ATA ACT GAA AAA TTT AAT CAA AAA TAT ATA GCT TAT AAG TTT TGT AAA	1785
Ile Thr Glu Lys Phe Asn Gln Lys Tyr Ile Ala Tyr Lys Phe Cys Lys	
565 570 575	
ATA AGT TTT GTG GAT ATT GTT GTG CAA GAA AAA GGC TTA AAA TTG TAT	1833
Ile Ser Phe Val Asp Ile Val Val Gln Glu Lys Gly Leu Lys Leu Tyr	
580 585 590 595	
TTA AAA ATG AAC TTG AAT GAA TTG CAA GAT GAA ATA AAG GAA AAA CTA	1881
Leu Lys Met Asn Leu Asn Glu Leu Gln Asp Glu Ile Lys Glu Lys Leu	
600 605 610	
AAA ATT AGA GAC GTT TCT AAT ATC GGT CGT CCA TGC GTT GGA AAC ATG	1929
Lys Ile Arg Asp Val Ser Asn Ile Gln Arg Pro Cys Val Gly Asn Met	
615 620 625	
GAA GTA GAG CTA GAA ACA AAA GAA AAT ATC CCT TAT TGT TTG GGA TTG	1977
Glu Val Glu Leu Glu Thr Lys Glu Asn Ile Pro Tyr Cys Leu Gly Leu	
630 635 640	
ATC AAG CAG GCT TTA GAA AAA CAG ATG GGT GGT AGG AAT AGG CAA TAAAA	2027
Ile Lys Gln Ala Leu Glu Lys Gln Met Gly Gly Arg Asn Arg Gln	
645 650 655	
ACCCAACCTTA TTCAAAATAA AGAGTATAAT TACAAATTAC TTAC	2071

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Met Asn Gly His Phe Ile Gly Ser Ile Leu Tyr Val Leu Asp Ser Asn	
1 5 10 15	
Thr His Ser Asn Asn Thr Leu Leu Ile Ile Asp Gly Gln Gln Arg Leu	
20 25 30	
Thr Thr Ile Thr Leu Leu Leu Ile Ala Leu Arg Asn His Leu Ser Glu	
35 40 45	
Glu Val Glu Ile Leu Glu Lys Phe Ser Arg Lys Glu Ile Glu Ser Tyr	
50 55 60	
Leu Ile Asn Ser Asn Lys Asp Gly Asp Lys Lys Phe Arg Leu Ile Leu	
65 70 75 80	
Ser Glu Ser Asp Lys Asp Thr Leu Leu Ser Leu Ile Asp Lys Asn Lys	
85 90 95	
Arg Lys Pro Ser Glu Pro Ser Val Lys Ile Val Glu Asn Phe Glu Leu	
100 105 110	
Phe Glu Lys Trp Ile Ser Glu Asn Thr Asp Lys Leu Glu Thr Ile Phe	
115 120 125	
Lys Gly Leu Lys Lys Leu Met Ile Val Trp Ile Ser Leu Asp Lys Gly	
130 135 140	
Lys Asp Asp Pro Gln Leu Ile Phe Glu Ser Met Asn Ser Lys Asp Ile	
145 150 155 160	

Glu	Leu	Thr	Gln	Thr 165	Asp	Leu	Ile	Arg	Asn 170	Tyr	Ile	Val	Met	Glu 175	Thr
Glu	Val	Glu	Lys 180	Gln	Glu	Asp	Phe	Tyr 185	Asn	Gln	Tyr	Trp	Arg 190	Ala	Met
Glu	Glu	Arg 195	Phe	Glu	Gln	Asn	Glu 200	Thr	Leu	Phe	Asn 205	Arg	Phe	Val	Arg
His	Tyr 210	Leu	Thr	Ile	Lys	Ile 215	Gly	Lys	Ile	Pro	Asn 220	Glu	Lys	Arg	Val
Tyr 225	Glu	Ala	Phe	Lys	Asp 230	Tyr	Arg	Gln	Lys	Lys 235	Gly	Ile	Glu	Ile	Glu 240
Asp	Leu	Leu	Lys 245	Asp	Leu	Gln	Lys	Tyr	Cys 250	Gly	Tyr	Phe	Cys	Gln 255	Ile
Ala	Phe	Lys	Lys 260	Glu	Asp	Asp	Lys	Asp 265	Leu	Asn	Lys	Ala	Leu 270	Ser	Phe
Leu	Val	Asn 275	Leu	Glu	Met	Asp	Val 280	Ile	Tyr	Pro	Leu	Leu 285	Leu	Glu	Leu
Tyr	Ser 290	Asp	Tyr	Lys	Asp	Gly 295	Val	Leu	Ser	Lys	Gln 300	Asp	Phe	Ile	Pro
Ile 305	Ile	Tyr	Leu	Ile	Glu 310	Ser	Tyr	Ile	Cys	Arg 315	Arg	Ala	Val	Cys	Gly 320
Leu	Gly	Thr	Asn 325	Ser	Leu	Asn	Lys	Val	Phe 330	Pro	Ser	Phe	Thr	Lys 335	His
Ile	Gln	Lys	Asp 340	Glu	Tyr	Phe	Lys	Ser 345	Leu	Lys	Ala	His	Phe 350	Val	Cys
Leu	Thr	Glu 355	Lys	Gln	Arg	Phe	Pro 360	Asn	Asn	Asp	Glu	Phe 365	Lys	Lys	Leu
Phe	Ile 370	Thr	Ile	Asp	Phe	Tyr 375	Lys	Phe	Lys	Lys	Asn 380	Lys	Tyr	Phe	Leu
Glu 385	Arg	Leu	Glu	Asn 390	Phe	Asp	Thr	Lys	Glu	Pro 395	Val	Asp	Thr	Gln	Lys 400
Cys	Asn	Ile	Glu 405	His	Ile	Met	Pro	Gln	Thr 410	Leu	Thr	Pro	Glu	Trp 415	Gln
Arg	Asp	Leu	Gly 420	Glu	Asn	Phe	Gln	Ala 425	Ile	His	Glu	Lys	Tyr 430	Leu	His
Thr	Ile	Gly 435	Asn	Leu	Thr	Leu	Thr 440	Gly	Tyr	Asn	Ser	Lys 445	Tyr	Ser	Asn
Asn	Ser 450	Phe	Gln	Glu	Lys	Arg 455	Asp	Met	Glu	Lys	Gly 460	Phe	Lys	Gln	Ser
Ser 465	Leu	Lys	Leu	Asn 470	Gln	Ser	Leu	Lys	Asp	Leu 475	Glu	Ser	Phe	Gly	Glu 480
Lys	Glu	Ile	Glu 485	Lys	Arg	Ala	Ser	Asp	Leu 490	Ala	Asp	Trp	Ala	Leu 495	Lys
Ile	Trp	Thr	Tyr 500	Pro	Ile	Leu	Glu	Ala 505	Glu	Thr	Leu	Glu	Glu 510	Tyr	Lys
Pro	Lys 515	Lys	Glu	Lys	Lys	Glu	Lys 520	Lys	Glu	Lys	Glu	Glu 525	Tyr	Lys	Leu
Lys	Lys 530	Glu	Lys	Lys	Val	Tyr 535	Asp	Leu	Ser	Ser	Tyr 540	Lys	Phe	Ser	Ser
Asp 545	Ser	Arg	Glu	Leu	Phe 550	Asp	Ile	Leu	Arg	Glu 555	Lys	Ile	Lys	Ala	Leu 560
Asp	Glu	Arg	Ile 565	Thr	Glu	Lys	Phe	Asn	Gln 570	Lys	Tyr	Ile	Ala	Tyr 575	Lys
Phe	Cys	Lys	Ile 580	Ser	Phe	Val	Asp	Ile 585	Val	Val	Gln	Glu	Lys 590	Gly	Leu
Lys	Leu	Tyr 595	Leu	Lys	Met	Asn	Leu 600	Asn	Glu	Leu	Gln	Asp 605	Glu	Ile	Lys
Glu	Lys 610	Leu	Lys	Ile	Arg	Asp 615	Val	Ser	Asn	Ile	Gly 620	Arg	Pro	Cys	Val

Gly	Asn	Met	Glu	Val	Glu	Leu	Glu	Thr	Lys	Glu	Asn	Ile	Pro	Tyr	Cys
625					630					635					640
Leu	Gly	Leu	Ile	Lys	Gln	Ala	Leu	Glu	Lys	Gln	Met	Gly	Gly	Arg	Asn
				645					650					655	
Arg	Gln														

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...558
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GTGGTGGCTG	AGTAGAAA	ATG	TTT	GAA	GCG	ACG	ACG	ATT	TTA	GGC	TAT	AGA	51
		Met	Phe	Glu	Ala	Thr	Thr	Ile	Leu	Gly	Tyr	Arg	
		1				5					10		
GGG GAA TTG AAT CAT AAA AAG TTC GCG CTC ATT GGA GGC GAT GGG CAG	99												
Gly Glu Leu Asn His Lys Lys Phe Ala Leu Ile Gly Gly Asp Gly Gln													
	15 20 25												
GTA ACT TTG GGT AAT TGC GTG GTC AAA GCC AAT GCG ACA AAA ATC AGA	147												
Val Thr Leu Gly Asn Cys Val Val Lys Ala Asn Ala Thr Lys Ile Arg													
	30 35 40												
AGC TTG TAT CAC AAC CAG GTT TTA AGC GGG TTT GCC GGA AGC ACC GCG	195												
Ser Leu Tyr His Asn Gln Val Leu Ser Gly Phe Ala Gly Ser Thr Ala													
	45 50 55												
GAC GCT TTT AGT TTG TTT GAT ATG TTT GAA CGC ATT TTA GAG AGC AAA	243												
Asp Ala Phe Ser Leu Phe Asp Met Phe Glu Arg Ile Leu Glu Ser Lys													
	60 65 70 75												
AAG GGG GAT TTG TTT AAA AGC GTG GTG GAT TTC AGT AAA GAA TGG CGC	291												
Lys Gly Asp Leu Phe Lys Ser Val Val Asp Phe Ser Lys Glu Trp Arg													
	80 85 90												
AAA GAT AAG TAT TTA CGC CGA CTG GAA GCG ATG ATG ATC GTT TTA AAC	339												
Lys Asp Lys Tyr Leu Arg Arg Leu Glu Ala Met Met Ile Val Leu Asn													
	95 100 105												
TTC GAT CAC ATT TTC ATT TTG AGC GGC ATG GGC GAT GTT TTA GAA GCT	387												
Phe Asp His Ile Phe Ile Leu Ser Gly Met Gly Asp Val Leu Glu Ala													
	110 115 120												
GAA GAC AAT AAG ATC GCT GCT ATT GGG AGT GGG GGG AAT TAC GCT TTA	435												

Glu	Asp	Asn	Lys	Ile	Ala	Ala	Ile	Gly	Ser	Gly	Gly	Asn	Tyr	Ala	Leu		
125						130					135						
AGC	GCG	GCT	AGG	GCT	TTA	GAT	CAT	TTC	GCT	CAT	TTA	GAG	CCT	AGA	AAA	483	
Ser	Ala	Ala	Arg	Ala	Leu	Asp	His	Phe	Ala	His	Leu	Glu	Pro	Arg	Lys		
140					145					150					155		
CTT	GTA	GAA	GAG	TCC	TTA	AAA	ATC	GCA	GGG	GAT	CTT	TGC	ATT	TAC	ACC	531	
Leu	Val	Glu	Glu	Ser	Leu	Lys	Ile	Ala	Gly	Asp	Leu	Cys	Ile	Tyr	Thr		
				160					165					170			
AAC	ACG	AAT	ATT	AAA	ATT	TTG	GAG	CTT	TAATGTCTAA	ATTGAATATG	ACCCAC	585					
Asn	Thr	Asn	Ile	Lys	Ile	Leu	Glu	Leu									
				175				180									
GAGAAATTGT	CGC															598	

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

Met	Phe	Glu	Ala	Thr	Thr	Ile	Leu	Gly	Tyr	Arg	Gly	Glu	Leu	Asn	His		
1				5					10					15			
Lys	Lys	Phe	Ala	Leu	Ile	Gly	Gly	Asp	Gly	Gln	Val	Thr	Leu	Gly	Asn		
			20					25					30				
Cys	Val	Val	Lys	Ala	Asn	Ala	Thr	Lys	Ile	Arg	Ser	Leu	Tyr	His	Asn		
			35				40					45					
Gln	Val	Leu	Ser	Gly	Phe	Ala	Gly	Ser	Thr	Ala	Asp	Ala	Phe	Ser	Leu		
			50			55				60							
Phe	Asp	Met	Phe	Glu	Arg	Ile	Leu	Glu	Ser	Lys	Lys	Gly	Asp	Leu	Phe		
65					70				75					80			
Lys	Ser	Val	Val	Asp	Phe	Ser	Lys	Glu	Trp	Arg	Lys	Asp	Lys	Tyr	Leu		
				85				90						95			
Arg	Arg	Leu	Glu	Ala	Met	Met	Ile	Val	Leu	Asn	Phe	Asp	His	Ile	Phe		
			100					105					110				
Ile	Leu	Ser	Gly	Met	Gly	Asp	Val	Leu	Glu	Ala	Glu	Asp	Asn	Lys	Ile		
			115				120					125					
Ala	Ala	Ile	Gly	Ser	Gly	Gly	Asn	Tyr	Ala	Leu	Ser	Ala	Ala	Arg	Ala		
			130			135					140						
Leu	Asp	His	Phe	Ala	His	Leu	Glu	Pro	Arg	Lys	Leu	Val	Glu	Glu	Ser		
145					150					155				160			
Leu	Lys	Ile	Ala	Gly	Asp	Leu	Cys	Ile	Tyr	Thr	Asn	Thr	Asn	Ile	Lys		
				165					170					175			
Ile	Leu	Glu	Leu														
			180														

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 34...396
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

TGTTTCATAG TAACAAATTG AAAATATACC ATT ATG TAT GGA GGT AAT GCT ATG	54
Met Tyr Gly Gly Asn Ala Met	
1 5	
GCT GAC ACA ATC AAT ACA ACT GAA GCA ACT CAT GAA ACA AAA AAA CCA	102
Ala Asp Thr Ile Asn Thr Thr Glu Ala Thr His Glu Thr Lys Lys Pro	
10 15 20	
AAC GCT TTT GTA AAT TTT TTC AAA AAC AAT TTG ACT GAT AAG CGT TAT	150
Asn Ala Phe Val Asn Phe Phe Lys Asn Asn Leu Thr Asp Lys Arg Tyr	
25 30 35	
GAT TCA TTA GGT CTC ATT GGA GCA GGG GTT TTA TGT TGT GTC TTG AGC	198
Asp Ser Leu Gly Leu Ile Gly Ala Gly Val Leu Cys Cys Val Leu Ser	
40 45 50 55	
GGT GCT ATG GGG ATT GTT GGG ATA ATC TTT GTC GCA ATA GGA ATC TTT	246
Gly Ala Met Gly Ile Val Gly Ile Ile Phe Val Ala Ile Gly Ile Phe	
60 65 70	
TTG TCT TTT TCT AAT ATC AAC TTA GTG AAA TTA GTT GAA AAA TTG TCC	294
Leu Ser Phe Ser Asn Ile Asn Leu Val Lys Leu Val Glu Lys Leu Ser	
75 80 85	
AAA AAA CAA TCT AAA GTG CCA ACA ACT GTC AAT AAC GAA ACT CAA AAA	342
Lys Lys Gln Ser Lys Val Pro Thr Val Asn Asn Glu Thr Gln Lys	
90 95 100	
TCT CAA GCA ACA AGC GTT ACC AAC GAA CCA ACT GAA GCC AAA GAG ACT	390
Ser Gln Ala Thr Ser Val Thr Asn Glu Pro Thr Glu Ala Lys Glu Thr	
105 110 115	
AAA GAT TGAGGCAAAA CAACGATTTT GACTGAAGAA AGAATGAGAG AAAATTTCAA AA	448
Lys Asp	
120	
AT	450

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

Met Tyr Gly Gly Asn Ala Met Ala Asp Thr Ile Asn Thr Thr Glu Ala
1 5 10 15
Thr His Glu Thr Lys Lys Pro Asn Ala Phe Val Asn Phe Phe Lys Asn
20 25 30
Asn Leu Thr Asp Lys Arg Tyr Asp Ser Leu Gly Leu Ile Gly Ala Gly
35 40 45
Val Leu Cys Cys Val Leu Ser Gly Ala Met Gly Ile Val Gly Ile Ile
50 55 60
Phe Val Ala Ile Gly Ile Phe Leu Ser Phe Ser Asn Ile Asn Leu Val
65 70 75 80
Lys Leu Val Glu Lys Leu Ser Lys Lys Gln Ser Lys Val Pro Thr Thr
85 90 95
Val Asn Asn Glu Thr Gln Lys Ser Gln Ala Thr Ser Val Thr Asn Glu
100 105 110
Pro Thr Glu Ala Lys Glu Thr Lys Asp
115 120

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 69...443
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

TAACCATTAG TTTCAAGCAG TATGAAAATC TTCTCCATAT CCATCAAAAAA GGTTGCGACA 60
ATGAAGTG ATG TGC AGA ACG CTC ATC TCT ATC GCT TTG TTA GAA AGC TCT 110
Met Cys Arg Thr Leu Ile Ser Ile Ala Leu Leu Glu Ser Ser
1 5 10
CTA GGG TTG AAC AAC AGG CGA GAA AAA TCC CTT AAA GAC ACT TCT TAT 158
Leu Gly Leu Asn Asn Arg Arg Glu Lys Ser Leu Lys Asp Thr Ser Tyr
15 20 25 30
TCC ATG TTT CAT ATC ACC CTA AAC ACC GCT AAA AAA TTC TAC CCT ACC 206
Ser Met Phe His Ile Thr Leu Asn Thr Ala Lys Lys Phe Tyr Pro Thr
35 40 45
TAC TCT AAA ACG CTC CTC AAA TTC AAA TTG CTA AAC GAT GTG GGT TTT 254
Tyr Ser Lys Thr Leu Leu Lys Phe Lys Leu Leu Asn Asp Val Gly Phe
50 55 60

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 31...2274
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

ATTTTATATC AAACACAGGT AGTAGGCACA	ATG GAA GAC TTT TTG TAT AAC ACC	54
	Met Glu Asp Phe Leu Tyr Asn Thr	
	1 5	
TTA TAT TTC ATA GAG GAT TAT AAG TTG GTT GTT ATT TTT AGT TTC ATA		102
Leu Tyr Phe Ile Glu Asp Tyr Lys Leu Val Val Ile Phe Ser Phe Ile		
10 15 20		
GGG TTA ATA GCG TTA TTT TTT CTT TAC AAA TTC ATA AAA GCT CAA AAA		150
Gly Leu Ile Ala Leu Phe Phe Leu Tyr Lys Phe Ile Lys Ala Gln Lys		
25 30 35 40		
AAG GCT TTT AAA GAT AAA GCT AAC CAG CCT CAA AAG AAA AAA AGC TTT		198
Lys Ala Phe Lys Asp Lys Ala Asn Gln Pro Gln Lys Lys Lys Ser Phe		
45 50 55		
AAA GAA ATC ATT ATA GAT GGG CTG AAA GAA AGG GTT AAA ACC TTT GGC		246
Lys Glu Ile Ile Ile Asp Gly Leu Lys Glu Arg Val Lys Thr Phe Gly		
60 65 70		
TTT TGG TTG CAA GCT ATA CTA TTA CTA TCC TAT TCT TTT ATC ACA TCA		294
Phe Trp Leu Gln Ala Ile Leu Leu Leu Ser Tyr Ser Phe Ile Thr Ser		
75 80 85		
GGA TTA TTT TTC TTG ATT CTC TTA GGT AAT TTT TAT GAT GAT AAT CGA		342
Gly Leu Phe Phe Leu Ile Leu Leu Gly Asn Phe Tyr Asp Asp Asn Arg		
90 95 100		
TCG CCT GAG AGC GAT GAT GAT CTT TTT GAT ATA TGG ATC TAT GCG ATA		390
Ser Pro Glu Ser Asp Asp Asp Leu Phe Asp Ile Trp Ile Tyr Ala Ile		
105 110 115 120		
CAA GAT TTT CCT AAT TAC TAT TTT AAA GCG CTT GGT TTT AGT TCA CTC		438
Gln Asp Phe Pro Asn Tyr Tyr Phe Lys Ala Leu Gly Phe Ser Ser Leu		
125 130 135		
AAG ATT TAT GGG TTC AAT ATA TCC TTA GTC GTA TAT GGT TCT ATT TTA		486
Lys Ile Tyr Gly Phe Asn Ile Ser Leu Val Val Tyr Gly Ser Ile Leu		
140 145 150		
TGC TCT TAT ATC TTC ATT ACC TTT TTT GTG TGG TTC TTA AAA TAC TTA		534
Cys Ser Tyr Ile Phe Ile Thr Phe Phe Val Trp Phe Leu Lys Tyr Leu		
155 160 165		
ACT CGG ACT AGA GAT ATA GGA GCG AAT AAA AAA GTT GAT GAT CTC TTT		582
Thr Arg Thr Arg Asp Ile Gly Ala Asn Lys Lys Val Asp Asp Leu Phe		
170 175 180		
GGT AGC GCG AGT TGG GAA ACT GAA GAG AAA ATG ATC AAA GCC AAA CTC		630
Gly Ser Ala Ser Trp Glu Thr Glu Glu Lys Met Ile Lys Ala Lys Leu		
185 190 195 200		

ATC Ile	ACG Thr	CCC Pro	AAC Asn	AAT Asn 205	AAA Lys	AAA Lys	CGC Arg	GCC Ala	TTT Phe 210	GAC Asp	AAA Lys	CGA Arg	GAG Glu	GTG Val 215	ATT Ile	678
GTA Val	GGC Gly	AGG Arg	CGT Arg 220	GGC Gly	TTG Leu	GGG Gly	GAT Asp	TTT Phe 225	ATC Ile	GCT Ala	TAC Tyr	GCA Ala	GGG Gly 230	CAG Gln	GCG Ala	726
TTC Phe	ATT Ile	GGC Gly 235	TTG Leu	ATT Ile	GCT Ala	CCT Pro	ACT Thr 240	AGA Arg	AGC Ser	GGT Gly	AAG Lys	GGG Gly 245	GTG Val	GGT Gly	TTC Phe	774
ATC Ile 250	ATG Met	CCC Pro	AAT Asn	ATG Met	ATC Ile	AAT Asn 255	TAT Tyr	CCT Pro	CAA Gln	AAT Asn	ATC Ile 260	GTT Val	GTG Val	TTT Phe	GAC Asp	822
CCT Pro 265	AAA Lys	GCT Ala	GAC Asp	ACT Thr	ATG Met 270	GAG Glu	ACT Thr	TGC Cys	GGA Gly	AAA Lys 275	ATC Ile	AGA Arg	GAA Glu	AAA Lys	CGC Arg 280	870
TTC Phe	AAC Asn	CAA Gln	AAA Lys 285	GTG Val	TTC Phe	ATC Ile	TAT Tyr	GAA Glu	CCT Pro 290	TTC Phe	TCC Ser	TTA Leu	AAA Lys	ACA Thr 295	CAC His	918
CGA Arg	TTT Phe	AAT Asn	CCT Pro 300	TTC Phe	GCT Ala	TAT Tyr	GTG Val	GAT Asp 305	TTT Phe	GGT Gly	AAT Asn	GAT Asp	GTG Val 310	GTT Val	TTG Leu	966
ACC Thr	GAA Glu	GAC Asp 315	ATA Ile	CTC Leu	TCT Ser	CAA Gln	ATT Ile 320	GAC Asp	ACA Thr	CGC Arg	CTA Leu	AAA Lys 325	GGG Gly	CAT His	GGC Gly	1014
ATG Met 330	GTG Val	GCT Ala	AGT Ser	GGA Gly	GGG Gly	GAT Asp 335	TTT Phe	TCC Ser	ACT Thr	CAA Gln	ATC Ile 340	TTT Phe	GGA Gly	TTA Leu	GCA Ala	1062
AAG Lys 345	CTC Leu	GTG Val	TTC Phe	CCT Pro	GAA Glu 350	AGA Arg	CCT Pro	AAT Asn	GAA Glu	AAA Lys 355	GAT Asp	CCT Pro	TTC Phe	TTT Phe	AGC Ser 360	1110
AAT Asn	CAA Gln	GCG Ala	CGA Arg 365	AAT Asn	CTT Leu	TTT Phe	GTC Val	ATC Ile	AAT Asn 370	TGC Cys	AAT Asn	ATT Ile	TAC Tyr	AGG Arg 375	GAT Asp	1158
CTC Leu	ATG Met	TGG Trp	ACT Thr 380	AAA Lys	AAG Lys	GGG Gly	CTT Leu	GAG Glu 385	TTT Phe	GTC Val	AAA Lys	AGA Arg	AAA Lys 390	AAA Lys	ATC Ile	1206
ATC Ile	ATG Met	CCT Pro 395	GAA Glu	ACA Thr	CCC Pro	ACG Thr	ATG Met	TTT Phe	TTC Phe	ATA Ile	GGT Gly	TCT Ser 405	ATG Met	GCA Ala	AGC Ser	1254
GGG Gly 410	ATC Ile	AAC Asn	TTG Leu	ATT Ile	GAT Asp	GAA Glu 415	GAC Asp	ACA Thr	AAC Asn	ATG Met	GAA Glu 420	AAA Lys	GTC Val	GTG Val	TCT Ser	1302
TTA Leu	ATG Met	GAA Glu	TTT Phe	TTT Phe	GGA Gly	GGT Gly	GAA Glu	GAA Glu	GAT Asp	AAG Lys	AGT Ser	GGC Gly	GAT Asp	AAT Asn	CTA Leu	1350

425				430				435				440					
AGA Arg	GTG Val	CTT Leu	AGT Ser	CCT Pro	GCC Ala	ACT Thr	AGA Arg	AAC Asn	ATG Met	TGG Trp	AAT Asn	AGC Ser	TTC Phe	AAG Lys	ACA Thr	1398	
				445					450					455			
ATG Met	GGC Gly	GGC Gly	GCT Ala	AGA Arg	GAA Glu	ACT Thr	TAT Tyr	AGC Ser	TCG Ser	GTT Val	CAA Gln	GGG Gly	GTA Val	TAC Tyr	ACT Thr	1446	
				460					465					470			
TCA Ser	GCC Ala	TTT Phe	GCG Ala	CCT Pro	TAT Tyr	AAT Asn	AAC Asn	GCA Ala	ATG Met	ATT Ile	AGA Arg	AAT Asn	TTC Phe	ACG Thr	AGC Ser	1494	
				475					480					485			
GCC Ala	AAT Asn	GAT Asp	TTT Phe	GAT Asp	TTC Phe	AGG Arg	CGT Arg	TTA Leu	AGG Arg	ATC Ile	GAT Asp	GAA Glu	GTG Val	AGT Ser	ATT Ile	1542	
				490					495					500			
GGT Gly	GTG Val	ATC Ile	GCT Ala	AAT Asn	CCT Pro	AAA Lys	GAA Glu	AGC Ser	ACT Thr	ATT Ile	GTT Val	GGA Gly	CCG Pro	ATA Ile	TTA Leu	1590	
				505					510					515			520
GAG Glu	CTG Leu	TTT Phe	TTC Phe	AAT Asn	GTG Val	ATG Met	ATT Ile	TAT Tyr	AGC Ser	AAT Asn	TTG Leu	ATT Ile	CTG Leu	CCA Pro	ATC Ile	1638	
				525					530					535			
CAT His	GAT Asp	CCA Pro	CAG Gln	TGC Cys	AAA Lys	AGA Arg	AGT Ser	TGC Cys	TTG Leu	ATG Met	CTC Leu	ATG Met	GAC Asp	GAA Glu	TTC Phe	1686	
				540					545					550			
ACT Thr	TTA Leu	TGT Cys	GGC Gly	TAT Tyr	TTA Leu	GAG Glu	ACC Thr	TTT Phe	GTT Val	AAA Lys	GCG Ala	GTA Val	GGG Gly	ATT Ile	ATG Met	1734	
				555					560					565			
GCA Ala	GAA Glu	TAC Tyr	AAC Asn	ATG Met	CGC Arg	CCC Pro	GCT Ala	TTT Phe	GTG Val	TTT Phe	CAA Gln	AGT Ser	AAG Lys	GCG Ala	CAA Gln	1782	
				570					575					580			
CTA Leu	GAG Glu	AAT Asn	GAC Asp	CCC Pro	CCA Pro	CTT Leu	GGT Gly	TAT Tyr	GGT Gly	AGG Arg	AAT Asn	GGC Gly	GCT Ala	AAG Lys	ACT Thr	1830	
				585					590					595			600
ATT Ile	TTA Leu	GAC Asp	AAC Asn	CTT Leu	TCT Ser	TTG Leu	AAT Asn	ATG Met	TAT Tyr	TAT Tyr	GGG Gly	ATT Ile	AAC Asn	AAC Asn	GAT Asp	1878	
				605					610					615			
AAC Asn	TAC Tyr	TAT Tyr	GAA Glu	CAT His	TTT Phe	GAA Glu	AAA Lys	CTT Leu	TCT Ser	AAG Lys	GTA Val	TTA Leu	GGG Gly	AAA Lys	TAC Tyr	1926	
				620					625					630			
ACA Thr	AGG Arg	CAA Gln	GAC Asp	GTG Val	AGC Ser	CGA Arg	AGC Ser	ATT Ile	GAT Asp	GAT Asp	AAT Asn	ACA Thr	GGT Gly	AAG Lys	ACC Thr	1974	
				635					640					645			
AAC Asn	ACT Thr	TCT Ser	ATC Ile	AGC Ser	AAC Asn	AAA Lys	GAG Glu	CGG Arg	TTT Phe	TTG Leu	ATG Met	ACC Thr	CCT Pro	GAT Asp	GAA Glu	2022	
				650					655					660			

TTG ATG ACT ATG GGC GAT GAG CTT ATC ATT CTA GAG AAT ACG CTC AAA	2070
Leu Met Thr Met Gly Asp Glu Leu Ile Ile Leu Glu Asn Thr Leu Lys	
665 670 675 680	
CCT ATC AAG TGC CAC AAG GCG CTT TAC TAT GAT GAT CCA TTC TTC ACC	2118
Pro Ile Lys Cys His Lys Ala Leu Tyr Tyr Asp Asp Pro Phe Phe Thr	
685 690 695	
GAT GAA CTC ATT AAG GTA AGT CCA AGC TTG AGC AAG AAA TAC AAA TTG	2166
Asp Glu Leu Ile Lys Val Ser Pro Ser Leu Ser Lys Lys Tyr Lys Leu	
700 705 710	
GGG AAA GTG CCT AAT CAA GCA ACT TTC TAT GAT GAT TTG CAA GCC GCT	2214
Gly Lys Val Pro Asn Gln Ala Thr Phe Tyr Asp Asp Leu Gln Ala Ala	
715 720 725	
AAA ACT AGA GGT GAA TTG AGT TAT GAT AAA TCT TTA GTG CCT GTG GGT	2262
Lys Thr Arg Gly Glu Leu Ser Tyr Asp Lys Ser Leu Val Pro Val Gly	
730 735 740	
TCA AGT GAA CTG TGATTAAGAC AAAATATCTT AACAAAAAGA AAATTAAAAG ATAAT	2319
Ser Ser Glu Leu	
745	
GATATAAATA	2329

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

Met Glu Asp Phe Leu Tyr Asn Thr Leu Tyr Phe Ile Glu Asp Tyr Lys	
1 5 10 15	
Leu Val Val Ile Phe Ser Phe Ile Gly Leu Ile Ala Leu Phe Phe Leu	
20 25 30	
Tyr Lys Phe Ile Lys Ala Gln Lys Lys Ala Phe Lys Asp Lys Ala Asn	
35 40 45	
Gln Pro Gln Lys Lys Lys Ser Phe Lys Glu Ile Ile Ile Asp Gly Leu	
50 55 60	
Lys Glu Arg Val Lys Thr Phe Gly Phe Trp Leu Gln Ala Ile Leu Leu	
65 70 75 80	
Leu Ser Tyr Ser Phe Ile Thr Ser Gly Leu Phe Phe Leu Ile Leu Leu	
85 90 95	
Gly Asn Phe Tyr Asp Asp Asn Arg Ser Pro Glu Ser Asp Asp Asp Leu	
100 105 110	
Phe Asp Ile Trp Ile Tyr Ala Ile Gln Asp Phe Pro Asn Tyr Tyr Phe	
115 120 125	
Lys Ala Leu Gly Phe Ser Ser Leu Lys Ile Tyr Gly Phe Asn Ile Ser	
130 135 140	
Leu Val Val Tyr Gly Ser Ile Leu Cys Ser Tyr Ile Phe Ile Thr Phe	
145 150 155 160	

Phe	Val	Trp	Phe	Leu	Lys	Tyr	Leu	Thr	Arg	Thr	Arg	Asp	Ile	Gly	Ala	
				165					170					175		
Asn	Lys	Lys	Val	Asp	Asp	Leu	Phe	Gly	Ser	Ala	Ser	Trp	Glu	Thr	Glu	
			180					185					190			
Glu	Lys	Met	Ile	Lys	Ala	Lys	Leu	Ile	Thr	Pro	Asn	Asn	Lys	Lys	Arg	
		195					200					205				
Ala	Phe	Asp	Lys	Arg	Glu	Val	Ile	Val	Gly	Arg	Arg	Gly	Leu	Gly	Asp	
	210					215					220					
Phe	Ile	Ala	Tyr	Ala	Gly	Gln	Ala	Phe	Ile	Gly	Leu	Ile	Ala	Pro	Thr	
225					230					235					240	
Arg	Ser	Gly	Lys	Gly	Val	Gly	Phe	Ile	Met	Pro	Asn	Met	Ile	Asn	Tyr	
			245						250					255		
Pro	Gln	Asn	Ile	Val	Val	Phe	Asp	Pro	Lys	Ala	Asp	Thr	Met	Glu	Thr	
		260						265					270			
Cys	Gly	Lys	Ile	Arg	Glu	Lys	Arg	Phe	Asn	Gln	Lys	Val	Phe	Ile	Tyr	
		275					280					285				
Glu	Pro	Phe	Ser	Leu	Lys	Thr	His	Arg	Phe	Asn	Pro	Phe	Ala	Tyr	Val	
	290					295					300					
Asp	Phe	Gly	Asn	Asp	Val	Val	Leu	Thr	Glu	Asp	Ile	Leu	Ser	Gln	Ile	
305					310					315					320	
Asp	Thr	Arg	Leu	Lys	Gly	His	Gly	Met	Val	Ala	Ser	Gly	Gly	Asp	Phe	
			325						330					335		
Ser	Thr	Gln	Ile	Phe	Gly	Leu	Ala	Lys	Leu	Val	Phe	Pro	Glu	Arg	Pro	
		340						345					350			
Asn	Glu	Lys	Asp	Pro	Phe	Phe	Ser	Asn	Gln	Ala	Arg	Asn	Leu	Phe	Val	
	355						360					365				
Ile	Asn	Cys	Asn	Ile	Tyr	Arg	Asp	Leu	Met	Trp	Thr	Lys	Lys	Gly	Leu	
	370					375					380					
Glu	Phe	Val	Lys	Arg	Lys	Lys	Ile	Ile	Met	Pro	Glu	Thr	Pro	Thr	Met	
385					390					395					400	
Phe	Phe	Ile	Gly	Ser	Met	Ala	Ser	Gly	Ile	Asn	Leu	Ile	Asp	Glu	Asp	
			405						410					415		
Thr	Asn	Met	Glu	Lys	Val	Val	Ser	Leu	Met	Glu	Phe	Phe	Gly	Gly	Glu	
		420						425					430			
Glu	Asp	Lys	Ser	Gly	Asp	Asn	Leu	Arg	Val	Leu	Ser	Pro	Ala	Thr	Arg	
	435						440					445				
Asn	Met	Trp	Asn	Ser	Phe	Lys	Thr	Met	Gly	Gly	Ala	Arg	Glu	Thr	Tyr	
	450					455					460					
Ser	Ser	Val	Gln	Gly	Val	Tyr	Thr	Ser	Ala	Phe	Ala	Pro	Tyr	Asn	Asn	
465					470					475					480	
Ala	Met	Ile	Arg	Asn	Phe	Thr	Ser	Ala	Asn	Asp	Phe	Asp	Phe	Arg	Arg	
			485						490					495		
Leu	Arg	Ile	Asp	Glu	Val	Ser	Ile	Gly	Val	Ile	Ala	Asn	Pro	Lys	Glu	
		500						505					510			
Ser	Thr	Ile	Val	Gly	Pro	Ile	Leu	Glu	Leu	Phe	Phe	Asn	Val	Met	Ile	
	515						520					525				
Tyr	Ser	Asn	Leu	Ile	Leu	Pro	Ile	His	Asp	Pro	Gln	Cys	Lys	Arg	Ser	
	530					535						540				
Cys	Leu	Met	Leu	Met	Asp	Glu	Phe	Thr	Leu	Cys	Gly	Tyr	Leu	Glu	Thr	
545					550					555					560	
Phe	Val	Lys	Ala	Val	Gly	Ile	Met	Ala	Glu	Tyr	Asn	Met	Arg	Pro	Ala	
			565						570					575		
Phe	Val	Phe	Gln	Ser	Lys	Ala	Gln	Leu	Glu	Asn	Asp	Pro	Pro	Leu	Gly	
		580						585					590			
Tyr	Gly	Arg	Asn	Gly	Ala	Lys	Thr	Ile	Leu	Asp	Asn	Leu	Ser	Leu	Asn	
		595					600					605				
Met	Tyr	Tyr	Gly	Ile	Asn	Asn	Asp	Asn	Tyr	Tyr	Glu	His	Phe	Glu	Lys	
	610					615					620					

Leu Ser Lys Val Leu Gly Lys Tyr Thr Arg Gln Asp Val Ser Arg Ser
 625 630 635 640
 Ile Asp Asp Asn Thr Gly Lys Thr Asn Thr Ser Ile Ser Asn Lys Glu
 645 650 655
 Arg Phe Leu Met Thr Pro Asp Glu Leu Met Thr Met Gly Asp Glu Leu
 660 665 670
 Ile Ile Leu Glu Asn Thr Leu Lys Pro Ile Lys Cys His Lys Ala Leu
 675 680 685
 Tyr Tyr Asp Asp Pro Phe Phe Thr Asp Glu Leu Ile Lys Val Ser Pro
 690 695 700
 Ser Leu Ser Lys Lys Tyr Lys Leu Gly Lys Val Pro Asn Gln Ala Thr
 705 710 715 720
 Phe Tyr Asp Asp Leu Gln Ala Ala Lys Thr Arg Gly Glu Leu Ser Tyr
 725 730 735
 Asp Lys Ser Leu Val Pro Val Gly Ser Ser Glu Leu
 740 745

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1037 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1008
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

TAAATTTGGA ATAAGAAC	ATG ACT GAA GAC AGA TTG AGT GCA GAA GAT AAA	51
	Met Thr Glu Asp Arg Leu Ser Ala Glu Asp Lys	
	1 5 10	
AAG TTT CTA GAA GTA GAA AGA GCT TTA AAA GAA GCG GCA TTA AAT CCT	99	
Lys Phe Leu Glu Val Glu Arg Ala Leu Lys Glu Ala Ala Leu Asn Pro		
	15 20 25	
CTA AGG CAT GCT ACT GAA GAA CTT TTT GGT GAT TTT TTA AAA ATG GAA	147	
Leu Arg His Ala Thr Glu Glu Leu Phe Gly Asp Phe Leu Lys Met Glu		
	30 35 40	
AAT ATC ACT GAG ATT TGT TAC AAT GGG AAC AAG GTT GTA TGG GTT TTA	195	
Asn Ile Thr Glu Ile Cys Tyr Asn Gly Asn Lys Val Val Trp Val Leu		
	45 50 55	
AAA AAT AAT GGC GAA TGG CAA CCA TTT GAT GTG AGA GAC AGG AAA GCC	243	
Lys Asn Asn Gly Glu Trp Gln Pro Phe Asp Val Arg Asp Arg Lys Ala		
	60 65 70 75	
TTT AGC CTG TCT CGT TTA ATG CAT TTT GCT CGG TGT TGT GCA AGT TTT	291	
Phe Ser Leu Ser Arg Leu Met His Phe Ala Arg Cys Cys Ala Ser Phe		
	80 85 90	

AAG AAA AAA ACA ATA GAC AAC TAT GAA AAT CCT ATT TTG AGC AGC AAT	339
Lys Lys Lys Thr Ile Asp Asn Tyr Glu Asn Pro Ile Leu Ser Ser Asn	
95 100 105	
TTA GCG AAT GGT GAA AGG GTG CAG ATT GTC CTT TCC CCT GTT ACA GTT	387
Leu Ala Asn Gly Glu Arg Val Gln Ile Val Leu Ser Pro Val Thr Val	
110 115 120	
AAT GAT GAA ACC ATT TCC ATA TCC ATA AGG ATA CCT AGC AAA ACA ACC	435
Asn Asp Glu Thr Ile Ser Ile Ser Ile Arg Ile Pro Ser Lys Thr Thr	
125 130 135	
TAT CCT CAT AGC TTC TTT GAA GAG CAA GGT TTT TAT AAT CTA CTA GAC	483
Tyr Pro His Ser Phe Phe Glu Glu Gln Gly Phe Tyr Asn Leu Leu Asp	
140 145 150 155	
AAC AAA GAA CAA GCG ATC AGC GCG ATT AAA GAT GGT ATT GCT ATT GGT	531
Asn Lys Glu Gln Ala Ile Ser Ala Ile Lys Asp Gly Ile Ala Ile Gly	
160 165 170	
AAA AAT GTG ATT GTT TGT GGT GGC ACA GGA AGC GGT AAA ACG ACT TAT	579
Lys Asn Val Ile Val Cys Gly Gly Thr Gly Ser Gly Lys Thr Thr Tyr	
175 180 185	
ATC AAA AGC ATC ATG GAG TTT ATC CCT AAA GAA GAA AGG ATC ATA TCC	627
Ile Lys Ser Ile Met Glu Phe Ile Pro Lys Glu Glu Arg Ile Ile Ser	
190 195 200	
ATT GAA GAC ACC GAA GAG ATT GTA TTC AAA CAC CAC AAA AAC TAC ACA	675
Ile Glu Asp Thr Glu Glu Ile Val Phe Lys His His Lys Asn Tyr Thr	
205 210 215	
CAG CTT TTT TTT GGT GGG AAT ATC ACC TCT GCT GAT TGC TTA AAG TCA	723
Gln Leu Phe Phe Gly Gly Asn Ile Thr Ser Ala Asp Cys Leu Lys Ser	
220 225 230 235	
TGT CTG AGA ATG CGG CCT GAT AGA ATC ATT TTA GGG GAA CTC AGA AGC	771
Cys Leu Arg Met Arg Pro Asp Arg Ile Ile Leu Gly Glu Leu Arg Ser	
240 245 250	
AGT GAG GCA TAC GAT TTT TAT AAT GTG CTT TGT AGC GGT CAT AAA GGC	819
Ser Glu Ala Tyr Asp Phe Tyr Asn Val Leu Cys Ser Gly His Lys Gly	
255 260 265	
ACA CTA ACC ACT CTG CAT GCA GGG AGC AGT GAA GAA GCG TTT ATC CGT	867
Thr Leu Thr Thr Leu His Ala Gly Ser Ser Glu Glu Ala Phe Ile Arg	
270 275 280	
TTG GCC AAC ATG AGT TCA TCT AAT AGC GCA GCA AGG AAT ATC AAG TTT	915
Leu Ala Asn Met Ser Ser Ser Asn Ser Ala Ala Arg Asn Ile Lys Phe	
285 290 295	
GAA AGT CTT ATT GAG GGC TTT AAA GAT TTG ATT GAT ATG ATT GTC CAT	963
Glu Ser Leu Ile Glu Gly Phe Lys Asp Leu Ile Asp Met Ile Val His	
300 305 310 315	
ATC AAC CAC CAC AAA CAG TGT GAT GAA TTT TAT ATC AAA CAC AGG TAGTA	1013
Ile Asn His His Lys Gln Cys Asp Glu Phe Tyr Ile Lys His Arg	

330

1037

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

-863-

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...5250
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

TAAATAAAAA	GCGTTAAGA	C	ATG	AAT	GAA	GAA	AAC	GAT	AAA	CTT	GAA	ACT	51
			Met	Asn	Glu	Glu	Asn	Asp	Lys	Leu	Glu	Thr	
			1				5					10	
TCT AAA AAA	GCC CAA CAA	GAT TCA	CCC CAA	GAT TTA	TCC AAT	GAA GAA							99
Ser Lys Lys	Ala Gln Gln	Asp Ser	Pro Gln	Asp Leu	Ser Asn	Glu Glu							
	15		20			25							
GCA ACA GAA	GCC AAT CAT	TTT GAA	AAT CTT	TTA AAA	GAA TCC	AAA GAA							147
Ala Thr Glu	Ala Asn His	Phe Glu	Asn Leu	Leu Lys	Glu Ser	Lys Glu							
	30		35			40							
AGC TCA GAT	CAT CAT CTT	GAC AAC	CCC ACA	GAA ACT	CAA ACC	CAT TTT							195
Ser Ser Asp	His His Leu	Asp Asn	Pro Thr	Glu Thr	Gln Thr	His Phe							
	45		50			55							
GAT GGA GAC	AAG TCA GAA	GAA ACC	CAA ACT	CAA ATG	GAT TCT	GAA GGT							243
Asp Gly Asp	Lys Ser Glu	Glu Thr	Gln Thr	Gln Met	Asp Ser	Glu Gly							
	60		65			70							
AAT GAA ACT	TCA GAA TCT	AGC AAT	GGC AGT	CTA GCA	GAC AAG	TTA TTC							291
Asn Glu Thr	Ser Glu Ser	Ser Asn	Gly Ser	Leu Ala	Asp Lys	Leu Phe							
	75		80			85							
AAA AAA GCC	AGA AAA TTA	GTT GAT	AAT AAA	AAA CCT	TTC ACT	CAG CAA							339
Lys Lys Ala	Arg Lys Leu	Val Asp	Asn Lys	Lys Lys	Pro Phe	Thr Gln							
	95		100			105							
AAG AAT TTA	GAT GAA GAA	ACC CAA	GAA CTG	AAC GAA	GAA GAC	GAT CAA							387
Lys Asn Leu	Asp Glu Glu	Thr Gln	Glu Leu	Asn Glu	Glu Asp	Asp Gln							
	110		115			120							
GAA AAT AAT	GAG TAT CAA	GAA GAA	ACT CAA	ACG GAC	TTA ATT	GAT GAT							435
Glu Asn Asn	Glu Tyr Gln	Glu Glu	Thr Gln	Thr Asp	Leu Ile	Asp Asp							
	125		130			135							
GAA ACT TCT	AAA AAA ACC	CAA CAA	CAT TCA	CCC CAA	GAT TTA	TCC AAT							483
Glu Thr Ser	Lys Lys Thr	Gln Gln	His Ser	Pro Gln	Asp Leu	Ser Asn							
	140		145			150							

GAA Glu 155	GAA Glu	GCA Ala	ACA Thr	GAA Glu	GCC Ala 160	AAT Asn	CAT His	TTT Phe	GAA Glu	AAT Asn 165	CTT Leu	TTA Leu	AAA Lys	GAA Glu	TCC Ser 170	531
AAA Lys	GAA Glu	AGC Ser	TCA Ser	GAT Asp 175	CAT His	CAT His	CTT Leu	GAC Asp	AAC Asn 180	CCC Pro	ACA Thr	GAA Glu	ACT Thr	CAA Gln 185	ACC Thr	579
AAT Asn	TTT Phe	GAT Asp	GGA Gly 190	GAC Asp	AAG Lys	TCA Ser	GAA Glu	GAA Glu 195	ACC Thr	CAA Gln	ACT Thr	CAA Gln	ATG Met 200	GAT Asp	TCT Ser	627
GAA Glu	GGT Gly	AAT Asn 205	GAA Glu	ACT Thr	TCA Ser	GAA Glu	TCT Ser 210	AGC Ser	AAT Asn	GGC Gly	AGT Ser	CTA Leu 215	GCA Ala	GAC Asp	AAG Lys	675
TTA Leu	TTC Phe 220	AAA Lys	AAA Lys	GCC Ala	AGA Arg	AAA Lys 225	TTA Leu	GTT Val	GAT Asp	AAT Asn	AAA Lys 230	AAA Lys	CCT Pro	TTC Phe	ACT Thr	723
CAG Gln 235	CAA Gln	AAG Lys	AAT Asn	TTA Leu	GAT Asp 240	GAA Glu	GAA Glu	ACC Thr	CAA Gln	GAA Glu 245	CTG Leu	AAC Asn	GAA Glu	GAA Glu	GAC Asp 250	771
GAT Asp	CAA Gln	GAA Glu	AAT Asn	AAT Asn 255	GAG Glu	TAT Tyr	CAA Gln	GAA Glu	GAA Glu 260	ACT Thr	CAA Gln	ACG Thr	GAC Asp	TTA Leu 265	ATT Ile	819
GAT Asp	GAT Asp	GAA Glu	ACT Thr 270	TCT Ser	AAA Lys	AAA Lys	ACC Thr	CAA Gln 275	CAA Gln	CAT His	TCA Ser	CCC Pro	CAA Gln 280	GAT Asp	TTA Leu	867
TCC Ser	AAT Asn	GAA Glu 285	GAA Glu	GCA Ala	ACA Thr	GAA Glu	GCC Ala 290	AAT Asn	CAT His	TTT Phe	GAA Glu 295	AAT Asn	CTT Leu	TTA Leu	AAA Lys	915
GAA Glu 300	TCC Ser	AAA Lys	GAA Glu	AGC Ser	TCA Ser	GAT Asp 305	CAT His	CAT His	CTT Leu	GAC Asp 310	AAC Asn	CCC Pro	ACA Thr	GAA Glu	ACT Thr	963
CAA Gln 315	ACC Thr	AAT Asn	TTT Phe	GAT Asp 320	GGA Gly	GAC Asp	AAG Lys	TCA Ser	GAA Glu	GAA Glu 325	ATA Ile	ACT Thr	GAC Asp	GAC Asp	TCT Ser 330	1011
AAC Asn	GAT Asp	CAA Gln	GAG Glu	ATT Ile 335	ATC Ile	AAA Lys	GGA Gly	AGC Ser	AAA Lys 340	AAG Lys	AAA Lys	TAT Tyr	ATT Ile	ATT Ile 345	GGT Gly	1059
GGC Gly	ATT Ile	GTA Val	GTC Val 350	GCT Ala	GTT Val	CTT Leu	ATC Ile	GTG Val 355	ATT Ile	ATT Ile	TTA Leu	TTT Phe	TCT Ser 360	AGA Arg	AGC Ser	1107
ATT Ile	TTT Phe	CAC His 365	TAC Tyr	TTC Phe	ATG Met	CCT Pro	TTG Leu 370	GAA Glu	GAT Asp	AAA Lys	AGC Ser	TCT Ser 375	CGT Arg	TTT Phe	AGC Ser	1155
AAA Lys	GAC Asp	AGG Arg	AAT Asn	CTT Leu	TAT Tyr	GTC Val	AAT Asn	GAT Asp	GAA Glu	ATC Ile	CAA Gln	ATA Ile	AGG Arg	CAA Gln	GAG Glu	1203

380	385	390	
TAT AAC CGA TTG CTG AAA GAA CGG AAT GAA AAA GGC AAT ATG ATC GAT Tyr Asn Arg Leu Leu Lys Glu Arg Asn Glu Lys Gly Asn Met Ile Asp 395 400 405 410			1251
AAG AAT CTT TTC TTC AAT GAC GAT CCC AAT AGA ACC TTA TAC AAC TAT Lys Asn Leu Phe Phe Asn Asp Asp Pro Asn Arg Thr Leu Tyr Asn Tyr 415 420 425			1299
TTG AAT ATT GCA GAA ATT GAG GAC AAA AAC CCG TTG AGA GCC TTT TAT Leu Asn Ile Ala Glu Ile Glu Asp Lys Asn Pro Leu Arg Ala Phe Tyr 430 435 440			1347
GAA TGT ATT AGT AAT GGT GGC AAC TAT GAA GAA TGT TTG AAG CTT ATC Glu Cys Ile Ser Asn Gly Gly Asn Tyr Glu Glu Cys Leu Lys Leu Ile 445 450 455			1395
AAA GAC AAA AAA CTT CAA GAT CAG ATG AAA AAG ACT CTA GAG GCT TAT Lys Asp Lys Lys Leu Gln Asp Gln Met Lys Lys Thr Leu Glu Ala Tyr 460 465 470			1443
AAC GAC TGC ATC AAA AAT GCC AAA ACT GAA GAA GAA AGG ATC AAG TGT Asn Asp Cys Ile Lys Asn Ala Lys Thr Glu Glu Glu Arg Ile Lys Cys 475 480 485			1491
TTA GAT TTA ATC AAA GAT GAA AAC CTA AAA AAA AGC TTA CTG AAC CAA Leu Asp Leu Ile Lys Asp Glu Asn Leu Lys Lys Ser Leu Leu Asn Gln 495 500 505			1539
CAA AAA GTT CAA GTG GCG CTA GAT TGT TTG AAA AAC GCT AAA ACC GAT Gln Lys Val Gln Val Ala Leu Asp Cys Leu Lys Asn Ala Lys Thr Asp 510 515 520			1587
GAA GAA CGA AAC GAG TGC CTA AAA CTC ATA AAT GAC CCT GAG ATT AGA Glu Glu Arg Asn Glu Cys Leu Lys Leu Ile Asn Asp Pro Glu Ile Arg 525 530 535			1635
GAG AAA TTC CGT AAG GAA TTA GAG CTT CAA AAA GAG CTT CAA GAG TAT Glu Lys Phe Arg Lys Glu Leu Glu Leu Gln Lys Glu Leu Gln Glu Tyr 540 545 550			1683
AAG GAT TGT ATC AAA AAC GCC AAA ACA GAA GCT GAG AAA AAC AAA TGC Lys Asp Cys Ile Lys Asn Ala Lys Thr Glu Ala Glu Lys Asn Lys Cys 555 560 565 570			1731
TTG AAA GGC TTG TCT AAA GAA GCT ATA GAG AGA TTG AAA CAG CAA GCG Leu Lys Gly Leu Ser Lys Glu Ala Ile Glu Arg Leu Lys Gln Gln Ala 575 580 585			1779
CTA GAT TGT TTG AAA AAC GCT AAA ACC GAT GAA GAA CGA AAC GAG TGC Leu Asp Cys Leu Lys Asn Ala Lys Thr Asp Glu Glu Arg Asn Glu Cys 590 595 600			1827
TTG AAA AAT ATT CCC CAA GAC TTG CAA AAA GAA CTA TTA GCT GAT ATG Leu Lys Asn Ile Pro Gln Asp Leu Gln Lys Glu Leu Ala Asp Met 605 610 615			1875

845	850	855	
ACC CCT GAA GCG AGA AAA CTT TTA GAA GAA GCT AAA AAA AGC GTT AAG Thr Pro Glu Ala Arg Lys Leu Leu Glu Glu Ala Lys Lys Ser Val Lys 860 865 870			2643
GCT TAY TTG GAT TGC GTA TCT CAA GCC AAA ACT GAA GCT GAG AAA AAA Ala Xaa Leu Asp Cys Val Ser Gln Ala Lys Thr Glu Ala Glu Lys Lys 875 880 885 890			2691
GAA TGC GAG AAA TTA CTC ACC CCT GAA GCG AGA AAA CTC TTA GAA GAA Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Glu 895 900 905			2739
GCT AAA GAG AGC GTT AAA GCT TAT AAA GAC TGC GTA TCA AAA GCT AGG Ala Lys Glu Ser Val Lys Ala Tyr Lys Asp Cys Val Ser Lys Ala Arg 910 915 920			2787
AAT GAA AAA GAG AAA AAA GAA TGC GAG AAA TTA CTC ACG CCT GAA GCG Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala 925 930 935			2835
AAA AAA CTT TTA GAG CAA CAA GTG CTA GAT TGT TTG AAA AAC GCT AAA Lys Lys Leu Leu Glu Gln Val Leu Asp Cys Leu Lys Asn Ala Lys 940 945 950			2883
ACC GAA GCT GAT AAA AAA AGG TGT GTC AAA GAT CTC CCT AAA GAC TTG Thr Glu Ala Asp Lys Lys Arg Cys Val Lys Asp Leu Pro Lys Asp Leu 955 960 965 970			2931
CAG AAA AAG GTT TTA GCT AAA GAG AGC GTT AAG GCT TAT TTG GAC TGC Gln Lys Lys Val Leu Ala Lys Glu Ser Val Lys Ala Tyr Leu Asp Cys 975 980 985			2979
GTA TCA AGA GCT AGG AAT GAA AAA GAG AAA AAA GAA TGC GAG AAA TTG Val Ser Arg Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu 990 995 1000			3027
CTC ACC CCT GAA GCG AAA AAA CTT TTA GAA GAA GCC AAA GAG AGT CTT Leu Thr Pro Glu Ala Lys Lys Leu Leu Glu Glu Ala Lys Glu Ser Leu 1005 1010 1015			3075
AAA GCT TAT AAA GAC TGC CTC TCT CAA GCT AGA AAT GAA GAA GAA AGG Lys Ala Tyr Lys Asp Cys Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg 1020 1025 1030			3123
AGA GCT TGC GAG AAA CTA CTC ACG CCT GAA GCG AGA AAA CTC TTA GAG Arg Ala Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu 1035 1040 1045 1050			3171
CAA GAA GTT AAG AAA AGC ATT AAG GCT TAT TTG GAC TGC GTA TCA AGA Gln Glu Val Lys Lys Ser Ile Lys Ala Tyr Leu Asp Cys Val Ser Arg 1055 1060 1065			3219
GCT AGG AAT GAA AAA GAG AAA AAA GAA TGC GAG AAA TTA CTC ACG CCT Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro 1070 1075 1080			3267

GAA GCG AGA AAA TTT TTA GCG AAG CAA GTG CTA AAT TGT TTG GAA AAA Glu Ala Arg Lys Phe Leu Ala Lys Gln Val Leu Asn Cys Leu Glu Lys 1085 1090 1095	3315
GCT GGA AAT GAA GAA GAA AGA AAA GCA TGT CTT AAA AAT CTC CCT AAA Ala Gly Asn Glu Glu Glu Arg Lys Ala Cys Leu Lys Asn Leu Pro Lys 1100 1105 1110	3363
GAC TTA CAG GAA AAT ATT TTA GCT AAA GAG AGT CTT AAA GCT TAT AAA Asp Leu Gln Glu Asn Ile Leu Ala Lys Glu Ser Leu Lys Ala Tyr Lys 1115 1120 1125 1130	3411
GAC TGC CTC TCT CAA GCT AGA AAT GAA GAA GAA AGG AGA GCT TGC GAG Asp Cys Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg Arg Ala Cys Glu 1135 1140 1145	3459
AAA CTA CTC ACG CCT GAA GCG AGA AAA CTC TTA GAG CAA GAA GTT AAG Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Gln Glu Val Lys 1150 1155 1160	3507
AAA AGC GTT AAG GCT TAT TTG GAC TGC GTA TCA AGA GCT AGG AAT GAA Lys Ser Val Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn Glu 1165 1170 1175	3555
AAA GAG AAA AAA GAA TGC GAG AAA TTA CTC ACG CCT GAA GCG AGA AAA Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys 1180 1185 1190	3603
TTT TTA GCG AAA GAA CTC CAA CAA AAA GAT AAA GCG ATC AAA GAT TGC Phe Leu Ala Lys Glu Leu Gln Gln Lys Asp Lys Ala Ile Lys Asp Cys 1195 1200 1205 1210	3651
TTG AAA AAC GCC GAT CCT AAC GAC AGA GCG GCT ATC ATG AAG TGT TTG Leu Lys Asn Ala Asp Pro Asn Asp Arg Ala Ala Ile Met Lys Cys Leu 1215 1220 1225	3699
GAT GGT TTG AGC GAT GAA GAG AAG CTC AAA TAC CTG CAA GAA GCT AGA Asp Gly Leu Ser Asp Glu Glu Lys Leu Lys Tyr Leu Gln Glu Ala Arg 1230 1235 1240	3747
GAA AAG GCT GTT GCG GAT TGT TTG GCT ATG GCT AAA ACC GAT GAA GAA Glu Lys Ala Val Ala Asp Cys Leu Ala Met Ala Lys Thr Asp Glu Glu 1245 1250 1255	3795
AAA AGG AAA TGC CAA AAC CTT TAT AGC GAT TTG ATC CAA GAA ATC CAA Lys Arg Lys Cys Gln Asn Leu Tyr Ser Asp Leu Ile Gln Glu Ile Gln 1260 1265 1270	3843
AAT AAA AGG ACA CAA AAC AAA CAA AAT CAA TTG AGT AAA ACA GAA AGG Asn Lys Arg Thr Gln Asn Lys Gln Asn Gln Leu Ser Lys Thr Glu Arg 1275 1280 1285 1290	3891
TTG CAT CAA GCA AGC GAG TGC TTG GAT AAC TTA GAT GAC CCT ACT GAT Leu His Gln Ala Ser Glu Cys Leu Asp Asn Leu Asp Asp Pro Thr Asp 1295 1300 1305	3939
CAA GAG GCC ATA GAG CAA TGT TTA GAG GGC TTG AGC GAT AGT GAA AGG Gln Glu Ala Ile Glu Gln Cys Leu Glu Gly Leu Ser Asp Ser Glu Arg	3987

1310										1315					1320					
GCG	CTA	ATT	CTA	GGA	ATT	AAA	CGA	CAA	GCT	GAT	GAA	GTG	GAT	CTG	ATT	4035				
Ala	Leu	Ile	Leu	Gly	Ile	Lys	Arg	Gln	Ala	Asp	Glu	Val	Asp	Leu	Ile					
1325					1330					1335										
TAT	AGC	GAT	CTA	AGA	AAC	CGT	AAA	ACC	TTT	GAT	AAC	ATG	GCG	GCT	AAA	4083				
Tyr	Ser	Asp	Leu	Arg	Asn	Arg	Lys	Thr	Phe	Asp	Asn	Met	Ala	Ala	Lys					
1340					1345					1350										
GGT	TAT	CCA	TTG	TTA	CCA	ATG	GAT	TTC	AAA	AAT	GGC	GGC	GAT	ATT	GCC	4131				
Gly	Tyr	Pro	Leu	Leu	Pro	Met	Asp	Phe	Lys	Asn	Gly	Gly	Asp	Ile	Ala					
1355					1360					1365					1370					
ACT	ATT	AAC	GCC	ACT	AAT	GTT	GAT	GCG	GAC	AAA	ATA	GCT	AGC	GAT	AAT	4179				
Thr	Ile	Asn	Ala	Thr	Asn	Val	Asp	Ala	Asp	Lys	Ile	Ala	Ser	Asp	Asn					
1375					1380					1385										
CCT	ATT	TAT	GCT	TCC	ATA	GAG	CCT	GAT	ATT	GCC	AAG	CAA	TAC	GAA	ACA	4227				
Pro	Ile	Tyr	Ala	Ser	Ile	Glu	Pro	Asp	Ile	Ala	Lys	Gln	Tyr	Glu	Thr					
1390					1395					1400										
GAA	AAA	ACC	ATT	AAG	GAT	AAG	AAT	TTA	GAA	GCT	AAA	TTA	GCT	AAG	GCT	4275				
Glu	Lys	Thr	Ile	Lys	Asp	Lys	Asn	Leu	Glu	Ala	Lys	Leu	Ala	Lys	Ala					
1405					1410					1415										
TTA	GGT	GGC	AAT	AAA	AAA	GAT	GAC	GAT	AAA	GAA	AAA	AGT	AAA	AAA	TCC	4323				
Leu	Gly	Gly	Asn	Lys	Lys	Asp	Asp	Asp	Lys	Glu	Lys	Ser	Lys	Lys	Ser					
1420					1425					1430										
ACA	GCA	GAA	GCT	AAA	GCA	GAA	AAC	AAT	AAG	ATA	GAC	AAA	GAT	GTC	GCA	4371				
Thr	Ala	Glu	Ala	Lys	Ala	Glu	Asn	Asn	Lys	Ile	Asp	Lys	Asp	Val	Ala					
1435					1440					1445					1450					
GAA	ACT	GCC	AAG	AAT	ATC	AGT	GAA	ATC	GCT	CTT	AAG	AAC	AAA	AAA	GAA	4419				
Glu	Thr	Ala	Lys	Asn	Ile	Ser	Glu	Ile	Ala	Leu	Lys	Asn	Lys	Lys	Glu					
1455					1460					1465										
AAG	AGT	GGG	GAA	TTT	GTA	GAT	GAA	AAT	GGT	AAT	CCC	ATT	GAT	GAC	AAA	4467				
Lys	Ser	Gly	Glu	Phe	Val	Asp	Glu	Asn	Gly	Asn	Pro	Ile	Asp	Asp	Lys					
1470					1475					1480										
AAG	AAA	GCA	GAA	AAA	CAA	GAT	GAA	ACA	AGC	CCT	GTC	AAA	CAG	GCC	TTT	4515				
Lys	Lys	Ala	Glu	Lys	Gln	Asp	Glu	Thr	Ser	Pro	Val	Lys	Gln	Ala	Phe					
1485					1490					1495										
ATA	GGC	AAG	AGT	GAT	CCC	ACA	TTT	GTT	TTA	GCG	CAA	TAC	ACC	CCC	ATT	4563				
Ile	Gly	Lys	Ser	Asp	Pro	Thr	Phe	Val	Leu	Ala	Gln	Tyr	Thr	Pro	Ile					
1500					1505					1510										
GAA	ATC	ACT	CTG	ACT	TCT	AAA	GTA	GAT	GCC	ACT	CTC	ACA	GGT	ATA	GTG	4611				
Glu	Ile	Thr	Leu	Thr	Ser	Lys	Val	Asp	Ala	Thr	Leu	Thr	Gly	Ile	Val					
1515					1520					1525					1530					
AGT	GGG	GTT	GTA	GCC	AAA	GAT	GTA	TGG	AAC	ATG	AAC	GGC	ACT	ATG	ATC	4659				
Ser	Gly	Val	Val	Ala	Lys	Asp	Val	Trp	Asn	Met	Asn	Gly	Thr	Met	Ile					
1535					1540					1545										

TTA TTA GAC AAA GGC ACT AAG GTG TAT GGG AAT TAT CAA AGC GTG AAA	4707
Leu Leu Asp Lys Gly Thr Lys Val Tyr Gly Asn Tyr Gln Ser Val Lys	
1550 1555 1560	
GGT GGC ACA CCC ATT ATG ACA CGC TTA ATG ATA GTC TTT ACT AAA GCC	4755
Gly Gly Thr Pro Ile Met Thr Arg Leu Met Ile Val Phe Thr Lys Ala	
1565 1570 1575	
ATT ACG CCT GAT GGT GTG ATA ATA CCT CTA GCA AAC GCT CAA GCA GCA	4803
Ile Thr Pro Asp Gly Val Ile Ile Pro Leu Ala Asn Ala Gln Ala Ala	
1580 1585 1590	
GGC ATG TTG GGT GAA GCA GGG GTA GAT GGC TAT GTG AAT AAT CAC TTT	4851
Gly Met Leu Gly Glu Ala Gly Val Asp Gly Tyr Val Asn Asn His Phe	
1595 1600 1605 1610	
ATG AAG CGC ATA GGC TTT GCT GTG ATA GCA AGC GTG GTT AAT AGC TTC	4899
Met Lys Arg Ile Gly Phe Ala Val Ile Ala Ser Val Val Asn Ser Phe	
1615 1620 1625	
TTG CAA ACT GCG CCT ATC ATA GCT CTA GAT AAA CTC ATA GGC CTT GGC	4947
Leu Gln Thr Ala Pro Ile Ile Ala Leu Asp Lys Leu Ile Gly Leu Gly	
1630 1635 1640	
AAA GGT AGA AGT GAA AGG ACA CCT GAA TTT AAT TAC GCT TTG GGT CAA	4995
Lys Gly Arg Ser Glu Arg Thr Pro Glu Phe Asn Tyr Ala Leu Gly Gln	
1645 1650 1655	
GCT ATC AAT GGT AGC ATG CAA AGT TCA GCT CAG ATG TCT AAT CAA ATT	5043
Ala Ile Asn Gly Ser Met Gln Ser Ser Ala Gln Met Ser Asn Gln Ile	
1660 1665 1670	
CTA GGG CAA CTG ATG AAT ATC CCC CCA AGT TTT TAC AAA AAC GAG GGC	5091
Leu Gly Gln Leu Met Asn Ile Pro Pro Ser Phe Tyr Lys Asn Glu Gly	
1675 1680 1685 1690	
GAT AGT ATT AAG ATT CTC ACA ATG GAC GAT ATT GAT TTT AGC GGT GTG	5139
Asp Ser Ile Lys Ile Leu Thr Met Asp Asp Ile Asp Phe Ser Gly Val	
1695 1700 1705	
TAT GAT GTT AAA ATT ACT AAC AAA TCT GTG GTA GAT GAA ATT ATC AAA	5187
Tyr Asp Val Lys Ile Thr Asn Lys Ser Val Val Asp Glu Ile Ile Lys	
1710 1715 1720	
CAA AGC ACC AAA ACT TTG TCT AGA GAA CAT GAA GAA ATC ACC ACA AGC	5235
Gln Ser Thr Lys Thr Leu Ser Arg Glu His Glu Glu Ile Thr Thr Ser	
1725 1730 1735	
CCC AAA GGT GGC AAT TAATTCAAGA GAAAGGATAA AATATATTCA TGTTACTAAA C	5291
Pro Lys Gly Gly Asn	
1740	
TCGGTTCTTT ACAAAATAAA AGACAAAACC AACAAACAGGC TCT	5334

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1743 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

Met	Asn	Glu	Glu	Asn	Asp	Lys	Leu	Glu	Thr	Ser	Lys	Lys	Ala	Gln	Gln
1				5				10						15	
Asp	Ser	Pro	Gln	Asp	Leu	Ser	Asn	Glu	Glu	Ala	Thr	Glu	Ala	Asn	His
			20					25					30		
Phe	Glu	Asn	Leu	Leu	Lys	Glu	Ser	Lys	Glu	Ser	Ser	Asp	His	His	Leu
		35					40					45			
Asp	Asn	Pro	Thr	Glu	Thr	Gln	Thr	His	Phe	Asp	Gly	Asp	Lys	Ser	Glu
	50					55				60					
Glu	Thr	Gln	Thr	Gln	Met	Asp	Ser	Glu	Gly	Asn	Glu	Thr	Ser	Glu	Ser
65					70				75					80	
Ser	Asn	Gly	Ser	Leu	Ala	Asp	Lys	Leu	Phe	Lys	Lys	Ala	Arg	Lys	Leu
				85				90					95		
Val	Asp	Asn	Lys	Lys	Pro	Phe	Thr	Gln	Gln	Lys	Asn	Leu	Asp	Glu	Glu
			100					105					110		
Thr	Gln	Glu	Leu	Asn	Glu	Glu	Asp	Gln	Glu	Asn	Asn	Glu	Tyr	Gln	
		115					120					125			
Glu	Glu	Thr	Gln	Thr	Asp	Leu	Ile	Asp	Asp	Glu	Thr	Ser	Lys	Lys	Thr
		130				135					140				
Gln	Gln	His	Ser	Pro	Gln	Asp	Leu	Ser	Asn	Glu	Glu	Ala	Thr	Glu	Ala
145					150					155				160	
Asn	His	Phe	Glu	Asn	Leu	Leu	Lys	Glu	Ser	Lys	Glu	Ser	Ser	Asp	His
				165					170					175	
His	Leu	Asp	Asn	Pro	Thr	Glu	Thr	Gln	Thr	Asn	Phe	Asp	Gly	Asp	Lys
			180					185					190		
Ser	Glu	Glu	Thr	Gln	Thr	Gln	Met	Asp	Ser	Glu	Gly	Asn	Glu	Thr	Ser
		195				200						205			
Glu	Ser	Ser	Asn	Gly	Ser	Leu	Ala	Asp	Lys	Leu	Phe	Lys	Lys	Ala	Arg
		210				215					220				
Lys	Leu	Val	Asp	Asn	Lys	Lys	Pro	Phe	Thr	Gln	Gln	Lys	Asn	Leu	Asp
225					230					235				240	
Glu	Glu	Thr	Gln	Glu	Leu	Asn	Glu	Glu	Asp	Asp	Gln	Glu	Asn	Asn	Glu
				245					250					255	
Tyr	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Leu	Ile	Asp	Asp	Glu	Thr	Ser	Lys
		260				265							270		
Lys	Thr	Gln	Gln	His	Ser	Pro	Gln	Asp	Leu	Ser	Asn	Glu	Glu	Ala	Thr
		275				280						285			
Glu	Ala	Asn	His	Phe	Glu	Asn	Leu	Leu	Lys	Glu	Ser	Lys	Glu	Ser	Ser
	290					295					300				
Asp	His	His	Leu	Asp	Asn	Pro	Thr	Glu	Thr	Gln	Thr	Asn	Phe	Asp	Gly
305					310					315					320
Asp	Lys	Ser	Glu	Glu	Ile	Thr	Asp	Asp	Ser	Asn	Asp	Gln	Glu	Ile	Ile
				325					330					335	
Lys	Gly	Ser	Lys	Lys	Lys	Tyr	Ile	Ile	Gly	Gly	Ile	Val	Val	Ala	Val
			340					345					350		
Leu	Ile	Val	Ile	Ile	Leu	Phe	Ser	Arg	Ser	Ile	Phe	His	Tyr	Phe	Met
		355				360						365			
Pro	Leu	Glu	Asp	Lys	Ser	Ser	Arg	Phe	Ser	Lys	Asp	Arg	Asn	Leu	Tyr
	370					375					380				
Val	Asn	Asp	Glu	Ile	Gln	Ile	Arg	Gln	Glu	Tyr	Asn	Arg	Leu	Leu	Lys
385					390					395					400

Leu	Leu	Glu	Glu	Ala	Lys	Lys	Ser	Val	Lys	Ala	Xaa	Leu	Asp	Cys	Val	865	870	875	880
Ser	Gln	Ala	Lys	Thr	Glu	Ala	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	885	890		895
Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Glu	Ala	Lys	Glu	Ser	Val	Lys	900	905		910
Ala	Tyr	Lys	Asp	Cys	Val	Ser	Lys	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Lys	915	920		925
Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys	Lys	Leu	Leu	Glu	Gln	930	935		940
Gln	Val	Leu	Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Glu	Ala	Asp	Lys	Lys	945	950		955
Arg	Cys	Val	Lys	Asp	Leu	Pro	Lys	Asp	Leu	Gln	Lys	Lys	Val	Leu	Ala	965	970		975
Lys	Glu	Ser	Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg	Asn	980	985		990
Glu	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys	995	1000		1005
Lys	Leu	Leu	Glu	Glu	Ala	Lys	Glu	Ser	Leu	Lys	Ala	Tyr	Lys	Asp	Cys	1010	1015		1020
Leu	Ser	Gln	Ala	Arg	Asn	Glu	Glu	Glu	Arg	Arg	Ala	Cys	Glu	Lys	Leu	1025	1030		1035
Leu	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Gln	Glu	Val	Lys	Lys	Ser	1045	1050		1055
Ile	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg	Asn	Glu	Lys	Glu	1060	1065		1070
Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Phe	Leu	1075	1080		1085
Ala	Lys	Gln	Val	Leu	Asn	Cys	Leu	Glu	Lys	Ala	Gly	Asn	Glu	Glu	Glu	1090	1095		1100
Arg	Lys	Ala	Cys	Leu	Lys	Asn	Leu	Pro	Lys	Asp	Leu	Gln	Glu	Asn	Ile	1105	1110		1115
Leu	Ala	Lys	Glu	Ser	Leu	Lys	Ala	Tyr	Lys	Asp	Cys	Leu	Ser	Gln	Ala	1125	1130		1135
Arg	Asn	Glu	Glu	Glu	Arg	Arg	Ala	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	1140	1145		1150
Ala	Arg	Lys	Leu	Leu	Glu	Gln	Glu	Val	Lys	Lys	Ser	Val	Lys	Ala	Tyr	1155	1160		1165
Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys	1170	1175		1180
Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Phe	Leu	Ala	Lys	Glu	Leu	1185	1190		1195
Gln	Gln	Lys	Asp	Lys	Ala	Ile	Lys	Asp	Cys	Leu	Lys	Asn	Ala	Asp	Pro	1205	1210		1215
Asn	Asp	Arg	Ala	Ala	Ile	Met	Lys	Cys	Leu	Asp	Gly	Leu	Ser	Asp	Glu	1220	1225		1230
Glu	Lys	Leu	Lys	Tyr	Leu	Gln	Glu	Ala	Arg	Glu	Lys	Ala	Val	Ala	Asp	1235	1240		1245
Cys	Leu	Ala	Met	Ala	Lys	Thr	Asp	Glu	Glu	Lys	Arg	Lys	Cys	Gln	Asn	1250	1255		1260
Leu	Tyr	Ser	Asp	Leu	Ile	Gln	Glu	Ile	Gln	Asn	Lys	Arg	Thr	Gln	Asn	1265	1270		1275
Lys	Gln	Asn	Gln	Leu	Ser	Lys	Thr	Glu	Arg	Leu	His	Gln	Ala	Ser	Glu	1285	1290		1295
Cys	Leu	Asp	Asn	Leu	Asp	Asp	Pro	Thr	Asp	Gln	Glu	Ala	Ile	Glu	Gln	1300	1305		1310
Cys	Leu	Glu	Gly	Leu	Ser	Asp	Ser	Glu	Arg	Ala	Leu	Ile	Leu	Gly	Ile	1315	1320		1325

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 22...825
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

AACAAATAAA GGAGTATTAA A ATG AAA CAA AGT TTG CGC GAA CAA AAA TTA	51
Met Lys Gln Ser Leu Arg Glu Gln Lys Leu	
1 5 10	
TTG AAA ATT TTA GAA AAT GAT GTC TTG ACG ATT TTG GAT AGT TTT TCT	99
Leu Lys Ile Leu Glu Asn Asp Val Leu Thr Ile Leu Asp Ser Phe Ser	
15 20 25	
AAT TAT CTT TTT GAA CTG AGA GAA GAG TTG GAC TTC ATA GAA GAA GAA	147
Asn Tyr Leu Phe Glu Leu Arg Glu Glu Leu Asp Phe Ile Glu Glu Glu	
30 35 40	
ATG GAA GGT GAA ATC ACC GAA CAA AAC CTT ACC GCT CTT TAT GAT TTT	195
Met Glu Gly Glu Ile Thr Glu Gln Asn Leu Thr Ala Leu Tyr Asp Phe	
45 50 55	
TCT AAT TTC TTA GAA GAC CAT GTC AAT GTA TTT TAT GAG AAT GTT TTG	243
Ser Asn Phe Leu Glu Asp His Val Asn Val Phe Tyr Glu Asn Val Leu	
60 65 70	
AAT ATA GAT GAT GTC AAA ACA GAA CAC CTT TAT TCA GGT CTC ATA GAT	291
Asn Ile Asp Asp Val Lys Thr Glu His Leu Tyr Ser Gly Leu Ile Asp	
75 80 85 90	
AGT CTT AAC GCT AAT CTT CAC TTT GTC AAG TCA TTT CTC AGT AAT CAG	339
Ser Leu Asn Ala Asn Leu His Phe Val Lys Ser Phe Leu Ser Asn Gln	
95 100 105	
GAT TTA GAC TTC CGC TTT TTT AAG GAA ATA AAC GAT GGG CAA GAT CCC	387
Asp Leu Asp Phe Arg Phe Phe Lys Glu Ile Asn Asp Gly Gln Asp Pro	
110 115 120	
CAA AAA ACA TTA TCA AGA TTA ATT CCT CTT CAA AGT GGG AAA AAT GAT	435
Gln Lys Thr Leu Ser Arg Leu Ile Pro Leu Gln Ser Gly Lys Asn Asp	
125 130 135	
GCA AGC TCG TTT AAA GCC AAT AAT TCT TTT GTT TCA TTA GTT TAT GTT	483
Ala Ser Ser Phe Lys Ala Asn Asn Ser Phe Val Ser Leu Val Tyr Val	
140 145 150	
TAT GTT TAC TTC ATG CTA GAA ACT ATC ATG CAG TCG TAT AGG ATT CTC	531
Tyr Val Tyr Phe Met Leu Glu Thr Ile Met Gln Ser Tyr Arg Ile Leu	
155 160 165 170	
AGA TTG CTA GAA AAA CCT ATC AAT AAC AAC ATA AGC GAG GAC ATG CAG	579

Arg	Leu	Leu	Glu	Lys	Pro	Ile	Asn	Asn	Asn	Ile	Ser	Glu	Asp	Met	Gln		
				175					180					185			
AAC	GAT	ATA	GAG	AAT	TTT	TTT	GTT	CAA	GCG	AAT	TTT	TTA	GAA	TAC	TAT	627	
Asn	Asp	Ile	Glu	Asn	Phe	Phe	Val	Gln	Ala	Asn	Phe	Leu	Glu	Tyr	Tyr		
			190					195					200				
GTT	CAG	AAC	AAA	ATA	TAC	CCA	ACC	AAT	CAT	GCC	TAT	GAC	TTC	ACG	CAT	675	
Val	Gln	Asn	Lys	Ile	Tyr	Pro	Thr	Asn	His	Ala	Tyr	Asp	Phe	Thr	His		
			205				210					215					
TTG	ATC	ATG	GAC	TCC	ATT	ATT	CCT	AAT	TGG	ATT	CAA	ACT	GAT	ATG	AGC	723	
Leu	Ile	Met	Asp	Ser	Ile	Ile	Pro	Asn	Trp	Ile	Gln	Thr	Asp	Met	Ser		
		220				225					230						
GTT	GAA	GCT	AAA	AAG	AAA	GAG	CTT	TTT	GAA	AAA	TAT	TTT	CAA	AAC	ATT	771	
Val	Glu	Ala	Lys	Lys	Lys	Glu	Leu	Phe	Glu	Lys	Tyr	Phe	Gln	Asn	Ile		
					240					245					250		
GAT	GAA	GTA	ACA	AAC	AAA	ATG	CTC	GAT	CAA	AAA	ANT	CAA	AAC	AAA	AGT	819	
Asp	Glu	Val	Thr	Asn	Lys	Met	Leu	Asp	Gln	Lys	Xaa	Gln	Asn	Lys	Ser		
				255					260					265			
AAC	GAT	TGAGTGGCGT	TAATGCGCTA	GAATAGTGCT	AAAAATAAGA	ATAAAGGAGT	CA	877									
Asn	Asp																

877

(2) INFORMATION FOR SEQ ID NO:626:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 268 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

Met	Lys	Gln	Ser	Leu	Arg	Glu	Gln	Lys	Leu	Leu	Lys	Ile	Leu	Glu	Asn		
1				5					10					15			
Asp	Val	Leu	Thr	Ile	Leu	Asp	Ser	Phe	Ser	Asn	Tyr	Leu	Phe	Glu	Leu		
			20					25					30				
Arg	Glu	Glu	Leu	Asp	Phe	Ile	Glu	Glu	Glu	Met	Glu	Gly	Glu	Ile	Thr		
			35				40					45					
Glu	Gln	Asn	Leu	Thr	Ala	Leu	Tyr	Asp	Phe	Ser	Asn	Phe	Leu	Glu	Asp		
		50				55					60						
His	Val	Asn	Val	Phe	Tyr	Glu	Asn	Val	Leu	Asn	Ile	Asp	Asp	Val	Lys		
				70						75				80			
Thr	Glu	His	Leu	Tyr	Ser	Gly	Leu	Ile	Asp	Ser	Leu	Asn	Ala	Asn	Leu		
				85					90					95			
His	Phe	Val	Lys	Ser	Phe	Leu	Ser	Asn	Gln	Asp	Leu	Asp	Phe	Arg	Phe		
			100					105					110				
Phe	Lys	Glu	Ile	Asn	Asp	Gly	Gln	Asp	Pro	Gln	Lys	Thr	Leu	Ser	Arg		
		115				120					125						
Leu	Ile	Pro	Leu	Gln	Ser	Gly	Lys	Asn	Asp	Ala	Ser	Ser	Phe	Lys	Ala		

130	135	140
Asn Asn Ser Phe Val	Ser Leu Val Tyr Val	Tyr Val Tyr Phe Met Leu
145	150	155
Glu Thr Ile Met Gln	Ser Tyr Arg Ile Leu Arg	Leu Leu Glu Lys Pro
165	170	175
Ile Asn Asn Asn Ile	Ser Glu Asp Met Gln Asn Asp	Ile Glu Asn Phe
180	185	190
Phe Val Gln Ala Asn	Phe Leu Glu Tyr Tyr Val	Gln Asn Lys Ile Tyr
195	200	205
Pro Thr Asn His Ala	Tyr Asp Phe Thr His Leu	Ile Met Asp Ser Ile
210	215	220
Ile Pro Asn Trp Ile	Gln Thr Asp Met Ser Val	Glu Ala Lys Lys Lys
225	230	235
Glu Leu Phe Glu Lys	Tyr Phe Gln Asn Ile Asp	Glu Val Thr Asn Lys
245	250	255
Met Leu Asp Gln Lys	Xaa Gln Asn Lys Ser	Asn Asp
260	265	

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...706
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

AAAAAATCAA TAAAGGGGT TTAGC	ATG CAA GCA GTA ATT TAT GGC AAG CAA	52
	Met Gln Ala Val Ile Tyr Gly Lys Gln	
	1 5	
GTG ATT ATG CAC CTT CTA AAC TCT CAT CAA GAA AAA TTG CAA GAA ATC		100
Val Ile Met His Leu Leu Asn Ser His Gln Glu Lys Leu Gln Glu Ile		
10 15 20 25		
TAT CTT TCT AAA GAA ATA GAC AAG AAA CTT TTT TTC GCG CTC AAA AAA		148
Tyr Leu Ser Lys Glu Ile Asp Lys Lys Leu Phe Phe Ala Leu Lys Lys		
30 35 40		
GCA TGC CCT AAT ATC ATC AAA GTG GAT AAT AAA AAA GCG CAA AGC TTG		196
Ala Cys Pro Asn Ile Ile Lys Val Asp Asn Lys Lys Ala Gln Ser Leu		
45 50 55		
GCT AAG GGG GGG AAT CAT CAA GGG GTT TTG GCT AAG GTG GAA CTG CCC		244
Ala Lys Gly Gly Asn His Gln Gly Val Leu Ala Lys Val Glu Leu Pro		
60 65 70		
TTA GCG GTT TCT TTA AAA GAG GTT AAA AAA GCT CAA AAA CTT TTG GTG		292
Leu Ala Val Ser Leu Lys Glu Val Lys Lys Ala Gln Lys Leu Leu Val		

75	80	85	
CTT TGC GGG ATT ACG GAT GTG GGG AAT ATT GGA GGT ATT TTT AGG AGC			340
Leu Cys Gly Ile Thr Asp Val Gly Asn Ile Gly Gly Ile Phe Arg Ser			
90	95	100	105
GCG TAT TGC TTA GGA ATG GGT GGC GTT ATT TTA GAT TTT GCT AAA GAA			388
Ala Tyr Cys Leu Gly Met Gly Gly Val Ile Leu Asp Phe Ala Lys Glu			
	110	115	120
TTG GCT TAT GAG GGG ATT GTG CGA TCC AGC TTG GGG CTT ATG TAT GAT			436
Leu Ala Tyr Glu Gly Ile Val Arg Ser Ser Leu Gly Leu Met Tyr Asp			
	125	130	135
TTG CCT TTT AGC GTT ATG CCT AAC ACG CTG GAT TTA ATC AAT GAA TTG			484
Leu Pro Phe Ser Val Met Pro Asn Thr Leu Asp Leu Ile Asn Glu Leu			
	140	145	150
AAA ACG AGC GGG TTT TTA TGT TTG GGC GCG AGC ATG CAA GGC TCT AGT			532
Lys Thr Ser Gly Phe Leu Cys Leu Gly Ala Ser Met Gln Gly Ser Ser			
	155	160	165
CAA ATA GAA AAT CTA TCC TTA AAA AAA TGC GCT CTT TTT TTG GGG AGC			580
Gln Ile Glu Asn Leu Ser Leu Lys Lys Cys Ala Leu Phe Leu Gly Ser			
	170	175	185
GAG CAT GAG GGG TTG TCT AAA AAA ATC CTT GCT AAA ATG GAT ACT ATA			628
Glu His Glu Gly Leu Ser Lys Lys Ile Leu Ala Lys Met Asp Thr Ile			
	190	195	200
TTG AGC GTA AAA ATG CGA AGA GAT TTT GAT TCG CTC AAT GTG AGC GTG			676
Leu Ser Val Lys Met Arg Arg Asp Phe Asp Ser Leu Asn Val Ser Val			
	205	210	215
GCA GCA GGG ATC TTA ATG GAT AAA ATC AAC TAGGTGGTCA ATTGAATGGA ACA			729
Ala Ala Gly Ile Leu Met Asp Lys Ile Asn			
	220	225	
GAATAAA			736

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

Met	Gln	Ala	Val	Ile	Tyr	Gly	Lys	Gln	Val	Ile	Met	His	Leu	Leu	Asn
1				5					10					15	
Ser	His	Gln	Glu	Lys	Leu	Gln	Glu	Ile	Tyr	Leu	Ser	Lys	Glu	Ile	Asp
			20					25					30		
Lys	Lys	Leu	Phe	Phe	Ala	Leu	Lys	Lys	Ala	Cys	Pro	Asn	Ile	Ile	Lys
		35					40					45			

```

Val Asp Asn Lys Lys Ala Gln Ser Leu Ala Lys Gly Gly Asn His Gln
 50          55          60
Gly Val Leu Ala Lys Val Glu Leu Pro Leu Ala Val Ser Leu Lys Glu
 65          70          75          80
Val Lys Lys Ala Gln Lys Leu Leu Val Leu Cys Gly Ile Thr Asp Val
          85          90          95
Gly Asn Ile Gly Gly Ile Phe Arg Ser Ala Tyr Cys Leu Gly Met Gly
          100          105          110
Gly Val Ile Leu Asp Phe Ala Lys Glu Leu Ala Tyr Glu Gly Ile Val
          115          120          125
Arg Ser Ser Leu Gly Leu Met Tyr Asp Leu Pro Phe Ser Val Met Pro
          130          135          140
Asn Thr Leu Asp Leu Ile Asn Glu Leu Lys Thr Ser Gly Phe Leu Cys
          145          150          155          160
Leu Gly Ala Ser Met Gln Gly Ser Ser Gln Ile Glu Asn Leu Ser Leu
          165          170          175
Lys Lys Cys Ala Leu Phe Leu Gly Ser Glu His Glu Gly Leu Ser Lys
          180          185          190
Lys Ile Leu Ala Lys Met Asp Thr Ile Leu Ser Val Lys Met Arg Arg
          195          200          205
Asp Phe Asp Ser Leu Asn Val Ser Val Ala Ala Gly Ile Leu Met Asp
          210          215          220
Lys Ile Asn
225

```

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...290
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

```

AACCATGCCT TTTCATCGTC TCTATCAAAA ATG TTA GGG TCT AAA ACA TAT TCC      53
          Met Leu Gly Ser Lys Thr Tyr Ser
          1          5

GTT TTA AGA TCG TAT GAA AAA ACA TTC TCG CCT GAA GAG CTT TGC ATT      101
Val Leu Arg Ser Tyr Glu Lys Thr Phe Ser Pro Glu Glu Leu Cys Ile
          10          15          20

TTA ATG GGC AAA ACA TAC GAA TAC CCC ATC ATG CTT AAA GAA TTA TTG      149
Leu Met Gly Lys Thr Tyr Glu Tyr Pro Ile Met Leu Lys Glu Leu Leu
          25          30          35          40

ATG CTT TTG GCA AAC GCT AGG GGA TTG CTT GAA GCC TTG AAA GTG ATT      197
Met Leu Leu Ala Asn Ala Arg Gly Leu Leu Glu Ala Leu Lys Val Ile
          45          50          55

```

TTC AAC ATG CTT GGC TTG TCA AAA TTA AAA GAC AAA AGC CCG TTT TCT 245
Phe Asn Met Leu Gly Leu Ser Lys Leu Lys Asp Lys Ser Pro Phe Ser
60 65 70

TTG AGA GTG TTG AGC AGT TTC AAG GAA TCC AAA CGC CCC ATT ACA TAGAA 295
Leu Arg Val Leu Ser Ser Phe Lys Glu Ser Lys Arg Pro Ile Thr
75 80 85

AGCCTTACGA TTTTAAACA AACGCTCTAA AAAAAGCTTG TTCGTATGA 344

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

Met Leu Gly Ser Lys Thr Tyr Ser Val Leu Arg Ser Tyr Glu Lys Thr
1 5 10 15
Phe Ser Pro Glu Glu Leu Cys Ile Leu Met Gly Lys Thr Tyr Glu Tyr
20 25 30
Pro Ile Met Leu Lys Glu Leu Leu Met Leu Leu Ala Asn Ala Arg Gly
35 40 45
Leu Leu Glu Ala Leu Lys Val Ile Phe Asn Met Leu Gly Leu Ser Lys
50 55 60
Leu Lys Asp Lys Ser Pro Phe Ser Leu Arg Val Leu Ser Ser Phe Lys
65 70 75 80
Glu Ser Lys Arg Pro Ile Thr
85

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

CTGAATTCGA ATGAAAAGAA TTTTAGTCTC T 31

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

CCGCTCGAGT TAAAACTCAT AATTCAAAT

29

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

CGCGGATCCG AAGACATGTG CAACCGATG

29

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

CCGCTCGAGC TAAAAGTTTT GCAAAATCAC

30

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

CGCGGATCCG ATTTTACTTG AAAAATTAA AC

32

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

CCGCTCGAGT TAGAAAGTGT AGTTCAAATA C

31

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

GCGGATCCTT TTCTTCAATG TTTG

24

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

CCGCTCGAGT CAAAGTTTTA AACAAATTC

29